

;; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
;; FILE REFERENCE: MNI-131
;; CURRENT APPLICATION NUMBER: US/09/880,137
;; CURRENT FILING DATE: 2001-03-05
;; PRIOR APPLICATION NUMBER: US 60/186,706
;; PRIOR FILING DATE: 2000-03-03
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 410
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-137-3

Query Match 59.0%; Score 36; DB 4; Length 410;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQKVQLQKLGK 12
DB 99 RLQERLKKLGE 110

RESULT 23
US-09-880-137-1

; Sequence 1, Application US/09880137
; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Barstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/880,137

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186,706

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Bos taurus

US-09-880-137-1

Query Match 59.0%; Score 36; DB 4; Length 418;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQKVQLQKLGK 12
DB 99 RLQERLKKLGE 110

RESULT 24

US-09-880-137-2

; Sequence 2, Application US/09880137

; Patent No. 6640025

; GENERAL INFORMATION:

; APPLICANT: Barstein, Gabriel

; TITLE OF INVENTION: METHODS OF ASSAYING FOR G

; FILE REFERENCE: MNI-131

; CURRENT APPLICATION NUMBER: US/09/880,137

; CURRENT FILING DATE: 2001-03-05

; PRIOR APPLICATION NUMBER: US 60/186,706

; PRIOR FILING DATE: 2000-03-03

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-880-137-2

Query Match 59.0%; Score 36; DB 4; Length 418;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQKVQLQKLGK 12
DB 99 RLQERLKKLGE 110

RESULT 25

US-09-107-532A-6174

; Sequence 6174, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 6174:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 153 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...153

; SEQUENCE DESCRIPTION: SEQ ID NO: 6174:

US-09-107-532A-6174

Query Match 57.4%; Score 35; DB 4; Length 153;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQEKVLQKLGK 12
DB 40 AQEKLVKGGK 50

RESULT 26

US-09-702-953B-10

; Sequence 10, Application US/09702953B
; Patent No. 6673897
; GENERAL INFORMATION:
; APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
; TITLE OF INVENTION: NOVEL INHIBITORS OF NF-kappaB ACTIVATION
; FILE REFERENCE: 2676-4554US
; CURRENT APPLICATION NUMBER: US/09/702,953B
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: PCT/BE99/00055
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 98201472.2
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-702-953B-10

Query Match 57.4%; Score 35; DB 4; Length 228;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QEKVLQKLGKA 13
|||:|:|
Db 6 QEKELQLANKA 16

RESULT 27

US-09-880-137-8
; Sequence 8, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-8

Query Match 57.4%; Score 35; DB 4; Length 382;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
|||:|:|
Db 100 RLQDELLKRLQ 111

RESULT 28

US-09-107-532A-6398
; Sequence 6398, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street

CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denise
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6398:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...399
SEQUENCE DESCRIPTION: SEQ ID NO: 6398:
US-09-107-532A-6398

Query Match 57.4%; Score 35; DB 4; Length 399;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
|||:|:|
Db 13 QAREKKVQWGR 24

RESULT 29

US-09-880-137-4
; Sequence 4, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-137-4

Query Match 57.4%; Score 35; DB 4; Length 409;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
Db 100 RLQDLRLKLGQ 111

RESULT 30

US-09-880-137-7
; Sequence 7, Application US/09880137
; Patent No. 6640025

GENERAL INFORMATION:

; APPLICANT: Berstein, Gabriel
; TITLE OF INVENTION: METHODS OF ASSAYING FOR G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR LIGANDS AND MODULATORS
; FILE REFERENCE: MNI-131
; CURRENT APPLICATION NUMBER: US/09/880,137
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/186,706
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Homo sapiens mutation
US-09-880-137-7

Query Match 57.4%; Score 35; DB 4; Length 409;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
Db 100 RLQDLRLKLGQ 111

RESULT 31

US-09-328-352-6321
; Sequence 6321, Application US/09328352
; Patent No. 6562958

GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6321
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii

US-09-328-352-6321

Query Match 57.4%; Score 35; DB 4; Length 468;
Best Local Similarity 53.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGKA 13
Db 364 KAQEEAAQKKEA 376

RESULT 32

US-09-702-953B-4
; Sequence 4, Application US/09702953B
; Patent No. 6673897

GENERAL INFORMATION:

; APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
; TITLE OF INVENTION: NOVEL INHIBITORS OF NF-kappaB ACTIVATION
; FILE REFERENCE: 2676-4554US
; CURRENT APPLICATION NUMBER: US/09/702,953B

; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: PCT/BE99/00055
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 98201472.2
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-702-953B-4

Query Match 57.4%; Score 35; DB 4; Length 574;
Best Local Similarity 63.6%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 QEKVLQKLGKA 13
Db 352 QEKELQRLNKA 362

RESULT 33

US-09-702-953B-3
; Sequence 3, Application US/09702953B
; Patent No. 6673897

GENERAL INFORMATION:

; APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
; TITLE OF INVENTION: NOVEL INHIBITORS OF NF-kappaB ACTIVATION
; FILE REFERENCE: 2676-4554US
; CURRENT APPLICATION NUMBER: US/09/702,953B
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: PCT/BE99/00055
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 98201472.2
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-702-953B-3

Query Match 57.4%; Score 35; DB 4; Length 627;
Best Local Similarity 63.6%; Pred. No. 4.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 QEKVLQKLGKA 13
Db 405 QEKELQRLNKA 415

RESULT 34

US-09-702-953B-2
; Sequence 2, Application US/09702953B
; Patent No. 6673897

GENERAL INFORMATION:

; APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
; TITLE OF INVENTION: NOVEL INHIBITORS OF NF-kappaB ACTIVATION
; FILE REFERENCE: 2676-4554US
; CURRENT APPLICATION NUMBER: US/09/702,953B
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: PCT/BE99/00055
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 98201472.2
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-702-953B-2

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US-09-702-953B-2
Query Match 57.4%; Score 35; DB 4; Length 647;
Best Local Similarity 53.6%; Pred. No. 4.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 QEKVLQKLGKA 13
   |||:|:|
Db 425 QEKSIQRLNKA 435

RESULT 35
US-09-914-259-61
; Sequence 61, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-61

Query Match 56.6%; Score 34.5; DB 4; Length 227;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 10; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 RAQEK---VLQKGLKA 13
   ||||:|:|
Db 44 RAQERLATVLQKLEEA 59

RESULT 36
US-107-532A-3730
; Sequence 3730, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6086:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:

US-09-702-953B-2
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3730:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:

US-09-107-532A-3730
Query Match 55.7%; Score 34; DB 4; Length 215;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQSKVLQK 9
   |||||:|
Db 205 RTQEKVLK 213

RESULT 37
US-09-107-532A-6086
; Sequence 6086, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6086:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...589
; SEQUENCE DESCRIPTION: SEQ ID NO: 6086:
US-09-107-532A-6086
Query Match 55.7%; Score 34; DB 4; Length 589;
Best Local Similarity 77.8%; Pred. No. 5.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QEKVLOKLG 11
DB 497 QEKVLETLG 505

RESULT 38
US-08-808-277A-3
; Sequence 3, Application US/08808277A
; Patent No. 5998374
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: LEE, IN-HEE
; APPLICANT: ZHAO, CHENGQUAN
; TITLE OF INVENTION: CLAVASPIRINS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,277A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 220002057300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-808-277A-3

Query Match 54.1%; Score 33; DB 2; Length 80;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 QEKVLOKLG 12
DB 27 EEKVQFLG 36

RESULT 39
US-08-746-160-3
; Sequence 3, Application US/08746160
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; Patent No. 6010876
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia I.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Lee, In-Hee
; TITLE OF INVENTION: CLAVANINS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,160
; FILING DATE: 06-NOV-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20563.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-746-160-3

Query Match 54.1%; Score 33; DB 3; Length 80;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 QEKVLOKLG 12
DB 27 EEKVQFLG 36

RESULT 40
US-08-659-254-2
; Sequence 2, Application US/08659254
; Patent No. 6194555
; GENERAL INFORMATION:
; APPLICANT: Stocco, Douglas M.
; APPLICANT: Clark, Dr. Barbara J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
; TITLE OF INVENTION: OF STEROIDOGENESIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue
; CITY: Austin
; STATE: TX
; COUNTRY: U.S.A.
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,254
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/538,960
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: 43375.0006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/499-6200
; TELEFAX: 512/499-6290
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 276 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-254-2

Query Match 54.1%; Score 33; DB 3; Length 276;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLQKLGK 12
Db 154 KVLQRIKG 161

RESULT 41
US-08-538-960-2
; Sequence 2, Application US/08538960
; Patent No. 5872230
; GENERAL INFORMATION:
; APPLICANT: Stocco, Douglas M.
; APPLICANT: Clark, Barbara J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: REGULATION OF STEROIDOGENESIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue
; CITY: Austin
; STATE: TX
; COUNTRY: U.S.A.
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,960
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: 43375.0002/DLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/499-6200
; TELEFAX: 512/499-6290
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; US-08-538-960-2

Query Match 54.1%; Score 33; DB 2; Length 284;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLQKLGK 12
Db 154 KVLQRIKG 161

RESULT 42
US-09-134-001C-4230
; Sequence 4230, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4230
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-4230

Query Match 54.1%; Score 33; DB 4; Length 296;
Best Local Similarity 46.2%; Pred. No. 4.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RAQKVLQKLGKA 13
Db 138 RDEKLIQSVSKA 150

RESULT 43
US-08-455-910-13
; Sequence 13, Application US/08855910
; Patent No. 6221640
; GENERAL INFORMATION:
; APPLICANT: Tao, Jianshi
; APPLICANT: Sassanfar, Mandana
; APPLICANT: Gallant, Paul L.
; APPLICANT: Shen, Xiaoyu
; APPLICANT: Avruch, Anthony S.
; APPLICANT: Yu, Russell V.
; APPLICANT: Nair, Shamila
; TITLE OF INVENTION: ENTEROCOCCAL AMINOACYL-CRNA SYNTHETASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,910
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;/ FILING DATE: 14-MAY-1997
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Brook, David E.
;/ REGISTRATION NUMBER: 22,592
;/ REFERENCE/DOCKET NUMBER: CP195-08
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (781) 861-6240
;/ TELEFAX: (781) 861-9540
;/ INFORMATION FOR SEQ ID NO: 13:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 423 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-855-910-13

Query Match 54.1%; Score 33; DB 3; Length 423;
Best Local Similarity 75.0%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKVQLKLG 11
Db 307 EEILQKLG 314
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RESULT 44
US-09-134-000C-5142
; Sequence 5142, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5142
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-5142

Query Match 54.1%; Score 33; DB 4; Length 427;
Best Local Similarity 75.0%; Pred. No. 6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKVQLKLG 11
Db 311 EEILQKLG 318
|:|||||

RESULT 45
US-08-477-451-18
; Sequence 18, Application US/08477451
; Patent No. 5928965
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter Pylori Cagi Region
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent in Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/477,451
;/ FILING DATE: 07-JUN-1995
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: McClung, Barbara G.
;/ REGISTRATION NUMBER: 33,113
;/ REFERENCE/DOCKET NUMBER: 0335.002
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 510-601-2708
;/ TELEFAX: 510-655-3542
;/ INFORMATION FOR SEQ ID NO: 18:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 464 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-477-451-18

Query Match 54.1%; Score 33; DB 2; Length 464;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RAEKVLQKLG 12
Db 269 KATKILESIGK 280
|:|||||

RESULT 46
US-08-313-075A-50
; Sequence 50, Application US/08313075A
; Patent No. 5639870
; GENERAL INFORMATION:
; APPLICANT: Holton, Timothy A.
; APPLICANT: Cornish, Edwina C.
; APPLICANT: Tanaka, Yoshikazu
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID
; TITLE OF INVENTION: PATHWAY ENZYMES AND USES THEREFOR
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,075A
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 1538/92
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 6698/93
; FILING DATE: 07-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PCT/AU93/00127
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9433
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR 50:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-313-075A-50

Query Match 54.1%; Score 33; DB 1; Length 496;
Best Local Similarity 50.0%; Pred. No. 7e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
Db 325 KAQELAQVIGK 336

RESULT 47
US-09-519-232-8
; Sequence 8, Application US/09519232
; Patent No. 6528702
; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Welisio, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Tesfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RTP2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-519-232-8

Query Match 54.1%; Score 33; DB 4; Length 586;
Best Local Similarity 41.7%; Pred. No. 8.1e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
Db 254 KISEKLERIGK 265

RESULT 48
US-09-107-532A-6359
; Sequence 6359, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
```

```
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-8277
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (3) LOCATION 1...822
; SEQUENCE DESCRIPTION: SEQ ID NO: 6359:
US-09-107-532A-6359

Query Match 54.1%; Score 33; DB 4; Length 822;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AQEKVLQKLG 11
Db 612 AQEQLQKFG 621

RESULT 49
US-09-543-681A-5053
; Sequence 5053, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5053
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5053

Query Match 54.1%; Score 33; DB 4; Length 826;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AQEKVLQKL 10
Db 193 AQSRVLQKL 201

RESULT 50
US-09-540-236-3299
; Sequence 3299, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
```

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 3299

; LENGTH: 1105

; TYPE: PRT

; ORGANISM: M.catarrahals

US-09-540-236-3299

Query Match 54.1%; Score 33; DB 4; Length 1105;

Best Local Similarity 60.0%; Pred. No. 1.5e+03;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QEKVLQKLGK 12

Db 117 EQKVEQKIGK 126

Search completed: March 4, 2004, 17:47:37

Job time : 15.4194 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:31:50 ; Search time 58.6452 Seconds
(without alignments)
86.723 Million cell updates/sec

Title: US-10-069-540A-2_COPY_138_155

Perfect score: 95

Sequence: 1 RIAXGRKLVVDVSARHH 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003s:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	130	4	ABG22449 Novel hum
2	95	100.0	130	4	ABG20881 Novel hum
3	95	100.0	130	4	ABG21407 Novel hum
4	95	100.0	130	4	ABG20318 Novel hum
5	95	100.0	252	4	AAB62101 Bar domai
6	95	100.0	404	2	AAW05392 Human SH3
7	95	100.0	414	4	ABG13005 Novel hum
8	95	100.0	425	4	ABG22456 Novel hum
9	95	100.0	434	2	AAW05391 Mouse SH3
10	95	100.0	431	2	AAW06602 Human box
11	95	100.0	451	2	AAW47295 Human Bin
12	95	100.0	451	2	AAW36881 Human Bin
13	95	100.0	451	2	AAW34504 Human Bin
14	95	100.0	453	6	ABR69631 Human CGD
15	95	100.0	482	6	ABU99771 Protein d
16	95	100.0	564	4	ABG62100 Human bri
17	95	100.0	572	4	ABG21411 Novel hum
18	95	100.0	588	7	ADD45931 Rat Prote
19	95	100.0	588	7	ADE60848 Rat Prote
20	95	100.0	588	7	ADE60840 Rat Prote
21	95	100.0	588	7	ADE60844 Rat Prote
22	95	100.0	588	7	ADE60852 Rat Prote
23	95	100.0	593	7	ADE60842 Human Pro
24	95	100.0	593	7	ADD45953 Human Pro
25	95	100.0	593	7	ADE60850 Human Pro

26	95	100.0	593	7	ADE60846	Human Pro
27	95	100.0	593	7	ADE60854	Human Pro
28	95	100.0	594	4	ABG20887	Novel hum
29	95	100.0	594	4	ABG20324	Novel hum
30	95	100.0	594	4	ABG22457	Novel hum
31	95	100.0	960	4	ABG20886	Novel hum
32	95	100.0	960	4	ABG20323	Novel hum
33	89	93.7	683	7	ADD44887	Rat Prote
34	89	93.7	695	5	AAE22091	Human amp
35	89	93.7	695	5	AAU75110	Synaptic
36	89	93.7	695	5	ADD44889	Human Pro
37	62	65.3	602	4	ABE63948	Drosophil
38	49	51.6	276	6	ADA48708	Rice prot
39	47	49.5	424	5	ABB91883	Herbicida
40	47	49.5	425	4	AAW48428	Protein A
41	47	49.5	468	3	AG41757	Arabidops
42	47	49.5	472	3	AG41756	Arabidops
43	47	49.5	587	3	AG41755	Arabidops
44	47	49.5	765	6	ABU24499	Protein e
45	45.5	47.9	521	5	ABP55425	Mouse pol
46	45.5	47.9	578	6	ABU96724	Human nuc
47	45.5	47.9	596	4	AAW95815	Human pro
48	45.5	47.9	742	7	ADB64808	Human pro
49	45.5	47.9	763	6	ABU00410	Human nov
50	44	46.3	161	4	AAU63157	Propionib
51	44	46.3	161	6	ABM59676	Propionib
52	44	46.3	297	6	ABU23306	Protein e
53	43.5	45.8	282	6	ABU47137	Protein e
54	43.5	45.8	282	6	ABU47874	Protein e
55	43	45.3	848	7	ADE54727	Rat Prote
56	42.5	44.7	304	6	ABU45447	Protein e
57	42	44.2	130	5	ABP28276	Streptoco
58	42	44.2	463	6	ABP57491	Mycobacte
59	42	44.2	463	6	ABU36480	Protein e
60	42	44.2	463	6	ABU34382	Protein e
61	42	44.2	634	3	AB333599	Modified
62	42	44.2	634	4	AAU04709	Modified
63	42	44.2	634	4	AAU05034	Modified
64	42	44.2	712	6	ABU29750	Protein e
65	42	44.2	721	7	ADC97262	E. faeciu
66	42	44.2	903	2	AAU28713	Detargete
67	42	44.2	906	2	AAU28712	Mutant ye
68	42	44.2	906	2	AAU28702	Yeast mul
69	42	44.2	906	4	AB20182	C. tropic
70	42	44.2	906	4	AB20181	C. tropica
71	42	44.2	906	4	AB20180	Candida t
72	42	44.2	906	4	AB20183	C. tropic
73	41.5	43.7	731	2	AAE60822	Meion pro
74	41.5	43.7	763	2	AAU24094	Mouse EPC
75	41	43.2	196	4	AG65249	Snowshoe
76	41	43.2	237	5	AB69788	Drosophil
77	41	43.2	237	5	ABU05849	M. tuberc
78	41	43.2	385	4	ABG11090	Novel hum
79	41	43.2	385	4	ABG16959	Novel hum
80	41	43.2	771	6	ABJ25622	Aspergill
81	41	43.2	905	6	ABJ26222	Aspergill
82	40.5	42.6	187	4	ABG02458	Novel hum
83	40.5	42.6	274	4	ABG17857	Novel hum
84	40.5	42.6	298	7	ABU94099	E. faeciu
85	40.5	42.6	306	6	ABU15207	Protein e
86	40	42.1	124	4	ABG08236	Novel hum
87	40	42.1	142	4	AAU64337	Propionib
88	40	42.1	142	6	ABM60856	Propionib
89	40	42.1	171	4	ABM64390	Amino aci
90	40	42.1	171	4	AAW40219	Human pol
91	40	42.1	216	4	AB93722	Human pro
92	40	42.1	244	4	ABG08238	Novel hum
93	40	42.1	259	6	AAW42005	Human pol
94	40	42.1	287	4	ABU11735	Human MDD
95	40	42.1	290	6	ABU70917	Human aci
96	40	42.1	294	3	AB307857	Amino aci
97	40	42.1	298	6	ABP97410	Thermoana
98	40	42.1	321	4	AAU54500	Propionib

99	40	42.1	321	6	ABM51019	Propionib
100	40	42.1	344	4	AA953186	Human pol
101	40	42.1	406	3	AA954209	Human TRA
102	40	42.1	406	7	ADB79885	Human act
103	40	42.1	414	3	AB07856	Amino aci
104	40	42.1	414	3	AB58368	Lung canc
105	40	42.1	414	5	AB343711	Human ova
106	40	42.1	436	6	AB089782	Novel hum
107	40	42.1	440	4	AB372014	Drosophil
108	40	42.1	460	3	AA343157	Human ORF
109	40	42.1	625	5	ABJ10986	Veysel sel
110	40	42.1	634	4	ABG15117	Novel hum
111	40	42.1	701	6	ABU44429	Protein e
112	40	42.1	735	4	ABE65024	Drosophil
113	40	42.1	752	6	ABR52722	Protein e
114	40	42.1	1059	4	ABE59330	Drosophil
115	40	42.1	1059	4	ABE67407	Drosophil
116	40	42.1	1059	4	ABE67408	Drosophil
117	39	41.1	89	6	ABU23366	Protein e
118	39	41.1	89	6	ABU17088	Protein e
119	39	41.1	95	6	AA436851	Acinetoba
120	39	41.1	147	4	AA40760	Human pol
121	39	41.1	210	4	ASG08543	Novel hum
122	39	41.1	245	5	ASP27803	Streptoco
123	39	41.1	245	6	ABU46473	Protein e
124	39	41.1	259	3	AGL13065	Arabidops
125	39	41.1	265	3	AGL13064	Arabidops
126	39	41.1	269	3	AGL13063	Arabidops
127	39	41.1	335	3	AGY59252	Human gly
128	39	41.1	335	3	AA310485	Human MPR
129	39	41.1	335	3	AGY90285	Human pep
130	39	41.1	335	4	AA38974	Human pol
131	39	41.1	392	3	AG474717	Arabidops
132	39	41.1	444	6	ABU34078	Protein e
133	39	41.1	450	4	ABE62490	Drosophil
134	39	41.1	460	4	ABE58088	Drosophil
135	39	41.1	471	6	ABJ25422	Aspergill
136	39	41.1	481	6	ABU26218	Protein e
137	39	41.1	493	3	AG474716	Arabidops
138	39	41.1	512	4	ABE60708	Drosophil
139	39	41.1	515	3	AGL17527	Arabidops
140	39	41.1	516	3	AG474715	Arabidops
141	39	41.1	523	3	AGL17526	Arabidops
142	39	41.1	525	3	AGL17525	Arabidops
143	39	41.1	565	6	ABJ26022	Aspergill
144	39	41.1	626	6	ABU52572	peanut Ar
145	39	41.1	708	4	ABE70030	Drosophil
146	39	41.1	708	4	ABE67226	Drosophil
147	39	41.1	853	6	ABU25701	Protein e
148	39	41.1	892	6	ABP96857	Escherich
149	39	41.1	981	3	AA979012	S. cerevi
150	38.5	40.5	52	4	AAU45370	Propionib

11-OCT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217.

23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

Dmanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

N-PSDB; AAS86636.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 52808; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIFO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

Sequence 130 AA;

ALIGNMENTS

RESULT 1	
ABG22449	
ID	ABG22449 standard; protein; 130 AA.
XX	
AC	ABG22449;
XX	
XX	
DT	18-FEB-2002 (first entry)
DE	
DE	Novel human diagnostic protein #22440.
XX	
KW	Human; chromosome mapping; gene mapping
KW	food supplement; medical imaging; diag
XX	
OS	Homo sapiens.
XX	
PN	WO200175067-A2.

XX 30-MAR-2001; 2001WO-US008631.
PF XX
XX 31-MAR-2000; 2000US-00540217.
PR XX
PR 23-AUG-2000; 2000US-00649167.
XX XX
XX (HYSE-) HYSEO INC.

(HYSE-) HYSEQ INC.
 Drmanac RT, Liu C, Tang YT;
 WPI; 2001-639362/73.
 N-PSDB: AAS85068.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

PS Claim 20; SEQ ID NO 51240; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AG00010-AG30377 represent novel human diagnostic amino acid sequences of the invention. Note: the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct_sequences](http://www.int/pub/published/pct_sequences)

```
Query Match      100.0%; Score 95; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 3
ABG21407
ID ABG21407 standard; protein; 130 AA.

Novel human diagnostic protein #21398.

XX	31-MAR-2000; 2000US-00540217.
PR	23-AUG-2000; 2000US-00649167.
XX	(HYSE-) HYSEQ INC.
XX	Drmanac RT, Liu C, Tang YT;
PI	
XX	WPI; 2001-639362/73.
DR	N-P8DB; AAS85594.
DR	
XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity.
PT	
XX	Claim 20; SEQ ID NO 51766; 103pp; English.
XX	

New isolated polynucleotide and encoded polypeptides, useful in PT diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess PT biodiversity.

PS Claim 20; SEQ ID NO 51766; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: the sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct/sequences](http://wipo.int/pub/published/pct/sequences)

Query Match	100.0%;	Score 95;	DB 4;	Length 130;
Best Local Similarity	100.0%;	Pred. No. 2.6e-08;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

RESULT 4
ABG20318
ID ABG20318 standard; protein; 130 AA.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
OS Homo sapiens.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS84505.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 50677; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 130 AA;

Query Match 100.0%; Score 95; DB 4; Length 130;

Best Local Similarity 100.0%; Pred. No. 2.6e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRGKLVYDSARHH 18

Db 111 RIAGRGKLVYDSARHH 128

RESULT 5

AAB62101

ID AAB62101 standard; protein; 252 AA.

XX AAB62101;

XX 29-MAY-2001 (first entry)

XX Bar domain of Bin1 protein.

XX Bridging integrator-2 protein; Bin2; cancer; leukemia; blood disorder;
KW hyperplastic disease; cytostatic; cell growth regulator; Bin1;
KW chromosome 4q22.1.

XX Homo sapiens.

XX WO200116158-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023723.

XX 31-AUG-1999; 99US-0151554P.

(WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX Prendergast GC, Ge K;

XX WPI; 2001-235087/24.

XX New bridging integrator-2 (Bin2) protein and nucleic acid molecules,
PT useful for regulating cell growth, and for diagnosing or treating
PT conditions associated with inappropriate expression of Bin2, e.g. cancers
PT or hepatocarcinoma.

XX Example 3; Fig 2; 62pp; English.

XX The invention provides a human bridging integrator-2 (Bin2) protein. The
CC protein can be expressed by standard recombinant methodology. The Bin2
CC proteins or peptides are useful in regulating cell growth, cell survival,
CC differentiation, endocytosis and actin organization. These peptides or
CC proteins are also useful for diagnosing or treating conditions associated
CC with inappropriate expression of Bin2, e.g. liver cancer, breast cancer,
CC hepatocarcinoma, myeloid and lymphoid leukemias or blood disorders. The
CC peptides, nucleic acid sequences or anti-Bin2 antibodies are useful for
CC diagnosing inappropriate expression of Bin2 Bin2 is also useful for
CC treating disorders associated with excessive Bin1 levels, e.g. liver,
CC colorectal, prostate or breast cancers, epithelia cell cancers, melanoma,
CC or hyperplastic disease states. The present sequence represents the Bar
CC domain of Bin1 used in homology studies with Bin2 protein

XX Sequence 252 AA;

Query Match 100.0%; Score 95; DB 4; Length 252;

Best Local Similarity 100.0%; Pred. No. 5.4e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRGKLVYDSARHH 18

Db 139 RIAGRGKLVYDSARHH 156

RESULT 6

AAW05392

ID AAW05392 standard; protein; 404 AA.

XX AAW05392;

XX 19-FEB-1998 (first entry)

XX Human SH3P9 protein.

XX Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
KW cellular signalling element; cellular structural element; malignancy;
KW protein identification; functional domain; protein screening;
KW cellular signal transduction process.

XX Homo sapiens.

XX WO9631625-A1.

XX 10-OCT-1996.

XX 04-APR-1996; 96WO-US004454.

XX 07-APR-1995; 95US-00417872.

XX 03-APR-1996; 96US-00630915.

XX (CYTO-) CYTOGEN CORP.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Sparks AB, Hoffman N, Kay BK, Fowlkes DM, McConnell SJ;

XX WPI; 1996-465045/46.

XX N-ESDB; AAT39792.

XX Identifying polypeptide(s) having specific functional domain (esp. SH3

PT domain) - comprises detecting selective binding to recognition unit,
 PT regardless of sequence homology.
 PS Claim 54; Fig 37; 174pp; English.
 XX
 CC AA005386-W05403 represent novel human and mouse Src-homology region 3
 CC (SH3) domain containing proteins that can be used in the method of the
 CC invention. SH3 domain containing proteins play a role in signalling and
 CC structural elements of cells. The method of the invention is for
 CC identifying polypeptides containing functional domains of interest
 CC (especially SH3 domains). The method comprises contacting a multivalent
 CC recognition unit (RU) complex with a number of peptides and identifying
 CC polypeptides having a selective binding affinity for the RU complex. The
 CC method is based on functional similarities and does not rely on sequence
 CC similarities. Prior methods only gave limited success for identifying
 CC proteins which contain an SH3 domain due to the minimal sequence homology
 CC among known SH3 proteins. It has been found that small peptide RUS in
 CC multivalent form have reduced specificity for a given functional domain
 CC compared to monomer RUS. Multivalent RU complexes are particularly suited
 CC to screening for polypeptides containing functional domains that are
 CC similar to, but not identical in sequence to, the original target
 CC functional domain. The new method enables proteins having a common
 CC function to be identified. Identification of novel SH3 proteins will be
 CC useful for a better understanding of cell growth, malignancy, signal
 CC transduction processes, etc. New candidate drugs can be identified, and
 CC their specificities (e.g. pharmacological activities) can be assessed
 CC using the method of the invention
 XX
 SQ Sequence 404 AA;

Query Match 100.0%; Score 95; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 9.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
 |||||
 Db 104 RIAKGRKLVYDSARHH 121

RESULT 7
 ABG13005
 ID ABG13005 standard; protein; 414 AA.

AC ABG13005;

XX 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #12996.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX WO200175067-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS77192.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess

PT biodiversity.
 XX Claim 20; SEQ ID NO 43364; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 414 AA;

Query Match 100.0%; Score 95; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 9.3e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18

Db 138 RIAKGRKLVYDSARHH 155

RESULT 8

ABG22456

ID ABG22456 standard; protein; 425 AA.

XX ABG22456;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22447.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS86643.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

PS Claim 20; SEQ ID NO 52815; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders CC involving aberrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic CC amino acid sequences of the invention. Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences XX

SQ Sequence 425 AA;

Query Match 100.0%; Score 95; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAKRGKLVYDSARHH 18
| | | | | | | | | | | | | | | | | |
Db 97 RIAKRGKLVYDSARHH 114

RESULT 9
AAW05391
ID AAW05391 standard; protein; 434 AA.

XX AC AAW05391;

XX DT 18-FEB-1998 (first entry)

XX DE Mouse SH3P9 protein.

XX Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
XX cellular signalling element; cellular structural element; malignancy;
XX protein identification; functional domain; protein screening;
XX cellular signal transduction process.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
XX Misc-difference 433 /note= "encoded by CTA"

XX PN WO9631625-A1.

XX PD 10-OCT-1996.

XX PF 04-APR-1996; 96WO-US004454.

XX PR 07-APR-1995; 95US-00417872.

XX PR 03-APR-1996; 96US-00630915.

XX PA (CVTO-) CVTOGEN CORP.

XX PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Sparks AB, Hoffman N, Kay BK, Fowlkes DM, McConnell SJ;

XX DR WPI; 1996-465045/46.

XX DR N-PSDB; AAT39791.

XX

PT Identifying polypeptide(s) having specific functional domain (esp. SH3
PT domain) - comprises detecting selective binding to recognition unit,
PT regardless of sequence homology.

XX Claim 54; Fig 35; 174pp; English.

XX AAW05386-W05403 represent novel human and mouse Src-homology region 3
CC (SH3) domain containing proteins that can be used in the method of the
CC invention. SH3 domain containing proteins play a role in signalling and
CC structural elements of cells. The method of the invention is for
CC identifying polypeptides containing functional domains of interest
CC (especially SH3 domains). The method comprises contacting a multivalent
CC recognition unit (RU) complex with a number of peptides and identifying
CC polypeptides having a selective binding affinity for the RU complex. The
CC method is based on functional similarities and does not rely on sequence
CC similarities. Prior methods only gave limited success for identifying
CC proteins which contain an SH3 domain due to the minimal sequence homology
CC among known SH3 proteins. It has been found that small peptide RUS in
CC multivalent form have reduced specificity for a given functional domain
CC compared to monomer RUS. Multivalent RU complexes are particularly suited
CC to screening for polypeptides containing functional domains that are
CC similar to, but not identical in sequence to, the original target
CC functional domain. The new method enables proteins having a common
CC function to be identified. Identification of novel SH3 proteins will be
CC useful for a better understanding of cell growth, malignancy, signal
CC transduction processes, etc. New candidate drugs can be identified, and
CC their specificities (e.g. pharmacological activities) can be assessed
CC using the method of the invention XX

SQ Sequence 434 AA;

Query Match 100.0%; Score 95; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAKRGKLVYDSARHH 18
| | | | | | | | | | | | | | | | | |
Db 139 RIAKRGKLVYDSARHH 156

RESULT 10

AAW06602
ID AAW06602 standard; protein; 451 AA.

XX AC AAW06602;

XX DT 07-FEB-1997 (first entry)

XX DE Human box-dependent myc-interacting protein (BIN1).

XX Box-dependent myc-interacting protein; BIN1; MIP-99; oncogene;
XX oncoprotein; breast cancer; liver cancer; apoptosis;
XX tumour suppressor protein; hyperplasia; diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX Domain 1. .222

FT /note= "polypeptide useful in constructs of the invention
FT (Claim 9)"

FT Domain 190. .250
FT /note= "polypeptide useful in constructs of the
FT invention (Claim 9)"

FT Domain 223. .251
FT /note= "polypeptide useful in constructs of the invention
FT (Claim 9)"

FT Domain 252. .265
FT /label= Nuclear localisation domain

FT /note= "polypeptide useful in constructs of the invention
FT (Claim 9)"

FT Domain 263. .397
FT /note= "polypeptide useful in constructs of the invention
FT (Claim 9)"

FT Domain 263. .397
FT /note= "polypeptide useful in constructs of the invention
FT (Claim 9)"

FT

CC of anti-Bau antiserum and antibodies to Bau, or to a desired fragment of
 CC the Bau protein, as diagnostic reagents, in gene therapy, and in
 CC screening and developing chemical compounds or proteins which may be used
 CC for the treatment of cancers characterized by Bau or BIN1, which regulate
 CC inappropriate MYC levels
 XX SQ Sequence 451 AA;

Query Match 100.0%; Score 95; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
 |||||
 Db 136 RIAKGRKLVYDSARHH 153

RESULT 13
 AAW94504
 ID AAW94504 standard; protein; 451 AA.

XX AC AAW94504;
 XX DT 22-APR-1999 (first entry)
 XX DE Human Binl protein.

XX KW Binl; brain-specific; box-dependent myc-interacting protein; cancer;
 XX KW diagnosis; hyperplastic disease; tumour suppressor; gene therapy;
 XX KW benign prostatic hypertrophy; neurodegeneration.

XX OS Homo sapiens.

XX PN WO9855151-A1.

XX PD 10-DEC-1998.

XX PF 04-JUN-1998; 98WO-US011647.

XX PR 06-JUN-1997; 97US-00870126.

XX PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX PI Prendergast GC, Sakamuro D;

XX DR WPI; 1999-059881/05.

XX N-PSDB; AAX16322.

PT New splice variant exons of Box-dependent myc-interacting polypeptide -
 PT associated with loss of tumour suppressor activity, used for diagnosis of
 PT cancer and in gene therapy.

XX Example 1; Page 81-82; 133pp; English.

XX The present invention describes Binl (Box-dependent myc-interacting
 CC protein 1) brain-specific alternative splice variants exon 12A, B, C and
 CC D. Binl specific antibodies (when labelled) are used to detect cancers or
 CC other hyperplastic conditions (e.g. benign prostatic hypertrophy)
 CC associated with a deficit of normal Binl and/or aberrant forms of Binl.
 CC The same diseases can also be diagnosed at the nucleic acid level using
 CC fragments of Binl nucleotide sequences in standard amplification and/or
 CC hybridisation assays. Cancers that can be detected are carcinomas and
 CC epithelial cell tumours, specifically of prostate, liver and colon/
 CC rectum, also melanoma. Binl nucleotide sequences, when included in a
 CC vector, and Binl proteins may also be used to treat these diseases, and
 CC also degenerative conditions such as neurodegeneration. Binl proteins may
 CC also be used to raise antibodies, and the nucleotide sequences can be
 CC used to express the corresponding proteins. Also anti-idiotypic
 CC antibodies can be used therapeutically, and more generally similar
 CC materials can be used to treat or diagnose any condition involving
 CC deregulation, defect or amplification of the c-myc oncogene. Binl
 CC nucleotide sequence, proteins and antibodies are also useful to screen
 CC for agents that may be used to treat Binl-related cancers. The present

CC sequence represents human Binl protein
 XX SQ Sequence 451 AA;

Query Match 100.0%; Score 95; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
 |||||
 Db 136 RIAKGRKLVYDSARHH 153

RESULT 14
 ABR69631
 ID ABR69631 standard; protein; 453 AA.

XX AC ABR69631;

XX DT 12-AUG-2003 (first entry)

XX DE Human CGDD-31 protein.

XX KW Human; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;
 XX KW neuroprotective; cerebroprotective; anti-HIV; anti-allergic;
 XX KW anti-inflammatory; gynaecological; cancer; atherosclerosis; epilepsy;
 XX KW Huntington's disease; stroke; AIDS; allergy; placenta; reproductive;
 XX KW CGDD; cell growth; cell differentiation; cell death.

XX OS Homo sapiens.

XX PN WO2003027263-A2.

XX PD 03-APR-2003.

XX PF 26-SEP-2002; 2002WO-US031095.

XX PR 28-SEP-2001; 2001US-0326389P.

XX PR 05-OCT-2001; 2001US-0327380P.

XX PR 03-OCT-2001; 2001US-0328186P.

XX PR 12-OCT-2001; 2001US-0329690P.

XX PR 26-OCT-2001; 2001US-0345384P.

XX PR 26-OCT-2001; 2001US-0348165P.

XX PR 02-NOV-2001; 2001US-0350219P.

XX PR 09-NOV-2001; 2001US-0344518P.

XX PR 09-NOV-2001; 2001US-0345143P.

XX PR 16-NOV-2001; 2001US-0332375P.

XX PR 03-DEC-2001; 2001US-0336908P.

XX PR 07-DEC-2001; 2001US-0340747P.

XX (INCY-) INCYTE GENOMICS INC.

XX Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Chawla NK;

XX Elliott VS, Emerling BM, Gandhi AR, Gietzen KJ, Gorvad AE;

XX Griffin JA, Hafala AJA, Ison CH, Kable AE, Kalafus DP;

XX Lehr-Mason PM, Lu DM, Marquis JP, Nguyen DB, Ramkumar J;

XX Richardson TW, Sapperstein SK, Swarnakar A, Tang YT, Tran UK;

XX Warren BA, Xu Y, Yao MG, Yue H, Yue H;

XX WPI; 2003-421159/39.

XX N-PSDB; ACC30608.

XX New human proteins associated with cell growth, differentiation, and
 PT death (CGDD), useful for diagnosing, treating and preventing diseases or
 PT conditions associated with the aberrant CGDD expression e.g. cancer,
 PT AIDS, or epilepsy.

XX Claim 1; Page 281-282; 350pp; English.

XX The invention relates to an isolated polypeptide associated with cell
 CC growth, differentiation and death (CGDD). Also disclosed are the
 CC polynucleotides encoding the polypeptides. The polypeptides and
 CC polynucleotides are useful in diagnosing, treating and preventing

CC diseases or conditions associated with the decreased expression or over
 CC expression of CGPD. Such diseases include cell proliferative (e.g.
 CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's
 CC disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and
 CC reproductive disorders, or disorders of the placenta. They are also
 CC useful in assessing the effects of exogenous compounds on the expression
 CC of nucleic acid and amino acid sequences of CGPD. The CGPD or its
 CC fragments are useful in screening compounds for effectiveness as an
 CC agonist or antagonist of the polypeptides, or in altering the expression
 CC of the target polynucleotide and compounds that specifically bind to or
 CC modulate the activity of the polypeptide. Microarrays consisting
 CC of polynucleotides of the invention are useful in monitoring and measuring
 CC protein-protein interactions, drug-target interactions, and gene
 CC expression profiles. Sequences given in records AAR69601-AAR69657
 CC represent CGPD polypeptides of the invention
 XX
 XX Sequence 453 AA;

Query Match 100.0%; Score 95; DB 6; Length 453;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSARHH 18
 |||||
 DB 139 RIAGRGKLVYDSARHH 156

RESULT 15
 ABUS9771
 ID ABUS9771 standard; protein; 482 AA.

AC ABUS9771;
 XX
 XX 10-JUL-2003 (first entry)
 XX
 XX Protein differentially expressed in cardiovascular disease #65.
 XX
 XX Cardiovascular disease; atherosclerosis; ischaemia; angina pectoris;
 KW myocardial infarction; cardiac; antiatheriosclerotic; antianginal;
 KW gene therapy; differential gene expression.
 XX
 XX Homo sapiens.
 OS
 XX WO2003031650-A2.
 PN
 XX 17-APR-2003.

XX 02-OCT-2002; 2002WO-EP011034.
 XX
 XX 08-OCT-2001; 2001GB-00024145.
 XX
 XX (FARB) BAYER AG.
 XX
 XX Munnes M, Gehrman M, Wick M, Schmitz G;
 PI WPI; 2003-403108/38.
 XX
 XX N-PSDB; ACA89944.
 DR
 XX
 XX Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
 PT angina, ischaemia, myocardial infarction or arteriosclerosis by detection
 PT of a polynucleotide in a biological sample comprises detecting a
 PT hybridisation complex.
 XX
 XX Claim 3; Page 433-435; 454pp; English.

XX The invention describes a method of predicting, diagnosing or prognosing
 CC a cardiovascular disease by detection of a polynucleotide in a biological
 CC sample comprises hybridising at least one of the polynucleotide to a
 CC nucleic acid material of a biological sample, thus forming a
 CC hybridisation complex, and detecting the hybridisation complex. The
 CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
 CC are useful for preparing compositions for preventing, predicting or
 CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.

CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
 CC This sequence represents a protein identified in the invention a being
 CC differentially expressed in individuals with cardiovascular disease
 XX
 XX Sequence 482 AA;

Query Match 100.0%; Score 95; DB 6; Length 482;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSARHH 18
 |||||
 DB 139 RIAGRGKLVYDSARHH 156

RESULT 16
 AAB62100
 ID AAB62100 standard; protein; 564 AA.

XX AAB62100;
 AC
 XX 29-MAY-2001 (first entry)
 DT
 XX Human bridging integrator-2 (Bin2) protein.

XX Bridging integrator-2 protein; Bin2; cancer; leukemia; blood disorder;
 KW hyperplastic disease; cytostatic; cell growth regulator;
 KW chromosome 4q22.1.
 XX
 XX Homo sapiens.

XX
 XX Key Location/Qualifiers
 XX Peptide 23..35
 XX /note= "specifically claimed fragment"
 XX Peptide 138..155
 XX /note= "specifically claimed fragment"

XX WO200116158-A2.
 PN
 XX 08-MAR-2001.
 PD
 XX 30-AUG-2000; 2000WO-US023723.
 XX
 XX 31-AUG-1999; 99US-0151554P.
 XX
 XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX Prendergast GC, Ge K;
 PI WPI; 2001-235087/24.
 XX
 XX N-PSDB; AAF57268.

XX New bridging integrator-2 (Bin2) protein and nucleic acid molecules,
 PT useful for regulating cell growth, and for diagnosing or treating
 PT conditions associated with inappropriate expression of Bin2, e.g. cancers
 PT or hepatocarcinoma.

XX Claim 1; Fig 1A-C; 62pp; English.

XX This represents a human bridging integrator-2 (Bin2) protein. The Bin2
 CC protein can be expressed by standard recombinant methodology. The Bin2
 CC proteins or peptides are useful in regulating cell growth, cell survival,
 CC differentiation, endocytosis and actin organization. These peptides or
 CC proteins are also useful for diagnosing or treating conditions associated
 CC with inappropriate expression of Bin2, e.g. liver cancer, breast cancer,
 CC hepatocarcinoma, myeloid and lymphoid leukemias or blood disorders. The
 CC peptides, nucleic acid sequences or anti-Bin2 antibodies are useful for
 CC diagnosing inappropriate expression of Bin2. Bin2 is also useful for
 CC treating disorders associated with excessive Bin1 levels, e.g. liver,
 CC colorectal, prostate or breast cancers, epithelia cell cancers, melanoma,
 CC or hyperplastic disease states

XX Sequence 564 AA;
 XX

Query Match 100.0%; Score 95; DB 4; Length 564;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIARGRKLVYDSARHH 18
 |||||
 DB 138 RIARGRKLVYDSARHH 155

RESULT 17
 ID ABG21411 standard; protein; 572 AA.
 XX
 AC ABG21411;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21402.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 XX
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS85598.
 DR

New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

Claim 20; SEQ ID NO 51770; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridization probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

Sequence 572 AA;
 XX
 SQ

Query Match 100.0%; Score 95; DB 4; Length 572;
 XX

Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIARGRKLVYDSARHH 18
 |||||
 DB 145 RIARGRKLVYDSARHH 162

RESULT 18
 ADD45951
 ID ADD45951 standard; protein; 588 AA.
 XX
 AC ADD45951;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein O08839, SEQ ID NO 11623.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 XX
 PR 01-NOV-2001; 2001US-0346382P.
 XX
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 XX WPI; 2003-268312/26.
 DR GENBANK; O08839.
 DR

New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 588 AA;
Query Match 100.0%; Score 95; DB 7; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RIAGRGRKLVYDSARHH 18
Db 139 RIAGRGRKLVYDSARHH 156
RESULT 19
ADE60848
ID ADE60848 standard; protein; 588 AA.
XX AC ADE60848;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein O08839, SEQ ID NO 6761.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KM Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GHEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; O08839.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that

CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences.
XX SQ Sequence 588 AA;
Query Match 100.0%; Score 95; DB 7; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RIAGRGRKLVYDSARHH 18
Db 139 RIAGRGRKLVYDSARHH 156
RESULT 20
ADE60840
ID ADE60840 standard; protein; 588 AA.
XX AC ADE60840;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein O08839, SEQ ID NO 6753.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KM Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GHEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; O08839.
XX PS New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX CC Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 588 AA;

Query Match 100.0%; Score 95; DB 7; Length 588;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRKLVDYDSARHH 18
 |||||
 Db 139 RIAGRKLVDYDSARHH 156

RESULT 21

ADE60844
 ID ADE60844 standard; protein; 588 AA.

XX AC ADE60844;
 XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein O08839, SEQ ID NO 6757.
 XX DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX OS Rattus norvegicus.

XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.

XX XX (GEO) GEN HOSPITAL CORP.
 XX FA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX DR WPI; 2003-268312/26.
 XX DR GENBANK; O08839.

XX PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 588 AA;

Query Match 100.0%; Score 95; DB 7; Length 588;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRKLVDYDSARHH 18
 |||||
 Db 139 RIAGRKLVDYDSARHH 156

RESULT 22

ADE60852
 ID ADE60852 standard; protein; 588 AA.

XX AC ADE60852;
 XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein O08839, SEQ ID NO 6765.
 XX DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX OS Rattus norvegicus.

XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.

XX XX (GEO) GEN HOSPITAL CORP.
 XX FA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX DR WPI; 2003-268312/26.
 XX DR GENBANK; O08839.

XX PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially

expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 588 AA;

Query Match 100.0%; Score 95; DB 7; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAKRGKLVYDSARHH 18
Db 139 RIAKRGKLVYDSARHH 156
|||||

RESULT 23
ADE60842
ID ADE60842 standard; protein; 593 AA.

XX AC ADE60842;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein Q99688, SEQ ID NO 6755.

XX KW Human; pain; neuronal tissue; gene therapy;
XX KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN W02003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (PARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; Q99688.

XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 593 AA;

Query Match 100.0%; Score 95; DB 7; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAKRGKLVYDSARHH 18
Db 139 RIAKRGKLVYDSARHH 156
|||||

RESULT 24

ADD45953

ID ADD45953 standard; protein; 593 AA.

XX AC ADD45953;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein Q99688, SEQ ID NO 11625.

XX KW Human; pain; neuronal tissue; gene therapy;

XX KM spinal segmental nerve injury; chronic constriction injury; CCI;

XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN W02003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (PARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; Q99688.

XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 593 AA;
 Query Match 100.0%; Score 95; DB 7; Length 593;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIARGRKLVYDSARHH 18
 Db 139 RIARGRKLVYDSARHH 156
 |||||

RESULT 25
 ADE60850
 ID ADE60850 standard; protein; 593 AA.

XX AC ADE60850;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human Protein Q99688, SEQ ID NO 6763.

XX KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.
 XX PN WO2003016475-A2.

XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.

XX PA (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; Q99688.

XX PI New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 593 AA;

Query Match 100.0%; Score 95; DB 7; Length 593;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIARGRKLVYDSARHH 18
 Db 139 RIARGRKLVYDSARHH 156
 |||||

RESULT 26
 ADE60846

ID ADE60846 standard; protein; 593 AA.

XX AC ADE60846;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein Q99688, SEQ ID NO 6759.

XX KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX PA (GHEO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.
 DR GENBANK; Q99688.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 593 AA;
 SQ
 Query Match 100.0%; Score 95; DB 7; Length 593;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIAGKGRKLVYDSARHH 18
 DB 139 RIAGKGRKLVYDSARHH 156
 RESULT 28
 ADE60854
 ID ADE60854 standard; protein; 593 AA.
 XX ADE60854;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Human Protein Q99688, SEQ ID NO 6767.
 XX
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; Chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 XX WO2003016475-A2.
 XX
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US025765.
 XX
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 PR

XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 XX GENBANK; Q99688.
 DR
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 593 AA;
 SQ
 Query Match 100.0%; Score 95; DB 7; Length 593;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIAGKGRKLVYDSARHH 18
 DB 139 RIAGKGRKLVYDSARHH 156
 RESULT 28
 ABG20887
 ID ABG20887 standard; protein; 594 AA.
 XX ABG20887;
 XX
 XX 13-FEB-2002 (first entry)
 DT
 DE Novel human diagnostic protein #20878.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200175067-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 PF

XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS85074.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 51246; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 594 AA;

Query Match 100.0%; Score 95; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSARHH 18
|||
DB 167 RIAGRGKLVYDSARHH 184

RESULT 29

ABG20324
ID ABG20324 standard; protein; 594 AA.

XX ABG20324;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #20315.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS84511.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 50893; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 594 AA;

Query Match 100.0%; Score 95; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSARHH 18
|||
DB 167 RIAGRGKLVYDSARHH 184

RESULT 30

ABG22457
ID ABG22457 standard; protein; 594 AA.

XX ABG22457;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22448.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS86644.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 52816; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 594 AA;

Query Match 100.0%; Score 95; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIAKRGKLVYDSARHH 18

Db 167 RIAKRGKLVYDSARHH 184

RESULT 31

ABG20886

ID ABG20886 standard; protein; 960 AA.

XX AC ABG20886;

XX DT 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #20877.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS85073.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 51245; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 960 AA;

Query Match 100.0%; Score 95; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIAKRGKLVYDSARHH 18

Db 238 RIAKRGKLVYDSARHH 255

RESULT 32

ABG20323

ID ABG20323 standard; protein; 960 AA.

XX AC ABG20323;

XX DT 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #20314.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX

DR WPI: 2001-639362/73.
DR N-PSDB; AAS84510.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 50682; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 960 AA;

Query Match 100.0%; Score 95; DB 4; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
Db 238 RIAKGRKLVYDSARHH 255

RESULT 33
ADD44887
ID ADD44887 standard; protein; 683 AA.
AC ADD44887;
XX
DT 29-JAN-2004 (first entry)
DE Rat Protein O08838, SEQ ID NO 10318.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-033347P.
XX
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX

DR WPI: 2003-268312/26.
DR GENBANK; O08838.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 683 AA;

Query Match 93.7%; Score 89; DB 7; Length 683;
Best Local Similarity 94.4%; Pred. No. 1.7e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
Db 134 RIAKGRKLVYDSARHH 151

RESULT 34
AAE22091
ID AAE22091 standard; protein; 695 AA.
AC AAE22091;
XX
DT 25-JUL-2002 (first entry)
DE Human amphiphsin-1 protein.
XX
KW Cellular senescence; amphiphsin-1 protein; caveolin-1 protein; human;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200221140-A1.
XX
PD 14-MAR-2002.
XX
PF 06-JUL-2001; 2001WO-KR001159.
XX
PR 08-SEP-2000; 2000KR-00053341.
PR 08-SEP-2000; 2000KR-00053342.
XX
PA (META-) METABOLIC ENG LAB CO LTD.
XX

PI Park S, Park W, Park J, Cho K, Kim D;
 XX WPI; 2002-362263/39.
 DR N-PSDB; RAD35148.
 XX
 PT Modulating cellular senescence in patient involves administering protein
 PT involved in cellular senescence e.g., amphiphysin protein or caveolin
 PT protein or polynucleotide encoding the proteins.
 XX
 PS Claim 23; Page 92-95; 103pp; English.
 XX
 CC The invention relates to a method of modulating cellular senescence in a
 CC patient. The method involves administering protein involved in cellular
 CC senescence e.g. amphiphysin-1 protein or caveolin-1 protein or
 CC polynucleotides encoding such proteins. The method is useful for
 CC detecting and modulating cellular senescence in a mammalian cell. It is
 CC also used in gene therapy. The present sequence is human amphiphysin-1
 CC protein
 CC
 SQ Sequence 695 AA;
 XX
 QY Query Match 93.7%; Score 89; DB 5; Length 695;
 Db Best Local Similarity 94.4%; Pred. No. 1.8e-06;
 Mismatches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 RIAKGRKLVYDSARHH 18
 134 RIAKGRKLVYDSARHH 151
 RESULT 35
 AAU75110
 ID AAU75110 standard; protein; 695 AA.
 AC AAU75110;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Synaptic vesicle and endocytosis associated protein, amphiphysin.
 XX
 KW MAPKAP-K3; AP-3 delta; APP-695; amyloid A4; Hsp8; heat shock protein 8;
 KW L130; NY-REN-58; P38 Alpha; P38 Beta; ERK3; KIAA0934; CDK9;
 KW cell cycle dependent kinase 9; CLK; C-NAP-1; clathrin heavy chain;
 KW amphiphysin; PN9109; KIAA1106; neurodegenerative disorder;
 KW non-insulin dependent diabetes mellitus; NIDDM; Alzheimer's disease;
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disorder;
 KW atherosclerosis; cardiac hypertrophy; hypoxic brain injury;
 KW yeast two-hybrid; signal transduction pathway; human; endocytosis;
 KW synaptic vesicle; mitogen activated protein kinase.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 93..273
 FT /note="This region binds the centrosomal Nek-2
 FT associated protein 1 (C-NAP1) (see ABK13313), the bait
 FT protein in a yeast two-hybrid assay, producing a complex
 FT Claimed in claim 1"
 XX
 PN WO200198524-A2.
 XX
 PD 27-DEC-2001.
 XX
 XX 21-JUN-2001; 2001WO-US019762.
 XX
 PR 22-JUN-2000; 2000US-0213245P.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 XX Heichman K, Bartel PL;
 XX WPI; 2002-122287/16.
 XX

PT New protein complexes comprising protein-protein interactions (e.g.
 PT MAPKAP-K3/AP-3 delta or C-NAP-1/clathrin HC), useful for diagnosing
 PT physiological generative disorders or screening drugs for these diseases.
 XX
 PS Example 11; Page; 60pp; English.
 XX
 CC The invention describes an isolated protein complex, comprising two
 CC proteins. The protein complex comprises: protein kinase MAPKAP-K3 and AP-
 CC 3 adaptor complex delta sub-unit; MAPKAP-K3 and amyloid A4 precursor
 CC protein, APP-695; MAPKAP-K3 and heat shock protein (Hsp) 8; leucine rich
 CC L130 and NY-REN-58; P38 Alpha and P38 Beta; protein kinase ERK3 and
 CC KIAA0934 (unknown function); ERK3 and cell cycle dependent kinase (CDK) 9
 CC ; ERK3 and protein kinase CLK; C-NAP-1 and Clathrin heavy chain; C-NAP-1
 CC and Amphiphysin; C-NAP-1 and novel protein PN9109 or C-NAP-1 and KIAA1106
 CC (unknown function) interactions. The protein complexes are useful for
 CC diagnosing physiological generative disorders, drug screening for agents
 CC that modulate the interaction of the proteins (thus identify drug
 CC targets), and identifying additional proteins in the pathway common to
 CC the proteins. These physiological disorders include non-insulin dependent
 CC diabetes mellitus (NIDDM), neurodegenerative disorders (e.g. Alzheimer's
 CC disease), inflammatory diseases (e.g. rheumatoid arthritis and
 CC inflammatory bowel disorder) and other human disease such as
 CC atherosclerosis, cardiac hypertrophy and hypoxic brain injury. This
 CC sequence represents the synaptic vesicle and endocytosis associated
 CC protein amphiphysin, residues 93-273 of which binds to the bait protein
 CC centrosomal Nek-2 associated protein 1 (C-NAP1) (see ABK13313) in a yeast
 CC two-hybrid assay for determining components of signal transduction
 CC pathways and forms an interaction claimed in claim 1 of the invention.
 CC Note: This sequence does not appear in the specification but has been
 CC obtained from a reference given in the invention
 XX
 SQ Sequence 695 AA;
 XX
 QY Query Match 93.7%; Score 89; DB 5; Length 695;
 Db Best Local Similarity 94.4%; Pred. No. 1.8e-06;
 Mismatches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 RIAKGRKLVYDSARHH 18
 134 RIAKGRKLVYDSARHH 151
 RESULT 36
 ADD44889
 ID ADD44889 standard; protein; 695 AA.
 XX ADD44889;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P49418, SEQ ID NO 10320.
 XX
 DE Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX

us-10-069-540a-2 copy 138 155.rag

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XX	06-JUL-1999	99US-0142390P

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Query Match 49.5%; Score 47; DB 3; Length 472;
 Best Local Similarity 53.3%; Pred. No. 20;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRGKRLVDYDSARHH 18
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 Db 170 KAGREVDYLGTRHH 184

RESULT 43
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 ID AAG41755 standard; protein; 587 AA.

XX AC AAG41755;
 XX DT 18-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 51991.
 XX KW Protein identification; signal transduction pathway; metabolic pathway;
 XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
 XX KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX FN EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PF 25-FEB-2000; 2000EP-00301439.
 XX PR 25-FEB-1999; 99US-0121825P.
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PR	23-JUN-1999;	99US-0140353P.	PR	31-AUG-1999;	99US-0151303P.
PR	23-JUN-1999;	99US-0140354P.	PR	01-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-0152363P.
PR	28-JUN-1999;	99US-0140823P.	PR	10-SEP-1999;	99US-0153700P.
PR	29-JUN-1999;	99US-0140991P.	PR	13-SEP-1999;	99US-0153758P.
PR	30-JUN-1999;	99US-0141287P.	PR	15-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0141842P.	PR	16-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-0155133P.
PR	06-JUL-1999;	99US-0142290P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155569P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-01444085P.	PR	07-OCT-1999;	99US-0158029P.

PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 25-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 49.5%; Score 47; DB 3; Length 587;
 Best Local Similarity 53.3%; Pred. NO. 25;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KGRKLVYDSARHH 18
 |||||
 DB 285 KAGREVADVLGTRHH 299

RESULT 44
 ABU24499
 ID ABU24499 standard; protein; 765 AA.

AC ABU24499;

DT 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #10026.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

KW Clostridium botulinum.

OS WO200277183-A2.

PN 03-OCT-2002.

PD 21-MAR-2002; 2002WO-US009107.

PF 21-MAR-2001; 2001US-00915242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KJ, Zyskind JW;

PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA28369.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25, SEQ ID NO 52423; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *X. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 765 AA;

Query Match 49.5%; Score 47; DB 6; Length 765;

Best Local Similarity 61.5%; Pred. NO. 33;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGRKLVYDSAR 16

DB 422 KGRKLVYDSAR 434

RESULT 45

ABP55425

ID ABP55425 standard; protein; 521 AA.

AC ABP55425;

DT 04-FEB-2003 (first entry)

DE Mouse polycomb gene enhancer 84-57.31 protein SEQ ID NO:2.

XX Mouse; polycomb gene enhancer 84-57.31; embryonic development deformity;
 tumour.

OS Mus sp.

XX CN1342699-A.

XX 03-APR-2002.

XX 12-SEP-2000; 2000CN-00125168.

XX 12-SEP-2000; 2000CN-00125168.

PA (30DE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-529776/57.

DR N-PSDB; ABQ83917.

XX A novel mouse polycarb gene enhancer 84-57.31 polypeptide, and the
PT polynucleotide encoding it, useful for treating several diseases e.g.
PT embryonic development deformity and tumors.

XX Claim 1; Page 26-27 (Disclosure); 34pp; Chinese.

XX The present sequence represents mouse polycarb gene enhancer 84-57.31
CC (1). Also described is a process for preparing (I) using DNA
CC recombination techniques. (I) can be used for treating several diseases
CC e.g. embryonic development deformity and tumors

XX Sequence 521 AA;

Query Match 47.9%; Score 45.5; DB 5; Length 521;

Best Local Similarity 43.5%; Pred. No. 40;

Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

QY 1 RIAKRGKLV-----DYDSARHH 18

Db 143 RVGRGGRVLLDRAHSDYDSVFFH 165

RESULT 46

ABU96724

ID ABU96724 standard; protein; 578 AA.

XX

AC ABU96724;

DT 25-JUL-2003 (first entry)

XX Human nucleic acid-associated protein (NAAP) #33.

XX Human; nucleic acid-associated protein; cytostatic; antiarteriosclerotic;
KW anticonvulsant; neurotropic; neuroprotective; cerebroprotective; anti-HIV;
KW anti-allergic; anti-inflammatory; thyromimetic; gene therapy;
KW cell proliferative disorder; cancer; atherosclerosis;
KW neurological disorder; epilepsy; Huntington's disease; stroke;
KW immune disorder; inflammatory disorder; AIDS; allergy;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
KW protein-protein interaction; drug-target interaction;
KW gene expression profile.

XX Homo sapiens.

XX WO2003023003-A2.

XX 20-MAR-2003.

XX 05-SEP-2002; 2002WO-US028540.

XX 07-SEP-2001; 2001US-0317792P.

XX 07-SEP-2001; 2001US-0317912P.

XX 14-SEP-2001; 2001US-032270P.

XX 21-SEP-2001; 2001US-0324040P.

XX 28-SEP-2001; 2001US-0326732P.

XX 19-OCT-2001; 2001US-0346716P.

XX 25-JAN-2002; 2002US-0351749P.

XX 22-FEB-2002; 2002US-0359498P.

XX (INCY-) INCYTE GENOMICS INC.

XX Tang YT, Jackson JL, Griffin JA, Elliott VS, Forsythe IJ;

XX Becha SD, Richardson TW, Lee EA, Sprague WW, Emerling BM;

XX Thangavelu K, Warren BA, Tran UK, Xue H, Xu Y, Yue H, Li JX;

XX Hafalia AJA, Sanjanwala B, Marquis JP, Gorvad AE, Lee SX, Ison CH;

XX Baughn MR, Chawla NK, Nguyen DB, Swarnakar A, Zebarjadian Y, Shah P;

PI

PI Thornton M, Yao MG, Khan FA, Gandhi AR, Yang J, Kable AE;

XX Burford N, Ramkumar J;

XX WPI; 2003-313243/30.

DR N-PSDB; ACA98972.

XX

XX New human nucleic acid associated proteins (NAAP), useful for diagnosing,

PT treating and preventing diseases or conditions associated with the

PT aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or

PT infections.

XX

XX Claim 1; Page 296-297; 345pp; English.

XX

XX The invention describes a novel human isolated nucleic acid-associated

CC polypeptide (NAAP). The polypeptides and polynucleotides are useful in

CC diagnosing, treating and preventing diseases or conditions associated

CC with the decreased expression or overexpression of NAAP, such as cell

CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.

CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,

CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)

CC disorders, or infections. These are also useful in assessing the effects

CC of exogenous compounds on the expression of nucleic acid and amino acid

CC sequences of NAAP. The NAAP or its fragments are useful in screening

CC compounds for effectiveness as agonist or antagonist of the polypeptides,

CC or in altering the expression of the target polynucleotide and compounds

CC that specifically bind to or modulate the activity of the polypeptide.

CC The microarray is useful in monitoring or measuring protein-protein

CC interactions, drug-target interactions, and gene expression profiles.

CC This is the amino acid sequence of a novel human nucleic acid-associated

CC protein (NAAP)

XX

XX Sequence 578 AA;

SQ

Query Match 47.9%; Score 45.5; DB 6; Length 578;

Best Local Similarity 43.5%; Pred. No. 44;

Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

QY 1 RIAKRGKLV-----DYDSARHH 18

Db 408 RVGRGGRVLLDRAHSDYDSVFFH 430

RESULT 47

AAB95815

ID AAB95815 standard; protein; 596 AA.

XX

AC AAB95815;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:18813.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

XX

PR 27-AUG-1999; 99JP-00300253.

XX

PR 11-JAN-2000; 2000JP-00118776.

XX

PR 02-MAY-2000; 2000JP-00183767.

XX

PR 09-JUN-2000; 2000JP-00241899.

XX

XX (HELI-) HELIX RES INST.

XX

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 PT
 XX
 PS Claim 8; SEQ ID NO 18813; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer, and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent cDNAs. All of which are used in the exemplification of the present invention
 XX
 CC Sequence 596 AA;
 XX
 SQ
 Query Match 47.9%; Score 45.5; DB 4; Length 596;
 Best Local Similarity 43.5%; Pred. No. 46;
 Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;
 QY 1 RIAGRGKLV-----DYDSARHH 18
 DB 241 RVGGRGVLLDRAHSDYDSVFHH 263
 RESULT 48
 ADB64808
 ID ADB64808 standard; protein; 742 AA.
 XX
 AC ADB64808;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human protein encoded by clone OCBF20016810.
 XX
 KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
 KW
 XX Homo sapiens.
 OS
 XX EP1308459-A2.
 FN
 XX 07-MAY-2003.
 PD
 XX 28-MAR-2002; 2002EP-00007401.
 PF
 XX 05-NOV-2001; 2001JP-00379298.
 PR
 XX 25-JAN-2002; 2002US-00350978.
 XX
 XX (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuka K, Nagai K, Irie R, Tamechika I, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;
 XX
 DR WPI; 2003-450961/43.
 DR N-PSDB; AD362838.
 XX
 PT New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
 PT
 XX
 PS Claim 1; Page; 222pp; English.
 XX
 CC The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotides and encoded proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes encoding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours). The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
 CC
 XX
 SQ Sequence 742 AA;
 Query Match 47.9%; Score 45.5; DB 7; Length 742;
 Best Local Similarity 43.5%; Pred. No. 59;
 Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;
 QY 1 RIAGRGKLV-----DYDSARHH 18
 DB 387 RVGGRGVLLDRAHSDYDSVFHH 409
 RESULT 49
 ABU00410
 ID ABU00410 standard; protein; 763 AA.
 XX
 AC ABU00410;
 XX
 DT 17-JAN-2003 (first entry)
 XX
 DE Human novel polypeptide #503.
 XX
 KW Human; genetic disorder; gene mapping; medical imaging; cancer; neurodegenerative disorder; lymphoid cell disorder; osteoporosis; Parkinson's disease; Alzheimer's disease; bone degenerative disorder; osteoarthritis; periodontal disease; liver fibrosis; viral infection; fungal infection; bacterial infection; autoimmune disease; diabetes; atopic dermatitis.
 KW
 XX Homo sapiens.
 OS
 XX WO200274961-A1.
 FN
 XX 26-SEP-2002.
 PD
 XX 14-MAR-2002; 2002WO-US005109.
 PF
 XX

PR 15-MAR-2001; 2001US-00810173.
PA (HYSE-) HYSEQ INC.
PI Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,
PI Wehrman T, Wang J, Wang D, Drmanac RT;
DR WPI; 2003-040556/03.
DR N-PSDB; ABX05488.
XX New isolated polypeptides and polynucleotides, useful for preventing,
PT treating or ameliorating medical conditions, such as cancer,
PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative
PT disorders, and infections.
PS Claim 9; SEQ ID NO 1029; 235pp; English.
XX The invention relates to human polynucleotides and the polypeptides they
CC encode. The polynucleotides and polypeptides are useful in diagnostics,
CC forensics, gene mapping, medical imaging, identification of mutations,
CC and producing many other types of data and traits, assessing biodiversity
CC amino acid sequences. They are also useful for products dependent on DNA and
CC ameliorating medical conditions. They are also useful for preventing, treating or
CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell
CC pericardial disease, osteoporosis, osteoarthritis, bone degenerative disorders,
CC bacterial disease, liver fibrosis, infections (e.g. viral, fungal or
CC Sequences ABG9988-ABG9999 and ABU0010-ABU0043 represent human
CC polypeptides of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied by the European Patent Office
XX Sequence 763 AA;
SQ
Query Match
Best Local Similarity 47.9%; Score 45.5; DB 6; Length 763;
Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;
QY 1 RIAGRGKLV-----DVDSARHH 18
Db 408 RVGGRGVLLDRAHSYDSVFFH 430
RESULT 50
AAU63157
ID AAU63157 standard; protein; 161 AA.
AC AAU63157;
XX
DT 27-FEB-2002 (first entry)
DE Propionibacterium acnes immunogenic protein #24053.
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
OS Propionibacterium acnes.
XX WO200181581-A2.
PN
XX
PD 01-NOV-2001.
XX
PP
PR 20-APR-2001; 2001WO-US012865.
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
DR N-PSDB; AAS59632.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
PS
XX Example 1; SEQ ID NO 24352; 1069pp; English.
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 161 AA;
Query Match
Best Local Similarity 46.3%; Score 44; DB 4; Length 161;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 6 GRKLVYDSARHH 18
Db 27 GGELIALDSARHH 39

Search completed: March 4, 2004, 17:44:23
Job time : 64.6452 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:39:06 ; Search time 15.6774 Seconds

(without alignments)
110.442 Million cell updates/sec

Title: US-10-069-540A-2_COPY_138_155

Perfect score: 95

Sequence: 1 RIAGRGKLVVDYDSARRH 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

PIR 78.*

1: piri.*

2: piri2.*

3: piri3.*

4: piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	482	JCS593	amphiphysin II2 -
2	89	93.7	682	S22700	amphiphysin - chic
3	89	93.7	695	S62400	amphiphysin (clone
4	69	72.6	461	T22946	hypothetical prote
5	49.5	52.1	130	F91120	hypothetical prote
6	48	50.5	159	F84259	hypothetical prote
7	47	49.5	424	F84658	probable protein k
8	47	49.5	578	T51888	asparagine synthas
9	47	49.5	578	T50812	asparagine synthas
10	45	47.4	288	S40975	hypothetical prote
11	44	46.3	225	PC2237	protein-glutamine
12	43.5	45.8	282	AB0828	probable transcrip
13	43	45.3	284	T40661	yeast reduced viab
14	43	45.3	270	T43000	RV5161 protein hom
15	43	45.3	397	S62579	probable plasma me
16	43	45.3	848	I55498	testicular dynamin
17	42	44.2	252	B69497	conserved hypotet
18	42	44.2	463	D70933	hypothetical prote
19	42	44.2	906	S32607	trifunctional enzy
20	42	44.2	1193	F83264	hypothetical prote
21	42	44.2	1957	A59294	skeletal myosin -
22	41.5	43.7	731	A59294	cucumis (EC 3.4.
23	41	43.2	92	1MNVSU	nonstructural prot
24	41	43.2	196	T13595	hypothetical prote
25	41	43.2	237	E70945	hypothetical prote
26	41	43.2	402	T25732	hypothetical prote
27	41	43.2	407	C71055	probable RNA methy
28	41	43.2	974	D89057	protein K09H11.1
29	41	43.2	1001	T50914	hypothetical membr

30	40.5	42.6	306	1	H65033	hypothetical prote
31	40.5	42.6	306	2	C91057	hypothetical prote
32	40.5	42.6	306	2	G85901	hypothetical prote
33	40.5	42.6	315	2	A71288	probable methylene
34	40.5	42.6	393	2	AC2896	oxidoreductase Atu
35	40.5	42.6	408	2	F97671	probable oxidoredu
36	40.5	42.6	458	2	S77016	sensory transducti
37	40	42.1	225	2	B35387	hypothetical prote
38	40	42.1	264	2	AG3175	hypothetical prote
39	40	42.1	308	2	E81288	hypothetical prote
40	40	42.1	426	2	H70390	conserved hypotet
41	40	42.1	651	2	T49986	lectin-like protei
42	40	42.1	752	2	S56146	GCN20 protein - ye
43	40	42.1	830	2	T18860	hypothetical prote
44	39.5	41.6	229	2	H64367	dolichyl-phosphate
45	39	41.1	97	2	T31023	conserved hypotet
46	39	41.1	99	2	G83986	hypothetical prote
47	39	41.1	165	2	A86199	hypothetical prote
48	39	41.1	219	2	T01186	protein kinase (EC
49	39	41.1	224	2	T01185	protein kinase (EC
50	39	41.1	259	2	T49291	hypothetical prote
51	39	41.1	394	2	AF2650	conserved hypotet
52	39	41.1	420	2	E97432	hypothetical prote
53	39	41.1	459	2	E71443	probable DNA-bindi
54	39	41.1	461	2	B95388	Probable (EC 1.1.1
55	39	41.1	512	2	S48828	lethal-3 protein,
56	39	41.1	559	2	T02825	probable membrane
57	39	41.1	639	2	B95945	probable glycosyl
58	39	41.1	756	2	T05829	hypothetical prote
59	39	41.1	781	2	T05206	hypothetical prote
60	39	41.1	796	2	C85220	hypothetical prote
61	39	41.1	918	2	S04255	regulatory protein
62	39	41.1	980	2	A38523	genome polyprotein
63	39	41.1	981	2	S55132	hypothetical prote
64	39	41.1	2894	2	C64474	hypothetical prote
65	38.5	40.5	64	2	C87511	hypothetical prote
66	38.5	40.5	427	2	A84155	hypothetical prote
67	38	40.0	136	2	A11104	B. subtilis YacZ p
68	38	40.0	136	2	A11466	B. subtilis YacZ p
69	38	40.0	203	2	JC1247	Grp-binding protei
70	38	40.0	224	2	B81783	hypothetical prote
71	38	40.0	252	2	F87259	hypothetical prote
72	38	40.0	299	2	G82393	transcription regu
73	38	40.0	389	2	D86424	43.3K hypotetical
74	38	40.0	431	2	S45038	protein disulfide-
75	38	40.0	440	2	JC4369	P5 protein precurs
76	38	40.0	464	2	B64970	Colanic acid biosy
77	38	40.0	464	2	H90984	hypothetical prote
78	38	40.0	464	2	C95830	hypothetical prote
79	38	40.0	503	2	B82880	multiple banded an
80	38	40.0	504	2	F71253	conserved hypotet
81	38	40.0	573	2	H99904	aerobic glycerol-3
82	38	40.0	620	2	H85431	Arpase-like protei
83	38	40.0	642	2	S18667	deoxyribodipyrimid
84	38	40.0	651	2	S35706	NADH oxidase (EC 1
85	38	40.0	715	2	A41511	staphylocoagulase
86	38	40.0	757	2	F87304	beta-N-acetylhexos
87	38	40.0	950	2	G83167	valyl-tRNA synthet
88	38	40.0	1433	2	G01946	nitric-oxide synth
89	38	40.0	1518	2	S37928	probable purine nu
90	38	40.0	2429	1	SJHUA	spectrin alpha cha
91	38	40.0	4574	2	G02520	plectin - human
92	38	40.0	4684	2	A59404	plectin [imported]
93	37.5	39.5	347	2	S33939	minor core protein
94	37.5	39.5	366	2	E72355	hypothetical prote
95	37.5	39.5	453	2	B97738	outer membrane pro
96	37.5	39.5	697	2	T00267	hypothetical prote
97	37.5	39.5	1249	2	T36294	hypothetical prote
98	37	38.9	89	1	H64116	ribosomal protein
99	37	38.9	91	2	F82522	hypothetical prote
100	37	38.9	112	2	T34589	hypothetical prote
101	37	38.9	113	2	S43583	F26F3.3 protein -
102	37	38.9	128	2	E69306	hypothetical prote

103 37 38.9 145 1 S23063 ribosomal protein
104 37 38.9 147 2 E90018 50S ribosomal prot
105 37 38.9 147 2 T16440 hypothetical prote
106 37 38.9 150 1 ORXYS1 cell division cont
107 37 38.9 163 2 S28136 gas vesicle protei
108 37 38.9 200 2 F71866 hypothetical prote
109 37 38.9 213 2 G82723 partition protein
110 37 38.9 227 2 AE2343 hypothetical prote
111 37 38.9 245 2 F83270 probable nucleosid
112 37 38.9 258 2 T09636 yscE protein - Lac
113 37 38.9 278 2 C72807 probable non-heme
114 37 38.9 315 2 S17952 acyltransferase (E
115 37 38.9 338 2 C75161 3-dehydroquinase
116 37 38.9 355 2 C64582 phospholipase A1 p
117 37 38.9 355 2 H71930 probable phospholi
118 37 38.9 369 2 H88535 protein B0523.4 [i
119 37 38.9 376 2 JN0745 site-specific DNA-
120 37 38.9 389 2 E90431 sulfolipid biosynt
121 37 38.9 392 2 C69544 conserved hypothet
122 37 38.9 394 2 C82951 conserved hypothet
123 37 38.9 397 2 G97075 probable transcrip
124 37 38.9 422 2 S58173 ketoacyl synthase
125 37 38.9 431 2 S19656 protein disulfide-
126 37 38.9 439 2 S44733 b0523.4 protein -
127 37 38.9 539 2 A64441 O-sialoglycoprotei
128 37 38.9 541 2 S76017 hypothetical prote
129 37 38.9 543 2 G87598 Tidd/FmbA family p
130 37 38.9 565 2 T47775 hypothetical prote
131 37 38.9 586 2 T02978 asparagine synthas
132 37 38.9 662 1 A49882 histidine decarbox
133 37 38.9 672 2 T12524 hypothetical prote
134 37 38.9 797 2 A70453 glutamate ammonia
135 37 38.9 808 2 F84038 phenylalanyl-tRNA
136 37 38.9 900 2 A72524 probable alanyl-tr
137 37 38.9 1139 2 S28277 hypothetical prote
138 37 38.9 1211 2 T27522 hypothetical prote
139 37 38.9 1526 2 T19473 hypothetical prote
140 37 38.9 1670 2 S71551 DNA-directed DNA p
141 36.5 38.4 124 2 F87429 hypothetical prote
142 36.5 38.4 349 2 E95858 conserved hypothet
143 36.5 38.4 431 2 E81053 seryl-tRNA synthet
144 36.5 38.4 431 2 E81822 serine-tRNA ligase
145 36.5 38.4 431 2 H84069 hypothetical prote
146 36.5 38.4 584 2 S06318 endoplasmic reticu
147 36.5 38.4 638 1 ISMSER protein disulfide-
148 36.5 38.4 643 1 S32476 protein disulfide-
149 36 37.9 87 2 T16008 hypothetical prote
150 36 37.9 89 1 R3EC15 ribosomal protein

ALIGNMENTS

RESULT 1
JC5593
amphiphysin II2 - human
C:Species: Homo sapiens (man)
C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jun-2000
C:Accession: JC5593
R;Tsutsui, K.; Maeda, Y.; Tsutsui, K.; Seki, S.; Tokunaga, A.
Biochem. Biophys. Res. Commun. 236, 178-183, 1997
A;Title: cDNA cloning of a novel amphiphysin isoform and tissue-specific expression of
A;Reference number: JC5593; MUID:97366618; PMID:9223448
A;Accession: JC5593
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-482 <TSU>
A;Cross-references: DBJ:AF001383; NID:g2199534; PIDN:AAB61363.1; PID:g2199535
A;Experimental source: fetal brain
C;Comment: This protein is involved in the synaptic vesicle recycling and in the regulat
C;Superfamily: amphiphysin; RVS161 protein homology
F;16-275/Domain: RVS161 protein homology <RVS>
F;410-481/Domain: SH3 #status predicted <SH3>

Query Match 100.0%; Score 95; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAXGRKLVYDSARHH 18
DB 139 RIAXGRKLVYDSARHH 156
|||||

RESULT 2

S22700
amphiphysin - chicken
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S22700
R;Lichte, B.; Veh, R.W.; Meyer, H.E.; Kilmann, M.W.
EMBO J. 11, 2521-2530, 1992
A;Title: Amphiphysin, a novel protein associated with synaptic vesicles.
A;Reference number: S22700; MUID:92331604; PMID:1628617
A;Accession: S22700
A;Molecule type: mRNA
A;Residues: 1-682 <LIC>
A;Cross-references: EMBL:X60422; NID:g62842; PIDN:CAA42953.1; PID:g62843
C;Superfamily: amphiphysin; RVS161 protein homology
F;11-270/Domain: RVS161 protein homology <RVS>

Query Match 93.7%; Score 89; DB 1; Length 682;
Best Local Similarity 94.4%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAXGRKLVYDSARHH 18
DB 134 RIAXGRKLVYDSARHH 151
|||||

RESULT 3

S82400
amphiphysin (clone 22-2) - human
C:Species: Homo sapiens (man)
C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S82400; I37166
R;David, C.; Solimena, M.; de Camilli, P.
PES Lett. 351, 73-79, 1994
A;Title: Autoimmunity in Stiff-Man Syndrome with breast cancer is targeted to the C-term
A;Reference number: S48686; MUID:94357284; PMID:8076697
A;Accession: S82400
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-695 <DAV>
A;Cross-references: EMBL:U07616; NID:g550449; PIDN:AAA21865.1; PID:g550450
R;Yamamoto, R.; Li, X.; Winter, S.; Francke, U.; Kilmann, M.W.
Hum. Mol. Genet. 4, 265-268, 1995
A;Title: Primary structure of human amphiphysin, the dominant autoantigen of paraneoplas
A;Reference number: I37166; MUID:95276740; PMID:7757077
A;Accession: I37166
A;Status: preliminary; translated from GB/EMBL/DDBT
A;Molecule type: mRNA
A;Residues: 1-695 <RES>
A;Cross-references: EMBL:X81438; NID:g662991; PIDN:CAA57197.1; PID:g662992
C;Genetics:
A;Gene: GDB:AMPH
A;Map position: 7p14-7p13
C;Superfamily: amphiphysin; RVS161 protein homology
F;11-270/Domain: RVS161 protein homology <RVS>

Query Match 93.7%; Score 89; DB 2; Length 695;
Best Local Similarity 94.4%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAXGRKLVYDSARHH 18
|||||

Db 134 RIAKGRKLVYDVSARHH 151

RESULT 4

T22946

hypothetical protein F58G6.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000

C:Accession: T22946

R:Illyod, C.

submitted to the EMBL Data Library, December 1995

A:Reference number: Z19641

A:Accession: T22946

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-461 <WIL>

A:Cross-references: EMBL:Z68217; PIDN:CAA92465.1; GSPDB:GN00022; CESP:F58G6.1

A:Experimental source: clone F58G6

C:Genetics:

A:Gene: CESP:F58G6.1

A:Map position: 4

A:Introns: 19/3; 57/3; 96/3; 130/3; 157/3; 186/3; 219/3; 271/3; 302/3; 335/3; 357/3

C:Superfamily: amphiphysin; RVSI61 protein homology

Query Match

Best Local Similarity 72.6%; Score 69; DB 2; Length 461;

Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDVSARH 17

Db 130 KIEKGRKLVYDSAKN 146

RESULT 5

F91120

hypothetical protein ECS3934 [imported] - *Escherichia coli* (strain O157:H7, substrain R)

C:Species: *Escherichia coli*

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C:Accession: F91120

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F91120

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-130 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA37357.1; PID:G13363407; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 050952

C:Genetics:

A:Gene: ECS3934

Query Match

Best Local Similarity 52.1%; Score 49.5; DB 2; Length 130;

Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 5 RGRKLVYDVSARHH 18

Db 84 RGRGLGKGYDEARHH 100

RESULT 6

F84259

hypothetical protein Vng1031c [imported] - *Halobacterium* sp. NRC-1

C:Species: *Halobacterium* sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: F84259

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of *Halobacterium* species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: F84259

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-169 <STO>

A:Cross-references: GB:AE004437; NID:G10580584; PIDN:AAG19442.1; GSPDB:GN00138

C:Genetics:

A:Gene: VNG1031C

C:Superfamily: conserved hypothetical protein MJ1050

Query Match

Best Local Similarity 50.5%; Score 48; DB 2; Length 169;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 AKRGRKLVYDVSARHH 18

Db 44 ADRGSKIVDVDAVRDH 59

RESULT 7

F84658

probable protein kinase [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002

C:Accession: F84658

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84658

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-424 <STO>

A:Cross-references: GB:AE002093; NID:G3075390; PIDN:AAC14522.1; GSPDB:GN00139

C:Genetics:

A:Gene: Atg26290

A:Map position: 2

C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match

Best Local Similarity 49.5%; Score 47; DB 2; Length 424;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRGRKLVYDVSARHH 18

Db 382 KEGKKFVDINKFRHH 396

RESULT 8

T51888

asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) [validated] - *Arabidopsis thali*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000

C:Accession: T51888

R:Lam, H.M.; Hsieh, M.H.; Coruzzi, G.

Plant J. 16, 345-353, 1998

A:Title: Reciprocal regulation of distinct asparagine synthetase genes by light and meta

A:Reference number: Z24846

A:Accession: T51888

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-578 <LAM>

A:Cross-references: EMBL:AF095452; PIDN:AAC72836.1

C:Genetics:

A:Gene: ASN3

C:Function:

A:Description: EC 6.3.5.4 [validated, MUID:99097830]

C:Superfamily: asparagine synthase (glutamine-hydrolyzing)

C:Keywords: ligase

Query Match 49.5%; Score 47; DB 2; Length 578;
 Best Local Similarity 53.3%; Pred. No. 12;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRGKRLVDYDSARHH 18
 |||:|
 DB 276 KAGREVADYLGTRHH 290
 |||:|

RESULT 9
 T50812
 asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) [similarity] - Arabidopsis thaliana
 N;Alternate names: protein F18D22 10; protein T31P16.230
 C;Species: Arabidopsis thaliana [mouse-ear cress]
 C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 19-Jul-2002
 C;Accession: T50812; T50028
 R;Bevan, M.; Volkart, G.; Grymonprez, B.; Voet, M.; Robben, J.; Bancroft, I.; Mewes, H.
 submitted to the Protein Sequence Database, July 2000
 A;Reference number: Z25241
 A;Accession: T50812
 A;Molecule type: DNA
 A;Residues: 1-578 <BEV1>
 A;Cross-references: EMBL:AL360334
 A;Experimental source: cultivar Columbia; BAC clone F18D22
 R;Bevan, M.; Zimmermann, W.; Gruenisen, A.; Wambutt, R.; Kalicki, J.; Wohlmann, P.; Smith, J.
 submitted to the Protein Sequence Database, May 2000
 A;Reference number: Z25027
 A;Accession: T50028
 A;Molecule type: DNA
 A;Residues: 138-578 <BEV2>
 A;Cross-references: EMBL:AL356332; GSPDB:GN00063; ATSP:T31P16.230
 A;Experimental source: cultivar Columbia; BAC clone T31P16
 C;Genetics:
 A;Gene: ATSP:T31P16.230
 A;Map position: 5
 A;Introns: 27/2; 73/3; 105/3; 153/1; 185/1; 216/3; 270/3; 371/3; 416/3; 443/3; 473/3; 500/3
 C;Superfamily: asparagine synthase (glutamine-hydrolyzing)
 C;Keywords: asparagine biosynthesis; ligase
 F;2-578/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>
 F;2/Active site: Cys #status predicted

Query Match 49.5%; Score 47; DB 2; Length 578;
 Best Local Similarity 53.3%; Pred. No. 12;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRGKRLVDYDSARHH 18
 |||:|
 DB 276 KAGREVADYLGTRHH 290
 |||:|

RESULT 10
 S40975
 hypothetical protein F58A4.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
 C;Accession: S40975
 R;Berks, M.
 submitted to the EMBL Data Library, February 1992
 A;Reference number: S40973
 A;Accession: S40975
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-288 <BER>
 A;Cross-references: EMBL:Z22179; NID:G297956; PID:G297958
 C;Genetics:
 A;Introns: 31/2; 113/3; 214/3

Query Match 47.4%; Score 45; DB 2; Length 288;
 Best Local Similarity 41.2%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 IAKRGKRLVDYDSARHH 18
 |||:|
 DB 14 LAQSDRKLADYLLAQPDTARRH 34
 |||:|

RESULT 11
 T40661
 yeast reduced viability upon starvation protein 161 homolog, implicated in cell growth
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
 C;Accession: T40661
 R;Lyne, M.; Rajadream, M.A.; Barrell, B.G.; Rieger, M.
 submitted to the EMBL Data Library, November 1998
 A;Reference number: Z21889

Query Match 45.8%; Score 43.5; DB 2; Length 282;
 Best Local Similarity 47.6%; Pred. No. 23;
 Matches 10; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 2 IAKRGKRLVDYDSARHH 17
 |||:|
 DB 14 LAQSDRKLADYLLAQPDTARRH 34
 |||:|

RESULT 12
 T40661
 Probable transcription regulator yfhh [imported] - Salmonella enterica subsp. enterica
 C;Species: Salmonella enterica subsp. enterica serovar typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB0828
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulie, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A;Authors: Parkhill, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; White, N.; Farrar, S.; Moulie, S.; O'Garra, P.
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhi
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB0828
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-282 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD02774.1; PID:gi6503784; GSPDB:GN00176
 C;Genetics:
 A;Gene: yfhh
 C;Superfamily: hypothetical protein ybbh

Query Match 45.8%; Score 43.5; DB 2; Length 282;
 Best Local Similarity 47.6%; Pred. No. 23;
 Matches 10; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 2 IAKRGKRLVDYDSARHH 17
 |||:|
 DB 14 LAQSDRKLADYLLAQPDTARRH 34
 |||:|

RESULT 13
 T40661
 yeast reduced viability upon starvation protein 161 homolog, implicated in cell growth
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
 C;Accession: T40661
 R;Lyne, M.; Rajadream, M.A.; Barrell, B.G.; Rieger, M.
 submitted to the EMBL Data Library, November 1998
 A;Reference number: Z21889

DB 114 VGRNSTNLVDYSGRRHH 130
 |||:|

RESULT 11
 PC2237
 protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13), tissue-type - red sea bream
 N;Alternate names: transglutaminase
 C;Species: Chrysophrys major (red sea bream)
 C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 07-May-1999
 C;Accession: PC2237
 R;Yasueda, H.; Kumazawa, Y.; Motoki, M.
 Biosci. Biotechnol. Biochem. 58, 2041-2045, 1994
 A;Title: Purification and characterization of a tissue-type transglutaminase from red sea bream
 A;Reference number: PC2237; MUID:95078510; PMID:7765597
 A;Accession: PC2237
 A;Molecule type: protein
 A;Residues: 1-225 <YAS>
 A;Experimental source: liver
 A;Comment: This enzyme catalyzes a Ca2+-dependent acyl-transfer reaction in which the gamma-glutamyl group of a protein is transferred to an acceptor.
 C;Superfamily: protein-glutamine gamma-glutamyltransferase
 C;Keywords: aminoacyltransferase

Query Match 46.3%; Score 44; DB 2; Length 225;
 Best Local Similarity 63.2%; Pred. No. 15;
 Matches 12; Conservative 3; Mismatches 2; Indels 2; Gaps 2;

QY 2 IAKRGKRLVDYDSARHH 18
 |||:|
 DB 65 IAEQGRLLVDFDSRLHH 83
 |||:|

RESULT 12
 AB0828
 Probable transcription regulator yfhh [imported] - Salmonella enterica subsp. enterica
 C;Species: Salmonella enterica subsp. enterica serovar typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB0828
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulie, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A;Authors: Parkhill, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; White, N.; Farrar, S.; Moulie, S.; O'Garra, P.
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhi
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB0828
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-282 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD02774.1; PID:gi6503784; GSPDB:GN00176
 C;Genetics:
 A;Gene: yfhh
 C;Superfamily: hypothetical protein ybbh

Query Match 45.8%; Score 43.5; DB 2; Length 282;
 Best Local Similarity 47.6%; Pred. No. 23;
 Matches 10; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 2 IAKRGKRLVDYDSARHH 17
 |||:|
 DB 14 LAQSDRKLADYLLAQPDTARRH 34
 |||:|

RESULT 13
 T40661
 yeast reduced viability upon starvation protein 161 homolog, implicated in cell growth
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
 C;Accession: T40661
 R;Lyne, M.; Rajadream, M.A.; Barrell, B.G.; Rieger, M.
 submitted to the EMBL Data Library, November 1998
 A;Reference number: Z21889

A;Accession: T40661
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-264 <LYN>
 A;Cross-references: EMBL:AL034352; PIDN:CAA22181.1; GSPDB:GN00067; SPDB:SPBC725.09c
 A;Experimental source: strain 972h-; cosmid c725
 C;Genetics:
 A;Gene: SPDB:SPBC725.09c
 A;Map position: 2
 A;Introns: 16/3
 A;Superfamily: RVS161 protein; RVS161 protein homology
 P;4-255/Domain: RVS161 protein homology <RVS>

Query Match 45.3%; Score 43; DB 2; Length 264;
 Best Local Similarity 53.3%; Pred. No. 26;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IAKGRKLVYDSAR 16
 Db 132 ITRKHKLDDHDAVR 146

RESULT 14

T43000
 RVS161 protein homolog - fission yeast (Schizosaccharomyces pombe) (fragment)
 C;Species: Schizosaccharomyces pombe
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
 A;Accession: T43000
 R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
 DNA Res. 4, 363-369, 1997
 A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
 A;Reference number: 217233; MUID:98162722; PMID:9501391
 A;Accession: T43000
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-270 <YOS>
 A;Cross-references: EMBL:D89200; NID:g1749607; PIDN:BAAL3861.1; PID:g1749608
 A;Experimental source: strain PR745
 C;Superfamily: RVS161 protein; RVS161 protein homology
 P;10-261/Domain: RVS161 protein homology <RVS>

Query Match 45.3%; Score 43; DB 2; Length 270;
 Best Local Similarity 53.3%; Pred. No. 26;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IAKGRKLVYDSAR 16
 Db 138 ITRKHKLDDHDAVR 152

RESULT 15

S62579
 Probable plasma membrane iron permease - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2000
 C;Accession: S62579; T38101
 R;Murphy, L.; Niblett, D.; Harris, D.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: S62573
 A;Accession: S62579
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-397 <MUR>
 A;Cross-references: EMBL:Z67998; NID:g1067202; PIDN:CAA91954.1; PID:g1067209
 R;Back, A.; Reinhardt, R.; Murphy, L.; Niblett, D.; Harris, D.; Barrell, B.G.; Rajandrea
 submitted to the EMBL Data Library, November 1995
 A;Reference number: Z21769
 A;Accession: T38101
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-397 <MU2>
 A;Cross-references: EMBL:Z67998; NID:g1067202; PIDN:CAA91954.1; GSPDB:GN00066; SPDB:SPAC
 A;Experimental source: strain 972h-; cosmid c1f7

C;Genetics:
 A;Gene: SPAC1F7.07c
 A;Map position: 1R
 C;Superfamily: conserved probable membrane protein YBR207w

Query Match 45.3%; Score 43; DB 2; Length 397;
 Best Local Similarity 52.9%; Pred. No. 37;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IAKGRKLVYDSAR 16
 Db 323 IAKLGKVVDELAAS 339

RESULT 16

I55498
 testicular dynamin - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 02-Feb-2001
 C;Accession: I55498
 R;Nakata, T.; Takemura, R.; Hirokawa, N.
 J. Cell Sci. 105, 1-5, 1993

A;Title: A novel member of the dynamin family of GTP-binding proteins is expressed speci
 A;Reference number: I55498; MUID:93366923; PMID:8360266
 A;Accession: I55498
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-848 <RES>
 A;Cross-references: GB:D14076; NID:g391871; PIDN:BAAO3161.1; PID:g391872
 C;Superfamily: human dynamin II; pleckstrin repeat homology
 C;Keywords: alternative splicing; GTP binding; membrane trafficking; nucleotide binding;
 F;38-45/Region: nucleotide-binding motif A (P-loop)
 F;132-137/Region: nucleotide-binding motif B
 F;514-619/Domain: nucleotide-binding motif <PLK>

Query Match 45.3%; Score 43; DB 2; Length 848;
 Best Local Similarity 46.2%; Pred. No. 75;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 RGRKLVYDSAR 17
 Db 87 KGKKFTDFEVRH 99

RESULT 17

B69497
 conserved hypothetical protein AF1979 - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Jun-2003
 C;Accession: B69497
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woose, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: B69497
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-252 <KLE>

A;Cross-references: GB:AE000966; GB:AE000782; NID:g2689289; PIDN:AA889275.1; PID:g264856
 C;Superfamily: nucleotidyltransferase

Query Match 44.2%; Score 42; DB 2; Length 252;
 Best Local Similarity 63.6%; Pred. No. 35;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GRKLVYDSAR 16
 Db 30 GRKLVYDSAR 40

RESULT 18

RD0933
 hypothetical protein RV0573c - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Jun-2001
 C:Accession: D70933
 R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A: Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.
 A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A: Reference number: A70500; MUID: 98295987; PMID: 9634230
 A: Accession: D70933
 A: Status: preliminary; nucleic acid sequence not shown; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-463 <COL>
 A: Cross-references: GB:AL021942; GB:AL123456; NID: G3242298; PIDN: CAA17444.1; PID: G290963
 A: Experimental source: strain H37RV
 C: Geneticks:
 A: Gene: RV0573c
 C: Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF0821

Query Match 44.2%; Score 42; DB 2; Length 463;
 Best Local Similarity 50.0%; Pred. No. 62;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 AKRGKLVYDVSARHH 18
 |||||:|:|:|
 DB 148 AARGPVDVFGARRAH 163

RESULT 19

S32607
 trifunctional enzyme HDE, peroxisomal - Yeast (Candida tropicalis)
 N: Alternate names: trifunctional beta-oxidation enzyme HDE
 N: Contains: 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-hydroxyacyl-CoA epimerase
 C: Species: Candida tropicalis
 C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
 C: Accession: S32607; JH0474; JH0350; S18126
 R: Sloots, J.A.; Aitchison, J.D.; Rachubinski, R.A.
 Gene 105, 129-134, 1991
 A: Title: Glucose-responsive and oleic acid-responsive elements in the gene encoding the
 A: Reference number: S32607; MUID: 92039009; PMID: 1937002
 A: Accession: S32607
 A: Status: nucleic acid sequence not shown; translation not shown
 A: Molecule type: DNA
 A: Residues: 1-906 <AIT>
 A: Cross-references: EMBL: X57854; NID: G2669; PIDN: CAA40989.1; PID: G2670
 A: Note: nucleotide sequence submitted to the EMBL Data Library, February 1991
 R: Aitchison, J.D.; Sloots, J.A.; Nuttle, W.M.; Rachubinski, R.A.
 Gene 105, 135-136, 1991

A: Title: Sequence of the gene encoding Candida tropicalis peroxisomal trifunctional enzyme
 A: Reference number: JH0474; MUID: 92039010; PMID: 1937003
 A: Accession: JH0474
 A: Status: translation not shown
 A: Molecule type: DNA
 A: Residues: 1-906 <AI3>
 A: Cross-references: EMBL: X57854; NID: G2669; PIDN: CAA40989.1; PID: G2670
 R: Nuttle, W.M.; Aitchison, J.D.; Rachubinski, R.A.
 Gene 69, 171-180, 1988
 A: Title: cDNA cloning and primary structure determination of the peroxisomal trifunctional
 A: Reference number: JH0350; MUID: 89172062; PMID: 3267241
 A: Accession: JH0350
 A: Molecule type: mRNA
 A: Residues: 1-539; S' 541-906 <NUT>
 A: Cross-references: GB: M22765; NID: G695397; PIDN: AAA62847.1; PID: G695398
 A: Note: the authors translated the codon TCC for residue 540 as Phe

C: Geneticks:
 A: Gene: HDE
 C: Superfamily: peroxisomal trifunctional enzyme HDE; short-chain alcohol dehydrogenase
 C: Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; isomerase; mult

F: 9-194/Domain: short-chain alcohol dehydrogenase homology <SAD1>
 F: 323-498/Domain: short-chain alcohol dehydrogenase homology <SAD2>

Query Match 44.2%; Score 42; DB 1; Length 906;
 Best Local Similarity 46.7%; Pred. No. 1.2e+02;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAKRGKLVYDVSAR 16
 |||||:|:|:|
 DB 267 VAKRFSILYDDSR 281

RESULT 20

F83264
 hypothetical protein PA3063 [imported] - Pseudomonas aeruginosa (strain PA01)
 C: Species: Pseudomonas aeruginosa
 C: Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C: Accession: F83264
 R: Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A: Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A: Reference number: A82950; MUID: 20437337; PMID: 10984043
 A: Accession: F83264
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-1193 <STO>
 A: Cross-references: GB: AE004730; GB: AE004091; NID: G9949154; PIDN: AAG06451.1; GSPDB: GN001
 A: Experimental source: strain PA01
 C: Geneticks:
 A: Gene: PA3063

Query Match 44.2%; Score 42; DB 2; Length 1193;
 Best Local Similarity 63.6%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 KLVYDVSARHH 18
 |||||:|:|:|
 DB 81 KLGDFEQARHH 91

RESULT 21

A59294
 skeletal myosin - nematode (Onchocerca volvulus)
 N: Alternate names: major body wall myosin
 C: Species: Onchocerca volvulus
 C: Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
 C: Accession: A59294
 R: Werner, C.; Rajan, T.V.
 Mol. Biochem. Parasitol. 50, 255-260, 1992
 A: Title: Comparison of the body wall myosin heavy chain sequences from Onchocerca volvulus
 A: Reference number: A59294; MUID: 92158005; PMID: 1741012
 A: Accession: A59294
 A: Status: preliminary; not compared with conceptual translation
 A: Molecule type: mRNA
 A: Residues: 1-1957 <WER>
 A: Cross-references: GB: M74066; NID: G159892; PIDN: AAA29420.1; PID: G159893
 A: Experimental source: sex female
 C: Superfamily: myosin heavy chain; myosin motor domain homology
 F: 87-773/Domain: myosin motor domain homology <MMO>

Query Match 44.2%; Score 42; DB 2; Length 1957;
 Best Local Similarity 50.0%; Pred. No. 2.3e+02;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 AKRGKLVYDVSARHH 18
 |||||:|:|:|
 DB 1702 AERARKQADYDANEAH 1717

RESULT 22

A55800

cucumis (EC 3.4.21.25) precursor - muskmelon
C;Species: Cucumis melo (muskmelon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55800
R;Yamagata, H.; Masuzawa, T.; Nagaoaka, Y.; Ohnishi, T.; Iwasaki, T.
J. Biol. Chem. 269, 32725-32731, 1994
A;Title: Cucumis, a serine protease from melon fruits, shares structural homology with
P;616-731/Domain: carboxyl-terminal propeptide #status predicted <CTP>
P;615-616/Cleavage site: Thr-Gly (autolytic) #status predicted
A;Accession: A55800
A;Molecule type: mRNA
A;Residues: 1-731 <YAM>
A;Cross-references: EMBL:D32206
A;Note: it is uncertain whether Met-1 is the initiator or whether translation is initiated
C;Superfamily: subtilisin-like proteinase ag12; subtilisin homology
C;Keywords: hydrolase; signal sequence; and amino-terminal propeptide (fragment) #status predicted
F;1-110/Domain: signal sequence and amino-terminal propeptide (fragment) #status predicted
F;111-615/Product: cucumis #status predicted <WAT>
F;131-539/Domain: subtilisin homology #status atypical <SBT>
P;616-731/Domain: carboxyl-terminal propeptide #status predicted <CTP>
P;615-616/Cleavage site: Thr-Gly (autolytic) #status predicted
Query Match 43.7%; Score 41.5; DB 1; Length 731;
Best Local Similarity 61.1%; Pred. No. 1.1e+02; Indels 1; Gaps 1;
Matches 11; Conservative 0; Mismatches 6;
CY 2 IAKRGKLVYDSAR-HH 18
DB 35 IVYMGKLEPDPSAHLHH 52
RESULT 23
MNVOUS
nonstructural protein NS - snowshoe hare virus
C;Species: snowshoe hare virus
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 30-Sep-1993
C;Accession: A04105
R;Bishop, D.H.L.; Gould, K.G.; Akashi, H.; Clerx-van Haaster, C.M.
Nucleic Acids Res. 10, 3703-3713, 1982
A;Title: The complete sequence and coding content of snowshoe hare bunyavirus small (S)
A;Reference number: A93429; MUID:82274210; PMID:7050911
A;Accession: A04105
A;Molecule type: genomic RNA
A;Residues: 1-92 <BIS>
A;Note: this virus is a member of the California encephalitis serogroup of mosquito-transmitted bunyaviruses
C;Comment: The genome consists of a large (L) RNA, a medium (M) RNA, and a small (S) RNA
C;Superfamily: bunyavirus nonstructural protein
Query Match 43.2%; Score 41; DB 1; Length 92;
Best Local Similarity 37.5%; Pred. No. 20; Indels 2; Gaps 0;
Matches 6; Conservative 8; Mismatches 2;
CY 1 RIAKRGKLVYDSAR 16
DB 48 RVSQGRQILNLESGR 63
RESULT 24
T13595
hypothetical protein 80H7.10 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13595
R;Benos, P.
Submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17667
A;Accession: T13595
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-196 <BEN>
A;Cross-references: EMBL:AL031027; NID:e1313443; PID:e1427308; PIDN:CAB41536.1
C;Genetics:
A;Cross-references: FlyBase:FBgn0000481

A;Introns: 52/1; 96/3; 140/3
A;Note: EG:80H7.10
Query Match 43.2%; Score 41; DB 2; Length 196;
Best Local Similarity 64.3%; Pred. No. 41; Indels 4; Gaps 0;
Matches 9; Conservative 1; Mismatches 4;
CY 3 AKRGKLVYDSAR 16
DB 45 AWEGRKLEIDYDWAR 58
RESULT 25
E70945
hypothetical protein Rv2054 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: E70945
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Searles, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70945
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-237 <COL>
A;Cross-references: GB:AL021899; GB:AL123456; NID:93242282; PIDN:CAA17268.1; PID:93242282
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv2054
C;Superfamily: carboxymethylglutaminase
Query Match 43.2%; Score 41; DB 2; Length 237;
Best Local Similarity 52.9%; Pred. No. 49; Indels 6; Gaps 0;
Matches 9; Conservative 2; Mismatches 6;
CY 2 IAKRGKLVYDSARHH 18
DB 79 LTKRGALDDILAARDH 95
RESULT 26
T25732
hypothetical protein F25B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T25732
R;Gattung, S.
Submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid F25B4.
A;Reference number: Z20076
A;Accession: T25732
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-402 <GAT>
A;Cross-references: EMBL:U64842; PIDN:AAB37080.1; GSPDB:GN00023; CESP:F25B4.1
A;Experimental source: strain Bristol N2; clone F25B4
C;Genetics:
A;Gene: CESP:F25B4.1
A;Map position: 5
A;Introns: 25/2; 87/2; 289/1
C;Superfamily: aminomethyltransferase
Query Match 43.2%; Score 41; DB 2; Length 402;
Best Local Similarity 43.8%; Pred. No. 79; Indels 5; Gaps 0;
Matches 7; Conservative 4; Mismatches 5;
CY 2 IAKRGKLVYDSARH 17
DB 288 VAKRRETLDFPGASH 303

RESULT 27

C71055
Probable RNA methyltransferase - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: C71055
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: C71055
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-407 <KAW>
A:Cross-references: GB:AP000005; NID:G3236132; PIDN:BAA30237.1; PID:G3257554
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH137
C:Superfamily: hypothetical protein HI0333

Query Match 43.2%; Score 41; DB 2; Length 407;
Best Local Similarity 61.5%; Pred. No. 80;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IAKGRKLVVDYDS 14
:|||||:|:
Db 289 LAKGFKVGVGFD 301

RESULT 28

D89057
protein K09H11.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: D89057
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D89057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-974 <STO>
A:Cross-references: GB:chr_V; PIDN:AAB52261.1; PID:G1938424; GSPDB:GN00023; CESP:K09H11.
A:Gene: K09H11.1
A:Map position: 5

Query Match 43.2%; Score 41; DB 2; Length 974;
Best Local Similarity 72.7%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GRKLVVDYDSAR 16
|||||:|:
Db 862 GRKLVQVDSLR 872

RESULT 29

TS0914
hypothetical membrane protein [imported] - Rubrivivax gelatinosus
C:Species: Rubrivivax gelatinosus
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: TS0914
R:Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
submitted to the EMBL Data Library, November 1999
A:Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt
A:Reference number: 225270

A:Accession: TS0914
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1001 <NAG>
A:Cross-references: EMBL:AB034704; PIDN:BAA94067.1
A:Experimental source: strain Ili44
C:Genetics:
A:Note: ORF1001

Query Match 43.2%; Score 41; DB 2; Length 1001;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RIAKGRKLVVDYDSAR 16
:|||||:|:
Db 772 RFARQGRLFSRDDAR 787

RESULT 30

H65033
hypothetical protein in purL-dpj intergenic region - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C:Accession: H65033
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H65033
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-306 <BLAT>
A:Cross-references: GB:AE000342; GB:U00096; NID:G1788907; PIDN:AAC75614.1; PID:G1788913;
A:Experimental source: strain K-12, substrain MGL655
C:Genetics:
A:Gene: yfjH
C:Superfamily: hypothetical protein ybbH

Query Match 42.6%; Score 40.5; DB 1; Length 306;
Best Local Similarity 42.9%; Pred. No. 74;
Matches 9; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

Qy 2 IAKGRKLVVDY----DSARH 17
:|:|:|:|:
Db 38 LAQSDKKLADYLLQLQPDARH 58

RESULT 31

C91057
hypothetical protein ECs3427 [imported] - Escherichia coli (strain O157:H7, substrain R)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C:Accession: C91057
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatcori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036850.1; PID:G13362898; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs3427
C:Superfamily: hypothetical protein ybbH

Query Match 42.6%; Score 40.5; DB 2; Length 306;
Best Local Similarity 42.9%; Pred. No. 74;
Matches 9; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

A;Residues: 1-458 <KAN>
 A;Cross-references: EMBL:D64005; GB:AB001339; NID:q1001779; PIDN:BAA10708.1; PID:q100182
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Species: sensory transduction histidine kinase sll0798; sensor histidine kinase hcr
 C;Superfamily: sensor histidine kinase homology <SHK>
 F193-44/Domain: sensor histidine kinase homology <SHK>

Query Match 42.6%; Score 40.5; DB 2; Length 458;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 4 KGRKRLVDYDSARHH 18
 |||||
 DB 167 KGRSLVEYD---RH 178
 |||||

RESULT 37
 B35387
 hypothetical protein (korC 5' region) - plasmid RK2 (fragment)
 C;Species: plasmid RK2
 C;Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 19-Dec-1997
 C;Accession: B35387
 R;Kornacki, J.A.; Burlage, R.S.; Figurski, D.H.
 J. Bacteriol. 172, 3040-3050, 1990
 A;Title: The kil-kor regulon of broad-host-range plasmid RK2: nucleotide sequence, poly
 A;Reference number: A35387; MUID:90264294; PMID:2160396
 A;Accession: B35387
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-225 <KOR>
 A;Cross-references: GB:M32794

Query Match 42.1%; Score 40; DB 2; Length 225;
 Best Local Similarity 53.8%; Pred. No. 67;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIAKGRKRLVDYD 13
 |||||
 DB 196 RINRGRKVCYED 208
 |||||

RESULT 38
 AG3175
 hypothetical protein attE [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pl
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AG3175
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AG3175
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-264 <KUR>
 A;Cross-references: GB:AE008687; PIDN:AAL4821.1; PID:G17743560; GSPD3:GN00188
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: attE
 A;Genome: plasmid

Query Match 42.1%; Score 40; DB 2; Length 264;
 Best Local Similarity 57.1%; Pred. No. 78;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IAKGRKRLVDYDGA 15
 |||||
 DB 108 ITRGRKITDLDEA 121
 |||||

RESULT 39
 B81288
 hypothetical protein Cj1429c [imported] - Campylobacter jejuni (strain NCTC 11168)
 C;Species: Campylobacter jejuni
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 C;Accession: B81288
 R;Parkhill, J.; Wren, B.W.; Murgall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
 Nature 403, 665-668, 2000
 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hye
 A;Reference number: A81250; MUID:20150912; PMID:10688204
 A;Accession: B81288
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <PAR>
 A;Cross-references: GB:ALJ139078; GB:ALJ11168; NID:G6968723; PIDN:CAB73853.1; PID:G6968885
 A;Experimental source: serotype O2, strain NCTC 11168
 C;Genetics:
 A;Gene: Cj1429c
 C;Superfamily: Campylobacter jejuni hypothetical protein Cj1429c

Query Match 42.1%; Score 40; DB 2; Length 308;
 Best Local Similarity 42.9%; Pred. No. 89;
 Matches 6; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 2 IAKGRKRLVDYDGA 15
 |||||
 DB 124 MAQRGPKVIEYDAS 137
 |||||

RESULT 40
 H70390
 conserved hypothetical protein aq_1056 - Aquifex aeolicus
 C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 15-Jun-2001
 C;Accession: H70390
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
 V.
 Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:98196666; PMID:9537320
 A;Accession: H70390
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-426 <AQF>
 A;Cross-references: GB:AE000720; NID:G2983529; PIDN:AAC07117.1; PID:G2983542; GB:AE00065
 A;Experimental source: strain VFS
 C;Genetics:
 A;Gene: aq_1056
 C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF0821

Query Match 42.1%; Score 40; DB 2; Length 426;
 Best Local Similarity 41.2%; Pred. No. 1.2e+02;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 IAKGRKRLVDYDSARHH 18
 |||||
 DB 143 LVAKGKKLVDFGFRRAH 159
 |||||

RESULT 41
 T49986
 lectin-like protein kinase-like - Arabidopsis thaliana
 N;Alternate names: protein F12B17.120
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 15-Sep-2000
 C;Accession: T49986
 R;Bevan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A;Reference number: Z25026
 A;Accession: T49986
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-830 <WIL>
A;Cross-references: EMBL:Z79596; PIDN:CAB01857.1; GSPDB:GN00028; CESP:C02C6.1
A;Experimental source: clone C02C6
C;Genetics:
A;Gene: CESP:C02C6.1
A;Map position: X
A;Introns: 56/2; 131/1; 333/2; 501/2; 593/2; 686/3; 815/2
C;Superfamily: human dynamin II; pleckstrin repeat homology

Query Match 42.1%; Score 40; DB 2; Length 830;
Best Local Similarity 46.2%; Pred. NO. 2.2e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps

QY 4 KRGKRLVDYDSAR 16
| | | | | | | | | | | | | | | | | | | | | |
DB 88 KKGRFVDFDAVR 100

RESULT 44
H64367
dolichyl-phosphate mannose synthase - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: H64367
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.;
Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: H64367
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-229 <BUL>
A;Cross-references: GB:U67504; GB:L77117; NID:gi591248; PIDN:AA898538.1; PID:
C;Genetics:
A;Map position: REV482606-481917
C;Superfamily: Methanobacterium thermoautotrophicum dolichyl-phosphate mannose

Query Match 41.6%; Score 39.5; DB 2; Length 229;
Best Local Similarity 42.1%; Pred. NO. 82;
Matches 8; Conservative 6; Mismatches 4; Indels 1; Gaps

QY 1 RIAKRGKRLV-DYDSARHH 18
| | | | | | | | | | | | | | | | | | | | | |
DB 185 QLAKGKXIVEEVSVETH 203

RESULT 45
T31023
conserved hypothetical protein 108 - Sulfolobus sp. plasmid pNOB8
C;Species: Sulfolobus sp.
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31023
R;She, Q.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.
Extremophiles 2, 417-425, 1998
A;Title: Genetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid
A;Reference number: Z20959; MUID:99044580; PMID:9827331
A;Accession: T31023
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-97 <SHE>
A;Cross-references: EMBL:AJ010405; NID:e1351926; PID:e1351945; PIDN:CAA09129.1
A;Experimental source: strain NOB8H2
C;Genetics:
A;Genome: plasmid pNOB8

Db ||:|:|:|:|
77 RVSKGLEVDY 88

RESULT 46

G89986 hypothetical protein SA1779 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: G89986

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino

ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; PMID:21311952; PMID:11418146

A:Accession: G89986

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-99 <KUR>

A:Cross-references: GB:BA000018; PID:g13701763; PIDN:BA843056.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA1779

Query Match 41.1%; Score 39; DB 2; Length 99;

Best Local Similarity 50.0%; Pred. No. 46;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRGRKLVVDYDSARH 17

||:|:|:|:|

Db 35 KRDKLTYDASKH 48

RESULT 47

A86199 hypothetical protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A86199

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; PMID:21016719; PMID:11130712

A:Accession: A86199

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-165 <STO>

A:Cross-references: GB:AB005172; NID:g8927670; PIDN:AAF82161.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 41.1%; Score 39; DB 2; Length 165;

Best Local Similarity 53.3%; Pred. No. 73;

Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 KRGRKLVVDYDSARHH 18

||:|:|:|:|

Db 125 KHGYSNDYSYRHH 139

RESULT 48

T01186

protein kinase (EC 2.7.1.37) touselled 4 - maize (fragment)

N:Alternate names: touselled-like kinase 4

C:Species: Zea mays (maize)

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Sep-1999

C:Accession: T01186

R:Yoon, E.S.; Rivin, C.J.

submitted to the EMBL Data Library, July 1997

A:Description: Analysis of the maize TOUSLED-LIKE KINASE gene family.

A:Reference number: Z14254

C:Accession: T01186

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-219 <YOO>

A:Cross-references: EMBL:AF012889; NID:g2326230; PIDN:AAB66608.1; PID:g2326231

A:Experimental source: strain W22; seedling shoot

C:Genetics:

A:Gene: MTK-4

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C:Keywords: phosphotransferase

Query Match 41.1%; Score 39; DB 2; Length 219;

Best Local Similarity 60.0%; Pred. No. 95;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRGRKLVVDYD 13

||:|:|:|:|

Db 62 KRGRKLVVDYD 71

RESULT 49

T01185

protein kinase (EC 2.7.1.37) touselled 1 - maize (fragment)

N:Alternate names: touselled-like kinase 1

C:Species: Zea mays (maize)

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Sep-1999

C:Accession: T01185

R:Yoon, E.S.; Rivin, C.J.

submitted to the EMBL Data Library, July 1997

A:Description: Analysis of the maize TOUSLED-LIKE KINASE gene family.

A:Reference number: Z14254

C:Accession: T01185

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-224 <YOO>

A:Cross-references: EMBL:AF012888; NID:g2326228; PIDN:AAB66607.1; PID:g2326229

A:Experimental source: strain B73; ear

C:Genetics:

A:Gene: MTK-1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C:Keywords: phosphotransferase

Query Match 41.1%; Score 39; DB 2; Length 224;

Best Local Similarity 60.0%; Pred. No. 97;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRGRKLVVDYD 13

||:|:|:|:|

Db 67 KRGRKLVVDYD 76

RESULT 50

T49291

hypothetical protein T16L24.50 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49291

R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.;

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25017

A:Accession: T49291

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-259 <DAN>

A:Cross-references: EMBL:AL138659; GSPDB:GN00061; ATSP:T16L24.50

A:Experimental source: cultivar Columbia; BAC clone T16L24

C:Genetics:

A:Gene: ATSP:TI6L24.50

A:Map position: 3
A:introns: 47/3; 80/3; 131/2

Query Match 41.1%; Score 39; DB 2; Length 259;
Best Local Similarity 85.7%; Pred. NO. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 YDSARHH 18

|||:||||
Db 227 YDSRRHH 233

Search completed: March 4, 2004, 17:47:00
Job time : 20.6774 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:32:31 ; Search time 12.1935 Seconds
(without alignments)
76.865 Million cell updates/sec

Title: US-10-069-540a-2_COPY_138_155

Perfect score: 95

Sequence: 1 RIAGRGRKLVYDSARHH 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	95	100.0	588	1 BIN1 MOUSE
2	95	100.0	588	1 BIN1 RAT
3	95	100.0	593	1 BIN1 HUMAN
4	89	93.7	682	1 AMPH CHICK
5	89	93.7	683	1 AMPH RAT
6	89	93.7	695	1 AMPH HUMAN
7	45	47.4	288	1 YMH3 CAEL
8	43	45.3	204	1 COAE RALSO
9	43	45.3	264	1 HO3 SCHPO
10	43	45.3	357	1 YAK7 SCHPO
11	43	45.3	775	1 ANR5 MOUSE
12	43	45.3	848	1 DYN3 RAT
13	42	44.2	130	1 YC35 SXECO
14	42	44.2	906	1 FOX2 CANTR
15	41	43.2	92	1 VNST BUNSH
16	41	43.2	321	1 MIAA RHIL0
17	41	43.2	464	1 WCM SHIFL
18	40.5	42.6	282	1 YFHH ECOLI
19	40	42.1	406	1 SNX6 HUMAN
20	40	42.1	461	1 XLB2 ECOLI
21	40	42.1	752	1 GC20 YEAST
22	40	42.1	830	1 DYN1 CAEL
23	39.5	41.6	229	1 Y544 METJA
24	39	41.1	356	1 LEU3 RALSO
25	39	41.1	512	1 MSL3 DROME
26	39	41.1	776	1 ANR5 HUMAN
27	39	41.1	918	1 QAL5 NEUCR
28	39	41.1	980	1 POLG LIV
29	39	41.1	981	1 YM48 YEAST
30	39	41.1	2894	1 YD96 METJA
31	38	40.0	203	1 YPT1 VOICLA
32	38	40.0	359	1 FLI1 EUCLG
33	38	40.0	413	1 ARGJ BRAJA

34	38	40.0	1	PD46 RAT
35	38	40.0	1	PD46 HUMAN
36	38	40.0	1	WCAW_ECOLI
37	38	40.0	1	YH33_CHRVO
38	38	40.0	1	YAI8_TREPA
39	38	40.0	1	PHR_NEUCR
40	38	40.0	1	NAD0_THEBR
41	38	40.0	1	STC2_STAAR
42	38	40.0	1	SECA_MYCSM
43	38	40.0	1	NOS1_HUMAN
44	38	40.0	1	NOS1_RABIT
45	38	40.0	1	KKX1_YEAST
46	38	40.0	1	SPCA_HUMAN
47	38	40.0	1	PLE1_CRIGR
48	38	40.0	1	PLE1_HUMAN
49	37.5	39.5	347	1 VCOM_ADEL2
50	37	38.9	88	1 RS15_HAEIN
51	37	38.9	91	1 Y022_ARCFU
52	37	38.9	128	1 Y453_ARCFU
53	37	38.9	145	1 RL13_STACA
54	37	38.9	147	1 YV59_CAEL
55	37	38.9	150	1 CKS1_YEAST
56	37	38.9	163	1 GVH2_HALNI
57	37	38.9	163	1 PRXH_HALN2
58	37	38.9	278	1 PRXH_EPMO2
59	37	38.9	315	1 LXD1_POHLE
60	37	38.9	331	1 MAN1_MOUSE
61	37	38.9	338	1 AROB_PYRAB
62	37	38.9	365	1 ISEF_PROST
63	37	38.9	376	1 MCL1_CITPR
64	37	38.9	439	1 PD46_MESAU
65	37	38.9	525	1 PD46_HUMAN
66	37	38.9	532	1 YKF3_CAEL
67	37	38.9	535	1 GCP_METJA
68	37	38.9	541	1 Y537_SYNY3
69	37	38.9	585	1 ASNS_MAIZE
70	37	38.9	624	1 PPS1_CAVPO
71	37	38.9	662	1 DCHS_HUMAN
72	37	38.9	697	1 SYGB_BUCBP
73	37	38.9	761	1 FIXI_RHILV
74	37	38.9	808	1 SYFB_BACHD
75	37	38.9	892	1 SVA_PYRAE
76	37	38.9	900	1 SVA_AERPE
77	37	38.9	925	1 SVA_METAP
78	37	38.9	926	1 SVA_METMA
79	37	38.9	1139	1 INAI_CAEL
80	37	38.9	1671	1 DPOL_PYRKO
81	36.5	38.4	70	1 RPOZ_THETN
82	36.5	38.4	107	1 I14K_TORMA
83	36.5	38.4	269	1 ML22_LACLC
84	36.5	38.4	358	1 VCOM_ADE40
85	36.5	38.4	431	1 SYS_NEIMA
86	36.5	38.4	431	1 SYS_NEIMB
87	36.5	38.4	638	1 PD44_MOUSE
88	36.5	38.4	643	1 PD44_RAT
89	36	37.9	51	1 RL39_METKA
90	36	37.9	88	1 RS15_ECOLI
91	36	37.9	88	1 RS15_SALTY
92	36	37.9	114	1 YZ11_METJA
93	36	37.9	164	1 NUSB_CHLFE
94	36	37.9	182	1 SVA_SULAC
95	36	37.9	188	1 KCV_THEAC
96	36	37.9	211	1 HIS5_RHOSH
97	36	37.9	231	1 RL1_BACHD
98	36	37.9	249	1 YF57_METJA
99	36	37.9	260	1 END_RAT
100	36	37.9	299	1 DH3I_CAEL
101	36	37.9	299	1 NODP_RHITR
102	36	37.9	324	1 PARB_TREPA
103	36	37.9	354	1 DCUP_XLFT
104	36	37.9	368	1 HISX_PYRAE
105	36	37.9	398	1 CGB2_BOVIN
106	36	37.9	398	1 CGB2_MOUSE

Q63081	rattus norv
Q5084	homo sapien
P1244	escherichia
Q7x94	chromobacte
Q8381	treponema p
P27526	neurospora
P32382	thermoanaer
P17855	staphylococ
P1533	mycobacteri
P29475	homo sapien
O9132	oryctolagus
P34244	saccharomyc
P02549	homo sapien
Q9155	cricetus
Q15149	homo sapien
P36717	human adeno
P40389	haemophilus
Q0213	archaeoglob
Q29796	archaeoglob
Q00990	staphylococ
P50439	caenorhabdi
P20486	saccharomyc
Q8ht6	halobacteri
P33961	halobacteri
O64252	mycobacteri
P21309	photobacter
Q9wu40	mus musculu
Q9v1h9	pyrococcus
P72241	providencia
Q4845	citrobacter
P38660	mesocricetu
Q13087	homo sapien
P34266	caenorhabdi
Q58530	methanococc
P54148	synechocyst
P49094	zea mays (m
O54820	c.bifunctio
P19113	homo sapien
P59573	buchnera ap
Q33533	rhizobium l
Q8K896	bacillus ha
Q8zsv6	pyrobaculum
Q8y9X3	aeropyrum p
Q8cu79	methanosarc
Q8pwu0	methanosarc
Q30600	caenorhabdi
P77933	pyrococcus
Q8r9s7	thermoanaer
Q81499	torpedo mar
P50178	lactococcus
P48753	human adeno
Q9jt77	neisseria m
Q9jy95	neisseria m
P08003	mus musculu
P38659	rattus norv
Q8tuv3	methanopyru
P02371	escherichia
Q8xif9	salmonella
Q60273	methanococc
Q8kbs4	chlorobium
P35029	sulfolobus
Q9ht3	thermoplasm
O33565	rhodobacter
Q8ges5	bacillus ha
Q58952	methanococc
Q63190	rattus norv
Q9xti0	caenorhabdi
P52995	rhizobium t
Q83295	treponema p
Q87dvo	xylella fas
Q8zy17	pyrobaculum
O77689	bos taurus
P30276	mus musculu

RN [1] SEQUENCE FROM N.A. (ISOFORM IIA).
 RP TISSUE=Brain;
 RC MEDLINE=97341217; PubMed=9195986;
 RX Ramjaun A.R., Micheva K.D., Bouchalet I., McPherson P.S.;
 RA "Identification and characterization of a nerve terminal-enriched
 RT amphiphysin isoform."
 RL J. Biol. Chem. 272:16700-16706(1997).
 RN [2] SEQUENCE FROM N.A. (ISOFORMS IIA AND BIN1).
 RP TISSUE=Brain, and Skeletal muscle;
 RC MEDLINE=97327761; PubMed=9182667;
 RX Butler M.H., David C., Ochoa G.-C., Freyberg Z., Daniell L., Grabs D.,
 RA Crenona O., De Camilli P.;
 RT "Amphiphysin II (SH3P9; BIN1), a member of the amphiphysin/Rvs family,
 is concentrated in the cortical cytomatrix of axon initial segments
 and nodes of ranvier in brain and around T tubules in skeletal
 muscle."
 RL J. Cell Biol. 137:1355-1367(1997).
 RN [3] SEQUENCE FROM N.A. (ISOFORM BIN1).
 RP TISSUE=Skeletal muscle;
 RC MEDLINE=96376973; PubMed=8782822;
 RX Sakamuro D., Elliott K.J., Wechsler-Reya R., Prendergast G.C.;
 RA "BIN1 is a novel Myc-interacting protein with features of a tumour
 RT suppressor."
 RL Nat. Genet. 14:69-76(1996).
 RN [4] REVISIONS TO N-TERMINUS.
 RP Sakamuro D., Elliott K.J., Wechsler-Reya R., Prendergast G.C.;
 RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [5] SEQUENCE FROM N.A. (ISOFORMS IIB; IIC1; IIC2 AND IID).
 RP TISSUE=Brain;
 RC MEDLINE=98264340; PubMed=9603201;
 RX Ramjaun A.R., McPherson P.S.;
 RA "Multiple amphiphysin II splice variants display differential clathrin
 RT binding: identification of two distinct clathrin-binding sites."
 RL J. Neurochem. 70:2369-2376(1998).
 RN [6] SEQUENCE FROM N.A. (ISOFORMS I12 AND I13).
 RP TISSUE=Brain;
 RC MEDLINE=97366618; PubMed=9223448;
 RX Tsutsui K., Maeda Y., Tsutsui K., Seki S., Tokunaga A.;
 RA "cDNA cloning of a novel amphiphysin isoform and tissue-specific
 RT expression of its multiple splice variants."
 RL Biochem. Biophys. Res. Commun. 236:178-183(1997).
 RN [7] SEQUENCE FROM N.A. (ISOFORMS I13; I13; BIN1-10-13; BIN1-13 AND
 RP BIN1+12A).
 RC TISSUE=Fibroblast;
 RX Wechsler-Reya R.J., Sakamuro D., Zhang J., Duhadaway J.,
 RA Prendergast G.C.;
 RT "Structural analysis of the human BIN1 gene. Evidence for tissue-
 RT specific transcriptional regulation and alternate RNA splicing."
 RL J. Biol. Chem. 272:31453-31458(1997).
 RN [8] SEQUENCE FROM N.A. (ISOFORM I12).
 RP Zhang J., Du W., Wechsler-Reya R.J., Duhadaway J., Sakamuro D.,
 RA Prendergast G.C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [9] SEQUENCE OF 133-593 FROM N.A.
 RP TISSUE=Brain;
 RC Xu W., Gibbs R.A.;
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [10] CHARACTERIZATION.
 RP TISSUE=Skeletal muscle;
 RC MEDLINE=98078712; PubMed=9418903;
 RX Wechsler-Reya R.J., Elliott K.J., Prendergast G.C.;
 RA "A role for the putative tumor suppressor Bin1 in muscle cell
 RT differentiation."
 RL Mol. Cell. Biol. 18:566-575(1998).
 CC -!- FUNCTION: May be involved in regulation of synaptic vesicle
 endocytosis. May act as a tumor suppressor and inhibits
 malignant cell transformation.
 CC -!- SUBUNIT: Heterodimer with AMPH. Binds SH3GLB1 (By similarity).
 Binds to SYNJ1 and DNMI through its SH3 domain, and to clathrin
 through a region outside of the SH3 domain. Also binds to alpha-
 adaptin. Interacts with the N-terminal transactivation domain of
 MYC in a manner requiring the integrity of the conserved MYC box
 regions 1 and 2.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Isoform I1a is
 found in the cytoplasm while isoform BIN1 is nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 Event-Alternative splicing; Named isoforms=11;
 Comment=Additional isoforms seem to exist;
 Name=I1A;
 IsoId=O00499-1; Sequence=Displayed;
 Name=I1B;
 IsoId=O00499-2; Sequence=VSP_000246, VSP_000252;
 Name=I1C1;
 IsoId=O00499-3; Sequence=VSP_000249;
 Name=I1C2;
 IsoId=O00499-4; Sequence=VSP_000246, VSP_000249;
 Name=I1D;
 IsoId=O00499-5; Sequence=VSP_000248;
 Name=I1I2;
 IsoId=O00499-6; Sequence=VSP_000246, VSP_000253;
 Name=I1I3;
 IsoId=O00499-7; Sequence=VSP_000246, VSP_000250;
 Name=BIN1;
 IsoId=O00499-8; Sequence=VSP_000246, VSP_000247, VSP_000250;
 Name=BIN1-10-13;
 IsoId=O00499-9; Sequence=VSP_000246, VSP_000251;
 Name=BIN1-13;
 IsoId=O00499-10; Sequence=VSP_000246, VSP_000247, VSP_000251;
 Name=BIN1+12A;
 IsoId=O00499-11; Sequence=VSP_000246, VSP_000247, VSP_000253;
 CC -!- TISSUE SPECIFICITY: ISOFORM I1A IS EXPRESSED ONLY IN THE BRAIN
 WHERE IT IS CONCENTRATED IN AXON INITIAL SEGMENTS AND NODES OF
 RANVIER. ISOFORM BIN1 IS WIDELY EXPRESSED WITH HIGHEST EXPRESSION
 IN SKELETAL MUSCLE.
 CC -!- PTM: Phosphorylated by protein kinase C (By similarity).
 CC -!- SIMILARITY: Contains 1 BAR domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 DR EMBL; AF040415; AAC51345.1; -
 DR EMBL; AF070576; AAC28646.1; -
 DR EMBL; U68485; AAC17461.1; -
 DR EMBL; AF001383; AAC61363.1; -
 DR EMBL; AF043898; AAC39710.1; -
 DR EMBL; AF043899; AAC39711.1; -
 DR EMBL; AF043900; AAC39712.1; -
 DR EMBL; AF043901; AAC39713.1; -
 DR EMBL; U87558; AAB63263.1; -
 DR EMBL; AF068914; AAC24126.1; -
 DR EMBL; AF068915; AAC24127.1; -
 DR EMBL; AF068916; AAC24128.1; -
 DR EMBL; AF068917; AAC23750.1; -
 DR EMBL; AF068918; AAC23751.1; -
 DR EMBL; U84004; AAC23440.1; -
 DR EMBL; U83999; AAC23440.1; JOINED.
 DR EMBL; U84001; AAC23440.1; JOINED.
 DR EMBL; U84002; AAC23440.1; JOINED.
 DR EMBL; U84003; AAC23440.1; JOINED.

DR EMBL; U84004; AAC23441.1; ALT INIT.
 DR EMBL; U83999; AAC23441.1; JOINED.
 DR EMBL; U84001; AAC23441.1; JOINED.
 DR EMBL; U84002; AAC23441.1; JOINED.
 DR EMBL; U84003; AAC23441.1; JOINED.
 DR PIR; JCS593; JCS593.
 DR TRANSFAC; T03490; -.
 DR Genew; HGNC:1052; BIN1.
 DR MIM; 601248; -.
 DR GO; GO:0015629; C:actin cytoskeleton; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0006899; P:nonsselective vesicle transport; TAS.
 DR GO; GO:0000074; P:regulation of cell cycle; TAS.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR004148; BAR_dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00002; SH3; 1.
 DR CytoSkelton; SH3 domain; Coiled coil.
 FT DOMAIN 10 84 COILED COIL (POTENTIAL).
 FT DOMAIN 144 191 COILED COIL (POTENTIAL).
 FT DOMAIN 609 682 SH3.
 SQ SEQUENCE 682 AA; 75205 MW; 61617F494F38EB20 CRC64;
 Query Match 93.7%; Score 89; DB 1; Length 682;
 Best Local Similarity 94.4%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RIAKRGKRLVDYDSARHH 18
 Db 134 RIAKRGKRLVDYDSARHH 151
 RESULT 5
 AMPH_RAT
 ID AMPH_RAT STANDARD; PRT; 683 AA.
 AC Q08838;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amphiphysin.
 GN AMPH OR AMPH1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=98009145; PubMed=9348539;
 RA Wigge P., Kohler K., Vallis Y., Owen D., Hunt S.P., McMahon H.T.;
 RT "Amphiphysin heterodimers: potential role in clathrin-mediated
 endocytosis".
 RL Mol. Biol. Cell 8:2003-2015 (1997).
 CC -1- FUNCTION: May participate in mechanisms of regulated exocytosis in
 synapses and certain endocrine cell types. May control the
 properties of the membrane associated cytoskeleton (By

DR EMBL; U84004; AAC23441.1; ALT INIT.
 DR EMBL; U83999; AAC23441.1; JOINED.
 DR EMBL; U84001; AAC23441.1; JOINED.
 DR EMBL; U84002; AAC23441.1; JOINED.
 DR EMBL; U84003; AAC23441.1; JOINED.
 DR PIR; JCS593; JCS593.
 DR TRANSFAC; T03490; -.
 DR Genew; HGNC:1052; BIN1.
 DR MIM; 601248; -.
 DR GO; GO:0015629; C:actin cytoskeleton; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0006899; P:nonsselective vesicle transport; TAS.
 DR GO; GO:0000074; P:regulation of cell cycle; TAS.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR004148; BAR_dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00002; SH3; 1.
 DR CytoSkelton; SH3 domain; Coiled coil; Endocytosis;
 FT DOMAIN 15 42 COILED COIL (POTENTIAL).
 FT DOMAIN 193 267 COILED COIL (POTENTIAL).
 FT DOMAIN 378 421 CLATHRIN-BINDING
 FT DOMAIN 520 592 SH3.
 FT VARSPPLIC 174 204 Missing (in isoform IIB, isoform IIC2,
 isoform IIC2, isoform IIC3, isoform BIN1,
 isoform BIN1+12A, isoform BIN1-10-13 and
 isoform BIN1-13).
 FT VARSPPLIC 285 P -> PRKSKLFSRLRRKN (in isoform BIN1,
 isoform BIN1+12A and isoform BIN1-13).
 FT VARSPPLIC 335 /FTID=VSP_000247.
 FT VARSPPLIC 377 Missing (in isoform IID).
 FT VARSPPLIC 421 /FTID=VSP_000248.
 FT VARSPPLIC 421 Missing (in isoform IIC1 and isoform
 IIC2).
 Query Match 100.0%; Score 95; DB 1; Length 593;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RIAKRGKRLVDYDSARHH 18
 Db 139 RIAKRGKRLVDYDSARHH 156
 RESULT 4
 AMPH_CHICK
 ID AMPH_CHICK STANDARD; PRT; 682 AA.
 AC P50478;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amphiphysin.
 GN AMPH.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tetra-hybrid; TISSUE=Forebrain;
 RX MEDLINE=92331604; PubMed=1628617;
 RA Lichte B., Voh R.W., Meyer H.E., Kilimann M.W.;
 RT "Amphiphysin, a novel protein associated with synaptic vesicles".
 RL EMBO J. 11:2521-2530 (1992).
 CC -1- FUNCTION: May participate in mechanisms of regulated exocytosis in
 synapses and certain endocrine cell types. May control the

CC similarity).

CC -!- SUBUNIT: Heterodimer with BIN1. Binds SH3GLB1 (By similarity).

CC -!- SUBCELLULAR LOCATION: Peripheral membrane protein associated with

CC the cytoplasmic surface of synaptic vesicles (By similarity).

CC -!- SIMILARITY: Contains 1 BAR domain.

CC -!- SIMILARITY: Contains 1 SH3 domain.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; Y13381; CAA73808.1; -

CC InterPro; IPR003005; Amphiphysin.

CC InterPro; IPR003017; Amphiphysin_1.

CC InterPro; IPR006632; BAR.

CC InterPro; IPR004148; BAR_dom.

CC Pfam; PF03114; BAR; 1.

CC Pfam; PF00018; SH3; 1.

CC PRINTS; PR01251; AMPHIPHYSIN.

CC PRINTS; PR00452; SH3DOMAIN.

CC ProDom; PD003208; Amphiphysin_1; 1.

CC ProDom; PD000066; SH3; 1.

CC SMART; SM00721; BAR; 1.

CC SMART; SM00326; SH3; 1.

CC PROSITE; PS00002; SH3; 1.

CC CytoSkelton; SH3 domain; Coiled coil.

CC FT DOMAIN 10 83 COILED COIL (POTENTIAL).

CC FT DOMAIN 144 191 COILED COIL (POTENTIAL).

CC FT DOMAIN 610 683 SH3.

CC SQ SEQUENCE 683 AA; 74877 MW; 7FEA4A9E5A1F6631 CRC64;

Query Match 93.7%; Score 89; DB 1; Length 683;

Best Local Similarity 94.4%; Pred. No. 2 3e-07;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAGKGRKLVDYDSARHH 18

DB 134 RIAGKSRKLVDYDSARHH 151

RESULT 6

AMPH HUMAN STANDARD; PRT; 695 AA.

AC P49418; O43538;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Amphiphysin.

GN AMPH OR AMPHI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Cerebellum;

RX MEDLINE=94357284; PubMed=8076697;

RA David C., Solimena M., de Camilli P.;

RT "Autoimmunity in stiff-man syndrome with breast cancer is targeted to

RT the C-terminal region of human amphiphysin, a protein similar to the

RT yeast proteins, Rvs167 and Rvs161.";

RL FEBS Lett. 351:73-79(1994).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=95276740; PubMed=7757077;

RA Yamamoto R., Li X., Winter S., Francke U., Kilimann M.W.;

RT "Primary structure of human amphiphysin, the dominant autoantigen of

RT paraneoplastic stiff-man syndrome, and mapping of its gene (AMPH) to

RT Chromosome 7p13-p14.";

RL Hum. Mol. Genet. 4:265-268(1995).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=98174372; PubMed=9513187;

RA Floyd S.R., Butler M.H., Cremona O., David C., Freyberg Z., Zhang X.,

RA Solimena M., Tokunaga A., Ishizu H., Tsutsui K., De Camilli P.V.;

RT "Expression of amphiphysin 1, an autoantigen of paraneoplastic

RT neurological syndromes, in breast cancer.";

RL Mol. Med. 4:29-39(1998).

CC -!- FUNCTION: May participate in mechanisms of regulated exocytosis in

CC synapses and certain endocrine cell types. May control the

CC properties of the membrane associated cytoskeleton.

CC -!- SUBUNIT: Heterodimer of AMPH and AMPHI (By similarity).

CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC SURFACE OF

CC SYNAPTIC VESICLES.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1; Synonyms=128 kDa;

CC IsoId=P49418-1; Sequence=Displayed;

CC Name=2; Synonyms=108 kDa;

CC IsoId=P49418-2; Sequence=VSP_000245;

CC -!- TISSUE SPECIFICITY: Neurons, certain endocrine cell types and

CC spermatocytes.

CC -!- DISEASE: Patients with stiff-man syndrome, a rare disease of the

CC central nervous system characterized by progressive rigidity of

CC the body musculature with superimposed painful spasms, have

CC antibodies against AMPH.

CC -!- SIMILARITY: Contains 1 BAR domain.

CC -!- SIMILARITY: Contains 1 SH3 domain.

CC -----

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CC -----

CC EMBL; U07616; AAA21865.1; -

CC EMBL; X81438; CAA57197.1; -

CC EMBL; AF034996; AAC02977.1; -

CC PIR; S62400; S62400.

CC PDB; 1KY7; 12-JUN-02.

CC Genew; HGNC:471; AMPH.

CC MIN; 600418; -

CC GO; GO:0015629; C:actin cytoskeleton; TAS.

CC GO; GO:0008021; C:synaptic vesicle; TAS.

CC GO; GO:0006897; P:endocytosis; TAS.

CC GO; GO:0007268; P:synaptic transmission; TAS.

CC InterPro; IPR003005; Amphiphysin.

CC InterPro; IPR003017; Amphiphysin_1.

CC InterPro; IPR006632; BAR.

CC InterPro; IPR004148; BAR_dom.

CC InterPro; IPR001452; SH3.

CC Pfam; PF03114; BAR; 1.

CC Pfam; PF00018; SH3; 1.

CC PRINTS; PR01251; AMPHIPHYSIN.

CC PRINTS; PR00452; SH3DOMAIN.

CC ProDom; PD003208; Amphiphysin_1; 1.

CC ProDom; PD000066; SH3; 1.

CC SMART; SM00721; BAR; 1.

CC SMART; SM00326; SH3; 1.

CC PROSITE; PS00002; SH3; 1.

CC CytoSkelton; SH3 domain; Coiled coil; Alternative splicing;

CC 3D-structure.

CC FT DOMAIN 10 83 COILED COIL (POTENTIAL).

CC FT DOMAIN 144 191 COILED COIL (POTENTIAL).

CC FT DOMAIN 622 695 SH3.

CC FT VARSPLIC 425 466 Missing (in isoform 2).

CC FT /FTId=VSP_000245.

QY	2	IAKGRKLVYDSARH	18	
		DE	Protein hcb3 (Homolog of Bin3).	
		GN	HOB3 OR SPBC725.09C.	

OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP MEDLINE=21293007; PubMed=11274158;
 RX Routhier E.L., Burn T.C., Abbaszade I., Summers M., Albright C.F.,
 RA "Human BIN3 complements the F-actin localization defects caused by
 RT loss of Hob3p, the fission yeast homolog of Rvs16lp.";
 RL J. Biol. Chem. 276:21670-21677(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehraich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=PR745;
 RX MEDLINE=98162722; PubMed=9501991;
 RA Yoshikawa S., Kato K., Nakai K., Okayama H., Nojima H.;
 RA "Identification of open reading frames in Schizosaccharomycetes pombe
 RT cDNAs.";
 RL DNA Res. 4:363-369(1997).
 CC -!- FUNCTION: Involved in cytokinesis and septation where it has a
 CC role in the localization of F-actin.
 CC -!- SIMILARITY: Contains 1 BAR domain.
 CC
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 CC
 CC EMBL; AF275638; AAF86459.1; --
 CC EMBL; AL034352; CAA22181.1; --
 CC EMBL; D89200; RAAL3861.1; ALT_INIT.
 CC F01; T40661; T40661.
 CC GeneDB Spombe; SPBC725.09c; --
 CC InterPro; IPR003005; Amphiphysin.
 CC InterPro; IPR006632; BAR.
 CC Pfam; PF03114; BAR; 1.
 CC PRINTS; PR01251; AMPHIPHYSIN.

DR SMART; SM00721; BAR; 1.
 KW Septation; Cytoskeleton; Coiled coil.
 FT DOMAIN 25 65 COILED COIL (POTENTIAL).
 FT DOMAIN 165 187 COILED COIL (POTENTIAL).
 FT CONFLICT 93 93 Q -> L (IN REF. 3).
 FT CONFLICT 96 96 E -> K (IN REF. 3).
 SQ SEQUENCE 264 AA; 30094 MW; 845388582305AD4D CRC64;
 Query Match 45.3%; Score 43; DB 1; Length 264;
 Best Local Similarity 53.3%; Pred. No. 6.2;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 IAKRGKRLVDYDSAR 16
 Db 132 ITRNKKLHDDAMR 146
 RESULT 10
 YAK7 SCHPO STANDARD; PRT; 397 AA.
 ID YAK7 SCHPO
 AC Q09919; 1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein ClF7.07c in chromosome I.
 GN SPAC1F7.07C.
 OS Schizosaccharomycetes pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehraich H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe.";
 RL Nature 415:871-880(2002).
 RN [1]
 RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the FTR1 family.
 CC
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 CC EMBL; Z67998; CAA91954.1; --

Fri Mar 5 14:57:56 2004

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DR PIR: S62579; S62579.
DR GeneDB Spombe; SPAC1F7.07c; -.
DR InterPro: IPR004923; FTR1.
DR Pfam: PF03239; FTR1; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 61 81 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 292 312 POTENTIAL.
SQ SEQUENCE 397 AA; 44314 MW; 1D98E41AD1FD708F CRC64;

Query Match 45.3%; Score 43; DB 1; Length 397;
Best Local Similarity 52.9%; Pred. No. 9.6;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IAKRGKRLVDYDSARHH 18
||| ||| ||| |||
Db 323 IAKLGDKVLDLEMASSH 339

RESULT 11
ANR5_MOUSE STANDARD; PRT; 775 AA.
AC Q9D2J7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ankyrin repeat domain protein 5.
GN ANKRD5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/60; PubMed=11217851;
RX MEDLINE=21085660;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pasole G., Quackenbush J.,
RA Schirml L.M., Staehli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli K., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Havaehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
CC -!- SIMILARITY: Contains 8 ANK repeats.
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CC -----
CC EMBL: AK019547; BAB31791.1; -.
CC HSSP: P80144; 2MVO.
CC MGD: MGI:2441685; Ankr5.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR002048; EF-hand.
CC Pfam: PF00023; ank; 10.

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DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SMO0248; ANK; 10.
DR PROSITE; PS00088; ANK_REPEAT; 6.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat. 76 ANK 1.
FT REPEAT 47 213 ANK 2.
FT REPEAT 184 213 ANK 3.
FT REPEAT 217 246 ANK 4.
FT REPEAT 250 279 ANK 5.
FT REPEAT 524 553 ANK 6.
FT REPEAT 557 586 ANK 7.
FT REPEAT 590 619 ANK 8.
FT REPEAT 623 652 ANK 8.
SQ SEQUENCE 775 AA; 86903 MW; 51C11E1BC5151F00 CRC64;

Query Match 45.3%; Score 43; DB 1; Length 775;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IAKRGKRLVDYDSARHH 18
||| ||| ||| |||
Db 204 ILRGGEVNDNRHH 220

RESULT 12
DYN3_RAT STANDARD; PRT; 848 AA.
AC Q08877;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dynamin 3 (EC 3.6.1.50) (Dynamin, testicular) (T-dynamin).
GN DN3 OR DYN3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=93366923; PubMed=8360266;
RA Nakata T., Takamura R., Hirokawa N.;
RA "A novel member of the dynamin family of GTP-binding proteins is
RA expressed specifically in the testis.";
RT in producing microtubule-associated force-producing protein involved
RL J. Cell Sci. 105:1-5(1993).
CC -!- FUNCTION: Microtubule-associated force-producing protein involved
CC in producing microtubule bundles and able to bind and hydrolyze
CC GTP. Most probably involved in vesicular trafficking processes, in
CC particular endocytosis.
CC -!- CATALYTIC ACTIVITY: GTP + H(2)O = GDP + phosphate.
CC -!- SUBCELLULAR LOCATION: Microtubule-associated.
CC -!- TISSUE SPECIFICITY: Expressed in germ-cell-depleted testis,
CC indicating its expression in Sertoli cells.
CC -!- SIMILARITY: Belongs to the dynamin family.
CC -!- SIMILARITY: Contains 1 PH domain.
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CC -----
CC EMBL: D14076; BAA03161.1; -.
CC PIR: I55498; I55498.
CC HSSP: Q05193; 2DYN.
CC InterPro: IPR001401; Dynamin.
CC InterPro: IPR000375; Dynamin_central.
CC InterPro: IPR003130; GED.
CC InterPro: IPR001849; PH.
CC Pfam: PF00350; dynamin; 1.
CC Pfam: PF01031; dynamin_2; 1.

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DR Pfam; PF00212; GED; 1.
 DR Pfam; PF00169; PH; 1.
 DR PRINTS; PR00195; DYNAMIN.
 DR SMART; SM00053; DYNC; 1.
 DR SMART; SM00302; GED; 1.
 DR SMART; SM00233; PH; 1.
 DR PROSITE; PS00410; DYNAMIN; 1.
 DR PROSITE; PS00003; PH_DOMAIN; 1.
 KW Hydrolyase; Motor protein; GTP-binding; Microtubule; Multigene family;
 KW Endocytosis.
 FT NP_BIND 38 45 GTP (BY SIMILARITY).
 FT NP_BIND 136 140 GTP (BY SIMILARITY).
 FT NP_BIND 205 208 GTP (BY SIMILARITY).
 FT DOMAIN 515 621 PH.
 FT SEQUENCE 848 AA; 95595 MW; 802365F6FC685F6 CRC64;
 Query Match 45.3%; Score 43; DB 1; Length 848;
 Best Local Similarity 46.2%; Pred. No. 22;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 5 RGRKLVVDYDSARH 17
 : : : : :
 DB 87 KGKFTDFEVRH 99
 : : : : :
 RESULT 13
 YC35_SKECO STANDARD; PRT; 130 AA.
 AC 096805;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical 15.1 kDa protein ycf35.
 GN YCF35.
 OS Skeletonema costatum (Marine centric diatom).
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
 OC Thalassiosirophyceae; Thalassiosirales; Skeletonemataceae;
 OC Skeletonema.
 ON NCBI_TaxID=2843;
 OX 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIES-323;
 RX MEDLINE=20189624; PubMed=10727090;
 RA Tada N., Shibata S., Otsuka S., Namba K., Oyazui H.;
 RT "Comparison of gene arrangements of chloroplasts between two centric
 RT diatoms, Skeletonema costatum and Odontella sinensis.";
 RL DNA Seq. 10:343-347(1999).
 CC -1- SIMILARITY: Belongs to the ycf35 family.
 CC
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 CC
 CC EMBL; AJ132264; CAA10626.1; -
 DR EMBL; AJ132264; CAA10626.1; -
 KW Chloroplast; Hypothetical protein.
 SQ SEQUENCE 130 AA; 15110 MW; 9A86185636915727 CRC64;
 Query Match 44.2%; Score 42; DB 1; Length 130;
 Best Local Similarity 40.0%; Pred. No. 4.3;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 4 KRGKLVVDYDSARH 18
 : : : : :
 DB 29 KREKKAIDANNKXH 43
 : : : : :
 RESULT 14
 FOX2_CANTR

ID FOX2_CANTR STANDARD; PRT; 906 AA.
 AC P22414;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (Multifunctional
 DE beta-oxidation protein) (MPP) [Includes: 2-enoyl-CoA hydratase
 DE (EC 4.2.1.-); D-3-hydroxyacyl CoA dehydrogenase (EC 1.1.1.-)].
 OS Candida tropicalis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5492;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 20336 / PK233;
 RX MEDLINE=89172062; PubMed=3267241;
 RA Nuttley W.M., Aitchison J.D., Rachubinski R.A.;
 RT "cDNA cloning and primary structure determination of the peroxisomal
 RT trifunctional enzyme hydratase-dehydrogenase-epimerase from the yeast
 RT Candida tropicalis PK233.";
 RL Gene 69:171-180(1988).
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 20336 / PK233;
 RX MEDLINE=92039009; PubMed=1937002;
 RA Aitchison J.D., Sloots J.A., Nuttley W.M., Rachubinski R.A.;
 RT "Glucose-responsive and oleic acid-responsive elements in the gene
 RT encoding the peroxisomal trifunctional enzyme of Candida
 RT tropicalis.";
 RL Gene 105:129-134(1991).
 RN 13
 RP SIMILARITY TO SHORT CHAIN DEHYDROGENASES OF N-TERMINAL DOMAIN.
 RX MEDLINE=90367890; PubMed=2394320;
 RA Baker M.E.;
 RT "A common ancestor for Candida tropicalis and dehydrogenases that
 RT synthesize antibiotics and steroids.";
 RL FASEB J. 4:3028-3032(1990).
 CC -1- FUNCTION: Second trifunctional enzyme acting on the beta-oxidation
 CC pathway for fatty acids, possessing hydratase-dehydrogenase-
 CC epimerase activities. Converts trans-2-enoyl-CoA via D-3-
 CC hydroxyacyl-CoA to 3-ketoacyl-CoA.
 CC -1- PATHWAY: Fatty acid beta-oxidation cycle; step 2.
 CC -1- PATHWAY: Fatty acid beta-oxidation cycle; step 3.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Peroxisomal.
 CC -1- INDUCTION: By growth on N-alkanes or fatty acids.
 CC -1- DOMAIN: Contains two SDR domains.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC
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 CC
 CC EMBL; M22765; AAA62847.1; -
 DR EMBL; M22765; AAA62847.1; -
 DR EMBL; X57854; CAA40989.1; -
 DR PIR; S32607; S32607.
 DR HSPSP; O70351; 1E38.
 DR InterPro; IPR002198; ADH short.
 DR InterPro; IPR002539; MacO dehydratas.
 DR Pfam; PF00106; adh short; 2.
 DR Pfam; PF01575; MacO dehydratas; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 2.
 DR Fatty acid metabolism; Multifunctional enzyme; Oxidoreductase; NAD;
 KW Lyase; Isomerase; Peroxisome; Repeat.
 FT DOMAIN 5 228 SHORT-CHAIN DEHYDROGENASE LIKE 1.
 FT DOMAIN 319 532 SHORT-CHAIN DEHYDROGENASE LIKE 2.
 FT SITE 904 906 MICROBODY TARGETING SIGNAL (POTENTIAL).

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FT NP BIND      12 36 NAD (BY SIMILARITY).
FT ACT SITE    163 163 BY SIMILARITY.
FT NP BIND     326 350 NAD (BY SIMILARITY).
FT ACT SITE    467 467 BY SIMILARITY.
FT CONFLICT    540 540 F -> S (IN REF. 1).
SQ SEQUENCE    906 AA; 99469 MW; 65AB88C8671C967B CRC64;

Query Match      44.2%; Score 42; DB 1; Length 906;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAKRGKLVYDYSR 16
DB 267 VAKRFSEILDYDSR 281

RESULT 15
VNST_BUNSH
ID_VNST_BUNSH STANDARD; PRT; 92 AA.
AC P03514;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Nonstructural protein NS-S.
OS Bunyavirus snowshoe hare.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.
OX NCBI_TaxID=11580;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=82274210; PubMed=7050911;
RX Bishop D.H.L., Gould K.G., Akashi H., Clerx-Van Haaster C.M.;
RA "The complete sequence and coding content of snowshoe hare bunyavirus small (S) viral RNA species.";
RT Nucleic Acids Res. 10:3703-3713(1982).
RL [2]
RN SEQUENCE OF 1-47 FROM N.A.
RP MEDLINE=82216937; PubMed=7086954;
RX Clerx-Van Haaster C.M., Akashi H., Auperin D.D., Bishop D.H.L.;
RA "Nucleotide sequence analyses and predicted coding of bunyavirus genome RNA species.";
RT J. Virol. 41:119-128(1982).
RL [1]
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DR EMBL; J02390; -; NOT_ANNOTATED_CDS.
DR EMBL; J02393; -; NOT_ANNOTATED_CDS.
DR PIR; A04105; MNVUSH.
DR InterPro; IPR000797; Bunya_Nss.
DR Pfam; PF01104; Bunya_NS-S_1.
DR ProDom; PD002170; Bunya_Nss; 1.
KW Nonstructural protein.
SQ SEQUENCE 92 AA; 10490 MW; B5CCF0C9FD4FA8C1 CRC64;

Query Match      43.2%; Score 41; DB 1; Length 92;
Best Local Similarity 37.5%; Pred. No. 4.3;
Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 RIAKRGKLVYDYSR 16
DB 48 RVSRGQRILNLSGR 63

RESULT 16
MIAA_RHILO
ID MIAA_RHILO STANDARD; PRT; 321 AA.
AC Q98KJ4;
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase) (IPTase) (IPPT).
DE MIAA OR MLL1448.
GN Rhizobium loti (Mesorhizobium loti).
OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RX Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
CC -!- FUNCTION: Catalyzes the first step in the biosynthesis of 2-methylthio-N6-(delta(2)-isopentenyl)-adenosine (MS2T[6A]) adjacent to the anticodon of several tRNA species (by similarity).
CC -!- CATALYTIC ACTIVITY: isopentenyl diphosphate + tRNA = diphosphate + tRNA containing 6-isopentenyladenosine.
CC -!- SIMILARITY: Belongs to the Ipp transferase family.
-----
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-----
DR EMBL; AF002997; BAB48820.1; -.
DR HAMAP; MF_00185; -.
DR InterPro; IPR002627; IPPT.
DR Pfam; PF01715; IPPT; 1.
DR ProDom; PD004674; IPPT; 1.
DR TIGRFAMs; TIGR00174; miaA; 1.
KW Transferase; Nucleotidyltransferase; tRNA processing; ATP-binding; Complete proteome.
FT NP BIND 24 31 ATP (POTENTIAL).
SQ SEQUENCE 321 AA; 35410 MW; D7FA3E4E7F4EB12F CRC64;

Query Match      43.2%; Score 41; DB 1; Length 321;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKRGKLVYDYSR 16
DB 193 AERGRPLDROTAR 206

RESULT 17
WCAM_SHIFL
ID WCAM_SHIFL STANDARD; PRT; 464 AA.
AC P37775;
DT 01-OCT-1994 (Rel. 30, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Colanic acid biosynthesis protein wcam.
GN WCAM OR SF2106 OR S2229.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=301 / Serotype 2a;

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RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Cao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Xu J.;
RA "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=2457T / ATCC 700930 / Serotype 2a;
RC STRAIN=2590274; PubMed=12704152;
RX Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Maynew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RA "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T";
RL Infect. Immun. 71:2775-2786(2003).
RN [3]
RN SEQUENCE OF 156-464 FROM N.A.
RP STRAIN=PE577 / Serotype 2a;
RC MEDLINE=94131953; PubMed=7507920;
RX Morona R., Mavris M., Fallarino A., Manning P.A.;
RA "Characterization of the rfc region of Shigella flexneri.";
RT J. Bacteriol. 176:733-747(1994)
CC -!- PATHWAY: Sline polysaccharide colanic acid biosynthesis.
CC -----
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CC -----
CC EMBL; AE015226; AA043645.1; -
DR EMBL; AE016985; AAP17474.1; -
DR EMBL; X71970; CAA50765.1; -
KW Lipopolysaccharide biosynthesis; Complete proteome.
FT CONFLICT 395 395 E -> D (IN REF. 3).
FT CONFLICT 398 398 V -> L (IN REF. 3).
FT CONFLICT 455 464 INFLPERRE -> Y (IN REF. 3).
SQ SEQUENCE 464 AA; 51191 MW; 0EC3BA7001C7D43D CRC64;
Query Match 43.28; Score 41; DB 1; Length 464;
Best Local Similarity 41.28; Pred.No. 25;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 TAAKGRKLVDDYSARHH 18
DB 432 VNERRQSSVDIDRINH 448
: ||| |||
: ||| |||

RESULT 18
YFHH_ECOLI
ID YFHH_ECOLI STANDARD; PRT; 282 AA.
AC P37767; P76588;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative HTH-type transcriptional regulator yfhh.
GN YFHH OR B2561.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]_TaxID=562;
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RA Nashimoto H., Saito N.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.

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RN [2] SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE OF 1-91 FROM N.A.
RX STRAIN=NWL37;
RX MEDLINE=92293954; PubMed=1602968;
RA Foulsten L.K., Larsen N.W., Molin S., Andersson P.;
RA "Analysis of an Escherichia coli mutant strain resistant to the cell-
RT killing function encoded by the gef gene family.";
RL Mol. Microbiol. 6:895-905(1992).
RN [4]
RP IDENTIFICATION.
RX MEDLINE=95075659; PubMed=7984428;
RA Borodovsky M., Rudd K.B., Koonin E.V.;
RT "Intrinsic and extrinsic approaches for detecting genes in a
RT bacterial genome.";
RL Nucleic Acids Res. 22:4756-4767(1994).
CC -1- SIMILARITY: Contains 1 SIS domain.
CC -1- SIMILARITY: Contains 1 HTH rpir-type DNA-binding domain.
CC
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CC
CC -----
CC EMBL; D64044; BAA10911.1; ALT INIT.
CC EMBL; U36841; AAA79823.1; ALT INIT.
CC EMBL; AE000342; AAC75614.1; ALT INIT.
CC EMBL; X72336; -; NOT ANNOTATED_CDS.
CC EcoGene; EG12308; yfHh.
CC InterPro; IPR000281; HTH_Rpir.
CC InterPro; IPR001347; SIS.
CC Pfam; PF01418; HTH_6; 1.
CC Pfam; PF01380; SIS; 1.
CC KW Hypothetical protein; Transcription regulation; DNA-binding;
CC Complete proteome.
FT DOMAIN 1 110 HTH RPIR-TYPE.
FT DOMAIN 126 282 SIS.
FT DNA_BIND 37 56 H-T-H MOTIF (POTENTIAL).
SQ SEQUENCE 282 AA; 30707 MW; FF0AE2A0BF4E3C48 CRC64;
Query Match 42.6%; Score 40.5; DB 1; Length 282;
Best Local Similarity 42.9%; Pred. No. 18;
Matches 9; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 2 IAKGRKLVLDY-----DSAPH 17
:|: ||||| |::|
Db 14 LAQSDKKLADYLLIQDPAH 34

RESULT 19
SNX6_HUMAN
-ID SNX6 HUMAN STANDARD; PRT; 406 AA.
AC Q9UNH7; Q9Y449;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sorting nexin 6 (TRAF4-associated factor 2).
GN SNX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21378165; PubMed=11485546;
RA Teasdale R.D., Loci D., Houghton F., Karlsson L., Gleeson P.A.;
RT "A large family of endosome-localized proteins related to sorting
  nexin 1.";
RL Biochem. J. 358:7-16(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Toji S., Yano M., Kobayashi A., Tanai K.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21276432; PubMed=11279102;
RA Parks W.T., Frank D.B., Huff C., Haft C.R., Martin J., Meng X.,
  de Caestecker M.P., McNally J.G., Reddi A., Taylor S.I., Roberts A.B.,
  Wang T., Lechleider R.J.;
RA "Sorting nexin 6, a novel SNX, interacts with the transforming growth
  factor-beta family of receptor serine-threonine kinases.";
RL J. Biol. Chem. 276:19332-19339(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA [4]
CC -1- FUNCTION: May be involved in several stages of intracellular
  trafficking.
CC -1- SUBUNIT: Interacts with TGF-beta receptors.
CC -1- SIMILARITY: Belongs to the sorting nexin family.
CC -1- SIMILARITY: Contains 1 phox homology (PX) domain.
CC -----
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CC -----
DR EMBL; AF121856; RAD27829.1; -
DR EMBL; U83194; AAD24202.1; ALT_INIT.
DR Genew; HGNC:14970; SNX6.
DR MIM; 606098; -
DR GO; GO:0005622; C:intracellular; NAS.
DR GO; GO:0005478; F:intracellular transporter activity; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006886; P:intracellular protein transport; NAS.
DR GO; GO:0007175; P:negative regulation of EGF receptor activity; NAS.
DR InterPro; IPR001683; PX.
DR Pfam; PF00787; PX; 1.
DR PROSITE; PS50195; PX; 1.
DR TRANSPORT; Protein transport.
DR DOMAIN 26 173
FT SEQUENCE 406 AA; 46648 MW; E3659DB19C59E1BB CRC64;
SQ
Query Match 42.1%; Score 40; DB 1; Length 406;
Best Local Similarity 58.3%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KRGRKLVVDNSA 15
: |||||:::
Db 312 RRSRLVDYENA 323

RESULT 20
KLB2 ECOLI
ID KLB2 ECOLI STANDARD; PRT; 461 AA.
AC PS2605;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE KLB2 protein.
GN KLB2
OS Escherichia coli.
OC Plasmid Incp-alpha RK2.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
  Enterobacteriaceae; Escherichia.

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OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94282811; PubMed=8014987;
RA Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Quiney D.G.,
  Haas D., Hellinski D.R., Schwab H., Stanisich V.A., Thomas C.M.;
RT "Complete nucleotide sequence of Birmingham Incp alpha plasmids.
  Compilation and comparative analysis.";
RL J. Mol. Biol. 239:623-663(1994).
RN [2]
RP SEQUENCE OF 1-237 FROM N.A.
RA Larsen M.H., Figurski D.H.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP -1- DOMAIN: CONTAINS A DNA-BINDING REGION JOINED BY A SHORT VARIABLE
  SEGMENT TO A REGION SIMILAR TO E. COLI KORA AND TRBA.
CC -----
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CC -----
DR EMBL; L27758; -; NOT ANNOTATED_CDS.
DR EMBL; U05773; AAA57449.1; -
DR Plasmid; DNA-binding; Transcription regulation.
RX SEQUENCE 461 AA; 51165 MW; 10EBFB2F2E00BD81 CRC64;
SQ
Query Match 42.1%; Score 40; DB 1; Length 461;
Best Local Similarity 53.8%; Pred. No. 37;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIARKEGRKLVVDY 13
: |||||:::
Db 432 RINRGRKVCYD 444

RESULT 21
GC20 YEAST
ID GC20 YEAST STANDARD; PRT; 752 AA.
AC P43535;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE GCN20 protein.
GN GCN20 OR YFR009W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
  Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95347344; PubMed=7670463;
RA Vazquez de Aldana C.R., Marton M.J., Hinnebusch A.G.;
RT "GCN20, a novel ATP binding cassette protein, and GCN1 reside in a
  complex that mediates activation of the eIF-2 alpha kinase GCN2 in
  amino acid-starved cells.";
RL EMBO J. 14:3184-3199(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=5288C / AB972;
RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
  Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
  Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
  Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-268(1995).
RN [3]
RP -1- FUNCTION: Positive effector of the eIF-2-alpha kinase activity of
  GCN2.
CC -1- SUBUNIT: Component of a heteromeric complex that includes GCN1 and
  GCN20.

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CC -1- SIMILARITY: Belongs to the ABC transporter family, EF3 subfamily.
CC -----
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CC -----
CC EMBL; U19971; AAA75444.1; -
CC DR EMBL; D50617; BAA09248.1; -
CC DR PIR; S56146; S56146.
CC DR GERM; S0001905; GCM20.
CC DR GO; GO:0005830; Cytosolic ribosome (sensu Eukarya); IDA.
CC DR GO; GO:0006448; P-regulation of translational elongation; IMP.
CC DR InterPro; IPR003593; AAA_ATPase.
CC DR InterPro; IPR003439; ABC_transporter.
CC DR Pfam; PF00005; ABC_tran; 2.
CC DR ProDom; PD000006; ABC_transporter; 2.
CC DR SMART; SM00382; AAA; 2.
CC DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
CC DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
CC KW ATP-binding; Repeat.
CC FT NP_BIND 232 239 ATP (POTENTIAL).
CC FT NP_BIND 565 572 ATP (POTENTIAL).
CC FT NP_BIND 752 752 AA; 85027 MW; 486FED10305A572E CRC64;
CC SQ SEQUENCE 752 AA; 85027 MW; 486FED10305A572E CRC64;

Query Match 42.1%; Score 40; DB 1; Length 752;
Best Local Similarity 37.5%; Pred. No. 63;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSAR 16
DB 152 KVAXRNKFKYKZASK 167

RESULT 22
DYN1 CAEEL STANDARD; PRT; 830 AA.
ID P39055; Q95QY9;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DYN1 OR C02C6.1.
GN DYN-1 OR C02C6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=Bristol N2;
RX MEDLINE=97439883; PubMed=9284229;
RA Clark S.G.; Shurland D.L.; Meyerowitz E.M.; Bargmann C.I.;
RA van der Bliek A.M.;
RT "A dynamin GTPase mutation causes a rapid and reversible temperature-
RT inducible locomotion defect in C. elegans."
RL Proc. Natl. Acad. Sci. U.S.A. 94:10438-10443(1997).
RN [2]
RP REVISIONS TO C-TERMINUS.
RP van der Bliek A.M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC STRAIN=Bristol N2;
RA Swinburne J.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Microtubule-associated force-producing protein involved
CC in producing microtubule bundles and able to bind and hydrolyze
CC GTP. Most probably involved in vesicular trafficking processes, in
CC particular endocytosis.

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CC -1- CATALYTIC ACTIVITY: GTP + H(2)O = GDP + phosphate.
CC -1- SUBCELLULAR LOCATION: Microtubule-associated.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=a;
CC IsoId=P39055-1; Sequence=Displayed;
CC Name=b;
CC IsoId=P39055-2; Sequence=VSP_001329;
CC Notes=No experimental confirmation available;
CC -1- SIMILARITY: Belongs to the dynamin family.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -----
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CC -----
CC EMBL; U29031; AAB72228.2; -
CC DR EMBL; Z79596; CAB01857.1; -
CC DR EMBL; Z79596; CAC42251.1; -
CC DR PIR; T18860; T18860.
CC DR KSSP; Q05153; 2DYN.
CC DR WormPep; C02C6.1a; CE07833.
CC DR WormPep; C02C6.1b; CE07832.
CC DR InterPro; IPR001401; Dynamin.
CC DR InterPro; IPR000375; Dynamin_central.
CC DR InterPro; IPR003130; GED.
CC DR InterPro; IPR001849; PH.
CC DR Pfam; PF00350; dynamin_1.
CC DR Pfam; PF01031; dynamin_2; 1.
CC DR Pfam; PF02212; GED; 1.
CC DR Pfam; PF00169; PH; 1.
CC DR PRINTS; PR00195; DYNAMIN.
CC DR SMART; SM00053; DYNG; 1.
CC DR SMART; SM00302; GED; 1.
CC DR SMART; SM00233; PH; 1.
CC DR PROSITE; PS00410; DYNAMIN; 1.
CC DR PROSITE; PS00003; PH_DOMAIN; 1.
CC KW Hydrolase; Motor protein; GTP-binding; Microtubule; Multigene family;
CC Endocytosis; Alternative splicing.
CC FT NP_BIND 40 47 GTP (BY SIMILARITY).
CC FT NP_BIND 138 142 GTP (BY SIMILARITY).
CC FT NP_BIND 207 210 GTP (BY SIMILARITY).
CC FT DOMAIN 519 624 PH.
CC FT VARSPPLIC 817 830
CC FT VSP PPGGPPPNMAPP -> VPTPSNGAPEIPARQVPRPF
CC (in isoform b).
CC /FTID=VSP_001329.
CC FT CONFLICT 734 734 R -> P (IN REF. 1).
CC SQ SEQUENCE 830 AA; 93407 MW; FF681250E51AB8A5 CRC64;

Query Match 42.1%; Score 40; DB 1; Length 830;
Best Local Similarity 46.2%; Pred. No. 70;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 KEGRLVYDSAR 16
DB 88 KGHFRVDFDAVR 100

RESULT 23
Y544 METJA STANDARD; PRT; 229 AA.
ID Y544 METJA
AC Q57954;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0544.
GN MJ0544.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;

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OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervilave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL Science 273:1058-1073 (1996).
 CC -----
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 CC -----
 CC EMBL: U67504; AAB98538.1; --
 DR F1R; H64367; H64367.
 DR TIGR; M00544; --
 DR InterPro; IPR001173; Glyco trans 2; 1.
 DR Pfam; PF00535; Glycos transf 2; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 229 AA; 26470 MW; D276082D92FCE26F CRC64;
 Query Match 41.6%; Score 39.5; DB 1; Length 229;
 Best Local Similarity 42.1%; Pred. No. 21;
 Matches 8; Conservative 6; Mismatches 4; Indels 1; Gaps 1;
 QY 1 RIAGRGKLV-DYDSARHH 18
 Db 185 QLAQKAGKIVRYVSEYH 203
 RESULT 24
 LEU3 RALSO
 ID LEU3 RALSO STANDARD; PRT; 356 AA.
 AC Q8XXF5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydrogenase)
 DE (IMDH) (3-IPM-DH)
 GN LEUB OR LEUB1 OR RSC1988 OR RS03417.
 OS Ralstonia solanaceum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choigne N., Claudel-Renard C., Cunac S., Demange N.,
 RA Gaspin C., Lavie M., Molzan A., Robert C., Saurin W., Schiex T.,
 RA Signier P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weisenbach J., Beucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502 (2002).
 CC -/- FUNCTION: Catalyzes the oxidation of 3-carboxy-2-hydroxy-4-
 CC methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2-
 CC oxopentanoate. The product decarboxylates to 4-methyl-2-
 CC oxopentanoate.

CC -/- CATALYTIC ACTIVITY: 3-carboxy-2-hydroxy-4-methylpentanoate +
 CC NAD(+) = 3-carboxy-4-methyl-2-oxopentanoate + NADH.
 CC -/- PATHWAY: Leucine biosynthesis; third step.
 CC -/- SUBUNIT: Homodimer (By similarity).
 CC -/- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -/- SIMILARITY: Belongs to the isocitrate and isopropylmalate
 CC dehydrogenase family. Leub subfamily 1.
 CC -----
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 CC -----
 CC EMBL: AL646067; CAD15690.1; ALT_INIT.
 DR HAMAP; MF 01033; -- 1.
 DR InterPro; IPR001804; Isodh.
 DR InterPro; IPR004429; Leub.
 DR Pfam; PF00180; isodh; 1.
 DR TIGR; TIGR00169; leub; 1.
 DR PROSITE; PS00470; IDH IMDH; 1.
 KW Oxidoreductase; Leucine biosynthesis; NAD; Complete proteome.
 SQ SEQUENCE 356 AA; 38218 MW; 3FFA88BACD020E8A CRC64;
 Query Match 41.1%; Score 39; DB 1; Length 356;
 Best Local Similarity 61.5%; Pred. No. 41;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 3 AKRGKLVYDSDA 15
 Db 180 AKRGKLVYDSDA 192
 RESULT 25
 MSL3 DROME
 ID MSL3 DROME STANDARD; PRT; 512 AA.
 AC P50536; Q81Q74; Q9VSI8.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Male-specific lethal-3 protein.
 GN MSL-3 OR CG8631.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=95285767; PubMed=7768187;
 RA Gorman M., Franke A., Baker B.S.;
 RT "Molecular characterization of the male-specific lethal-3 gene and
 RT investigations of the regulation of dosage compensation in
 RT Drosophila.";
 RL Development 121:463-475 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.C., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burris K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fother C., Gabriellani A.C., Garg N.R., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mankulov G., Malshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "the genome sequence of *Drosophila melanogaster*.";
 RA Science 287:2185-2195 (2000).
 RA [3]
 RN REVISIONS, AND ALTERNATIVE SPLICING.
 RP MEDLINE=2426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RA "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RA systematic review";
 RA Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RA [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP STRAIN=Berkeley; TISSUE=Embryo;
 RC MEDLINE=2426066; PubMed=12537569;
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
 RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
 RA Rubin G.M., Celniker S.E.;
 RA "A *Drosophila* full-length cDNA resource";
 RA Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
 CC -1- FUNCTION: The MSL proteins are essential for elevating
 CC transcription of the single X chromosome in the male (X chromosome
 CC dosage compensation). Mle, msl-1 and msl-3 are co-localized on the
 CC X chromosome. Each of the MSL proteins requires all the other MSLs
 CC for wild-type X-chromosome binding.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; MSL-3 IS ASSOCIATED WITH HUNDREDS
 CC OF DISCRETE SITES ALONG THE LENGTH OF THE X CHROMOSOME IN MALES
 CC AND NOT IN FEMALES, AND IS ALSO ASSOCIATED WITH 10-20 AUTOSOMAL
 CC SITES IN MALES.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=A;
 CC IsoId=P50536-1; Sequences=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=P50536-2; Sequences=VSP 007640;
 CC Note=No experimental confirmation available;
 CC -1- SIMILARITY: Contains 1 chromo domain.
 CC
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CC DR EMBL; X81321; CA557101.1; -
 DR EMBL; AE003560; AAF50612.1; -
 DR EMBL; AE003560; AAN2073.1; -
 DR EMBL; AY071074; AAL48696.1; -
 DR PIR; S48828; S48828.
 DR FlyBase; FBgn0002775; msl-3.
 DR GO; GO:0016456; C:dosage compensation complex (sensu *Drosophila*); NAS.
 DR GO; GO:0003682; P:chromatin binding; IDA.
 DR GO; GO:0009047; P:dosage compensation, by hyperactivation of . . . ; NAS.
 DR InterPro; IPR000953; Chromo.
 DR InterPro; IPR008676; MRG.
 DR Pfam; PF05712; MRG; 1.
 DR SMART; SM00298; CHROMO; 1.
 DR PROSITE; PS00598; CHROMO 1; FALSE NEG.
 DR PROSITE; PS50013; CHROMO 2; FALSE NEG.
 KW Chromatin regulator; Nuclear protein; Transcription regulation;
 KW Alternative splicing.
 KW DOMAIN 11 90
 FT VARSPLIC 1 34
 CHROMO.
 MTELRDETFPLFKHGEIVLCYEPDKSKARVLYTSK -> MPQ
 (in isoform 2).
 /FTId=VSP 007640.
 FT CONFLICT 184 184 A -> T (IN REF. 1).
 FT CONFLICT 352 352 V -> G (IN REF. 1).
 FT SEQUENCE 512 AA; 58852 MW; 3101BC92B2339951 CRC64;
 Query Match 41.1%; Score 39; DB 1; Length 512;
 Best Local Similarity 46.2%; Pred. No. 61;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RIARGRKLVLDYD 13
 DB 203 RVSRRLRLIEYD 215
 RESULT 26
 ANRS HUMAN STANDARD; PRT; 776 AA.
 ID ANRS HUMAN STANDARD; PRT; 776 AA.
 AC Q3NU02; Q9H6Y9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ankyrin repeat domain protein 5.
 GN ANKRD5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharasliadho M.H., Leversha M.A., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElay K., Nickerson A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20."
 RN Nature 414:865-871(2001).
 RN
 RP SEQUENCE OF 329-776 FROM N.A.
 RC TISSUE=Colon;
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shiobara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 8 ANK repeats.
 CC
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 CC
 CC EMBL; AL109754; CAB97618.2;
 DR EMBL; AK025322; BAB15111.1; ALT_INIT.
 DR HSP; P80144; 2M0Y.
 DR Genew; HGNC:15803; ANKRD5.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002048; EF-hand.
 DR Pfam; PF00023; ank; 10.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 11.
 DR PROSITE; PSS0088; ANK_REPEAT; 6.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 KW ANK repeat; Repeat.
 FT REPEAT 47 76 ANK 1.
 FT REPEAT 184 213 ANK 2.
 FT REPEAT 217 246 ANK 3.
 FT REPEAT 250 279 ANK 4.
 FT REPEAT 524 553 ANK 5.
 FT REPEAT 557 586 ANK 6.
 FT REPEAT 590 619 ANK 7.
 FT REPEAT 623 652 ANK 8.
 SQ SEQUENCE 776 AA; 86664 MW; 2F71F35AC4D337B6 CRC64;
 Query Match 41.1%; Score 39; DB 1; Length 776;
 Best Local Similarity 41.2%; Pred. No. 96;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 OY 2 IAKRGKLVDSARHH 18
 DB 204 ILERGEVNAFNDRRH 220
 RESULT 27
 ID QALIS NEUCR STANDARD; PRT; 918 AA.
 AC P11637;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DE Quinate repressor.
 GN QA-1S.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A / FGSC 987;
 RX MEDLINE=89293848; PubMed=2525625;
 RA Geever R.F., Huie L., Baum J.A., Tyler B.M., Patel V.B.,
 RA Rutledge B.J., Case M.E., Giles N.H.;

RT "DNA sequence, organization and regulation of the qa gene cluster of
 RT Neurospora crassa.";
 RL J. Mol. Biol. 207:15-34(1989).
 CC -1- FUNCTION: Repressor for enzymes and proteins of quinate
 CC metabolism.
 CC
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 CC
 CC EMBL; X14603; CAA32753.1;
 DR PIR; S04255; S04255.
 DR InterPro; IPR001381; DQuinase I.
 DR InterPro; IPR000623; Shik_kinase.
 DR InterPro; IPR006151; Shikimate_DH.
 DR Pfam; PF01487; DQuinase I; 1.
 DR Pfam; PF01488; Shikimate_DH; 1.
 DR Pfam; PF01202; SKI; 1.
 KW Quinate metabolism; Transcription regulation; Repressor; DNA-binding.
 SQ SEQUENCE 918 AA; 100580 MW; 67EDA399CBF098B2 CRC64;
 Query Match 41.1%; Score 39; DB 1; Length 918;
 Best Local Similarity 58.3%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 7 RKLVDYDSARHH 18
 DB 127 RKIVLESEFHH 138
 RESULT 28
 ID POLG LIV STANDARD; PRT; 980 AA.
 AC P22338;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix
 DE protein (Envelope protein M); Major envelope protein E; Nonstructural
 DE proteins NS1] (Fragment).
 OS Louping ill virus (Lil).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxID=11086;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91082437; PubMed=1845834;
 RA Shiu S.Y.W., Ayres M.D., Gould E.A.;
 RT "Genomic sequence of the structural proteins of louping ill virus:
 RT comparative analysis with tick-borne encephalitis virus.";
 RL Virology 180:411-415(1991).
 CC -1- SUBUNIT: The virion of this virus is a nucleocapsid covered by a
 CC lipoprotein envelope. The envelope consists of two proteins:
 CC protein M and glycoprotein E. The nucleocapsid is a complex of
 CC protein C and mRNA.
 CC
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 CC
 CC EMBL; M59376; AAA46281.1;
 DR PIR; A38523; A38523.
 DR HSP; P14336; 1SVB.
 DR InterPro; IPR001122; Flavi_capsidC.
 DR InterPro; IPR000336; Flavi_glycoproteE.

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DR InterPro; IPR000069; Flavi M.
DR InterPro; IPR001157; Flavi NS1.
DR InterPro; IPR002535; Flavi Propep.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF01003; Flavi Capsid; 1.
DR Pfam; PF02832; Flavi Glycoprot; 1.
DR Pfam; PF00869; Flavi Glycoprot; 1.
DR Pfam; PF01004; Flavi M; 1.
DR Pfam; PF00948; Flavi NS1; 1.
DR Pfam; PF01570; Flavi Propep; 1.
DR ProDom; PD001556; Flavi Glycoprote; 1.
DR ProDom; PD001496; Flavi NS1; 1.
KW Polyprotein; Glycoprotein; Core protein; Coat protein;
FT INIT_MET 1 1
FT CHAIN 1 112
FT PROPEP 113 205
FT CHAIN 206 280
FT CHAIN 281 776
FT CHAIN 777 >980
FT TRANSMEM 101 112
FT TRANSMEM 247 259
FT TRANSMEM 266 280
FT TRANSMEM 738 751
FT DISULFID 283 310
FT DISULFID 340 385
FT DISULFID 372 401
FT DISULFID 466 570
FT DISULFID 587 618
FT CARBOHYD 144 144
FT CARBOHYD 434 434
FT CARBOHYD 861 861
FT NON_TER 980 980
SQ SEQUENCE 980 AA; 107234 MW; 2242B99364F3BFD9 CRC64;

Query Match 41.1%; Score 39; DB 1; Length 980;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 RGRKLVYDSARHH 18
DB 220 RGRKWLGDLSRTH 233

RESULT 29
YH48_YEAST STANDARD; PRT; 981 AA.
AC Q12751;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 113.2 kDa protein in S902-HSC82 intergenic region.
GN YMR185W OR YMR010.15.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8288c / AB572;
RX Bowden S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrall B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
XIII.1";
RL Nature 387:90-93 (1997).
RN [2]
RP SEQUENCE OF 650-981 FROM N.A.
RX MEDLINE=95373281; PubMed=7645348;

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RA Erkine A.M., Szent-Gyorgyi C., Simmons S.F., Gross D.S.;
RT "The upstream sequences of the HSP82 and HSC82 genes of Saccharomyces
RT cerevisiae; regulatory elements and nucleosome positioning motifs.";
RL Yeast 11:573-580 (1995).
RN [3]
RP SEQUENCE OF 976-981 FROM N.A.
RX MEDLINE=89384620; PubMed=2674684;
RA Borkovich K.A., Farrelly F.W., Finkelstein D.B., Taulien J.,
RA Lindquist S.;
RT "hsp82 is an essential protein that is required in higher
RT concentrations for growth of cells at higher temperatures.";
RL Mol. Cell. Biol. 9:3919-3930 (1989).
CC -----
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CC -----
CC EMBL; Z49808; CAA89918.1;
DR EMBL; U20349; AAA87904.1; ALT_INIT.
DR PIR; S55132; S55132.
DR GerMOnline; 142859;
DR SGD; S0004797; YMR185W.
DR InterPro; IPR008938; ARM.
KW Hypothetical protein.
SQ SEQUENCE 981 AA; 113248 MW; 13F29F65C6D4B53B CRC64;

Query Match 41.1%; Score 39; DB 1; Length 981;
Best Local Similarity 40.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 KRGKRLVDYDSARHH 18
DB 142 KKGOKSARVETPRWH 156

RESULT 30
YD96_METJA STANDARD; PRT; 2894 AA.
AC Q58791;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical protein MJ1396.
GN MJ1396.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Huft M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii";
RL Science 273:1058-1073 (1996).
CC -----
CC -!- SIMILARITY: Contains 20 Pbl1 repeats.
CC -----
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CC -----
DR EMBL: AF034806; AAC31359.1; --
DR InterPro: IPR002910; FLO_LFY.
DR Pfam: PF01698; FLO_LFY; 1.
KW Transcription regulation; Activator; DNA-binding;
KW Nuclear protein; Developmental protein.
SQ SEQUENCE 359 AA; 40929 MW; C9C768BE85076312 CRC64;

Query Match 40.0%; Score 38; DB 1; Length 359;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 RKLVDYDSARHH 18
   |||:|
Db 84 RRLLEADRRHH 95

RESULT 33
ARGJ_BRAJA STANDARD; PRT; 413 AA.
AC PS9610;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Arginine biosynthesis bifunctional protein argJ [Includes: Glutamate
DE N-acetyltransferase (EC 2.3.1.35) (Ornithine acetyltransferase)
DE (ornithine transacetylase) (OATase); Amino-acid acetyltransferase
DE (EC 2.3.1.1) (N-acetylglutamate synthase) (AGS)] [Contains: Arginine
DE biosynthesis bifunctional protein argJ alpha chain; Arginine
DE biosynthesis bifunctional protein argJ beta chain].
DE ARGJ OR BLA0206.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Ixiguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RA "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
CC -!- FUNCTION: Catalyzes two activities which are involved in the
CC cyclic version of arginine biosynthesis: the synthesis of
CC acetylglutamate from glutamate and acetyl-CoA, and of ornithine by
CC transacetylation between acetylornithine and glutamate (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: N(2)-acetyl-L-ornithine + L-glutamate = L-
CC ornithine + N-acetyl-L-glutamate.
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + L-glutamate = CoA + N-acetyl-L-
CC glutamate.
CC -!- PATHWAY: Arginine biosynthesis; first step.
CC -!- PATHWAY: Arginine biosynthesis; fifth step.
CC -!- SUBUNIT: Heterotetramer of two alpha and two beta chains (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- MISCELLANEOUS: Some bacteria possess a monofunctional argJ, i.e.,
CC capable of catalyzing only the fifth step of the arginine
CC biosynthetic pathway.
CC -!- SIMILARITY: Belongs to the argJ family.
CC -----
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DR EMBL: AP005935; BAC45471.1; --
DR HAMAP: MF_01106; --; 1.
DR InterPro: IPR002813; ArgJ.
DR Pfam: PF01960; ArgJ; 1.
DR ProDom: PD004193; ArgJ; 1.
DR TIGRfam: TIGR00120; ArgJ; 1.
KW Arginine biosynthesis; Multifunctional enzyme; Transferase;
KW Acyltransferase; Complete proteome.
FT CHAIN 1 194
   ARGinine BIOSYNTHESIS BIFUNCTIONAL
   PROTEIN ARGJ ALPHA CHAIN (BY SIMILARITY).
FT CHAIN 195 413
   ARGinine BIOSYNTHESIS BIFUNCTIONAL
   PROTEIN ARGJ BETA CHAIN (BY SIMILARITY).
FT SITE 194 195
   CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).
SQ SEQUENCE 413 AA; 42683 MW; F5B3BE3F558DCF33 CRC64;

Query Match 40.0%; Score 38; DB 1; Length 413;
Best Local Similarity 43.8%; Pred. No. 72;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSAR 16
   |||:|
Db 355 RVARGARDPDYDEAQ 370

RESULT 34
PDA6 RAT STANDARD; PRT; 431 AA.
AC Q63081;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein disulfide isomerase A6 precursor (EC 5.3.4.1) (Protein
DE disulfide isomerase P5) (Calcium-binding protein 1) (CaBP1
DE (Fragment)).
DE PDI A6 OR CABP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95181574; PubMed=7876340;
RA Fuelekrug J., Soennichsen B., Wuensch U., Arseven K., Van P.N.,
RA Soeling H.-D., Mieskes G.;
RA "CaBP1, a calcium binding protein of the thioredoxin family, is a
RT resident KDEL protein of the ER and not of the intermediate
RT compartment.";
RL J. Cell Sci. 107:2719-2727(1994).
CC -!- CATALYTIC ACTIVITY: Rearrangement of both intrachain and
CC interchain disulfide bonds in proteins to form the native
CC structures.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- SIMILARITY: Contains 2 thioredoxin domains.
CC -----
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CC -----
DR EMBL: X79328; CAA55891.1; --
DR FIR: S45038; S45038.
DR HSP: P07237; IMEK.
DR InterPro: IPR005788; Disulph isom.
DR InterPro: IPR000886; ER target_s.
DR InterPro: IPR006662; ThioRed.
DR InterPro: IPR006663; ThioRedox_dom2.
DR Pfam: PF00085; ThioRedox_2.
DR PRINTS: PR00421; THIOREDOXIN.
DR TIGRfam: TIGR01126; pdi_dom; 2.

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DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 2.
 KW Redox-active center; Isomerase; Endoplasmic reticulum; Repeat; Signal;
 KW Calcium-binding.
 FT NON_TER 1
 FT SIGNAL <1 10
 FT CHAIN 11 431
 FT DISULFID 46 49
 FT DISULFID 181 184
 FT DOMAIN 413 427
 FT SITE 428 431
 FT SITE 428 431
 FT SITE 428 431
 SQ SEQUENCE 431 AA; 47220 MW; 2CD07A233C90135C CRC64;
 Query Match 40.0%; Score 38; DB 1; Length 431;
 Best Local Similarity 43.8%; Pred. No. 75;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 RIAGKGRKLVYDSAR 16
 DB 232 KIFQGESFVDYDGR 247
 RESULT 35
 PDA6 HUMAN
 ID PDAC_HUMAN STANDARD; PRT; 440 AA.
 AC Q15084; Q99778;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein disulfide isomerase A6 precursor (EC 5.3.4.1) (Protein
 DE disulfide isomerase P5).
 GN PDIA6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RC TISSUE=Placenta;
 RX MEDLINE=96069616; PubMed=7590364;
 RA Hayano T., Kikuchi M.;
 RT "Cloning and sequencing of the cDNA encoding human P5";
 RL Gene 164:377-378(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 20-440 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97264341; PubMed=9110174;
 RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,

RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
 RT "Large-scale concatenation cDNA sequencing.";
 RL Genome Res. 7:333-358(1997).
 CC -1- CATALYTIC ACTIVITY: Rearrangement of both intrachain and
 CC interchain disulfide bonds in proteins to form the native
 CC structures.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- SIMILARITY: Contains 2 thioredoxin domains.
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 CC -----
 DR EMBL; D49489; BAA08450.1; -;
 DR EMBL; BC001312; AAH01312.1; -;
 DR EMBL; U79278; AAB50217.1; -;
 DR PIR; JC4369; JC4369.
 DR HSP; P07237; IMEX.
 DR GO; GO:0003756; P:protein disulfide isomerase activity; TAS.
 DR GO; GO:0006457; P:protein folding; TAS.
 DR InterPro; IPR005788; Disulph_ism.
 DR InterPro; IPR000886; ER_target_S.
 DR InterPro; IPR006662; Thioered.
 DR InterPro; IPR006663; Thioered_dom2.
 DR Pfam; PF00085; Thioered; 2.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TRIFAMS; TRIGR0126; pdl_dom; 2.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 2.
 DR Redox-active center; Isomerase; Endoplasmic reticulum; Repeat; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 440
 FT DISULFID 55 58 PROTEIN DISULFIDE ISOMERASE A6.
 FT DISULFID 190 193 REDOX-ACTIVE (BY SIMILARITY).
 FT DOMAIN 422 434 REDOX-ACTIVE (BY SIMILARITY).
 FT SITE 437 440 ASP/GLU-RICH (ACIDIC).
 FT CONFLICT 214 214 K -> R (IN REF. 3).
 SQ SEQUENCE 440 AA; 48121 MW; 06895409F0265D7C CRC64;
 Query Match 40.0%; Score 38; DB 1; Length 440;
 Best Local Similarity 43.8%; Pred. No. 77;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 RIAGKGRKLVYDSAR 16
 DB 241 KIFQGESFVDYDGR 256
 RESULT 36
 WCA6 ECOLI
 ID WCA6_ECOLI STANDARD; PRT; 464 AA.
 AC P71244; P76378;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Colanic acid biosynthesis protein wcaM.
 GN WCA6 OR B2043.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=96326333; PubMed=8759852;
 RA Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.;
 RT "Organization of the Escherichia coli K-12 gene cluster responsible
 RT for production of the extracellular polysaccharide colanic acid";
 RL J. Bacteriol. 178:4885-4893(1996).

RN [2]
 RP REVISIONS.
 RC STRAIN=K12;
 RA Reeves P.R.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12";
 RC Science 277:1453-1474 (1997).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Teggami H.,
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 460-Kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 40.1-50.0 min region on the linkage map";
 RC DNA Res. 3:379-392 (1996).
 CC -1- PATHWAY: Slime polysaccharide colanic acid biosynthesis.
 CC
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 CC
 DR EMBL; U38473; AAC77852.1; -;
 DR EMBL; AE000295; AAC75104.1; -;
 DR EMBL; D90842; BAA15897.1; -;
 DR PIR; B64970; B64970.
 DR EcoGene; EGI2651; wcaM.
 KW Lipopolysaccharide biosynthesis; Complete proteome.
 SQ SEQUENCE 464 AA; 51315 MW; 72A7655DC07368BE CRC64;

 Query Match 40.0%; Score 38; DB 1; Length 464;
 Best Local Similarity 35.3%; Pred. No. 82;
 Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

 QY 2 IAKRGKLYDYSARHH 18
 Db 432 VNEKQSSVDIDRINH 448

 RESULT 37
 YH33 CHRV
 ID YH33 CHRV STANDARD; PRT; 478 AA.
 AC QYNX94;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Hypothetical UPF0061 protein CV1733.
 GN CV1733.
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=2282850; PubMed=14500782;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,

RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brigidio M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantinatti F., Farias L.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Garginelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassem K., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of *Chromobacterium violaceum* reveals
 RT remarkable and exploitable bacterial adaptability";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).
 CC -1- SIMILARITY: Belongs to the UPF0061 (SELO) family.
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 CC
 DR EMBL; AE016916; AA059408.1; -;
 DR HAMAP; MF_00692; -; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 478 AA; 52250 MW; 34990A21225CED51 CRC64;

 Query Match 40.0%; Score 38; DB 1; Length 478;
 Best Local Similarity 63.6%; Pred. No. 84; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1;

 QY 8 KLVVDYSARHH 18
 Db 185 KLDYTIARHY 195

 RESULT 38
 YH18 TREPA
 ID YH18 TREPA STANDARD; PRT; 504 AA.
 AC O83981;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical UPF0144 protein TP1018.
 GN TP1018.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=9833770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
 RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,


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RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RL spirochete.";
RL Science 281:375-388(1998).
CC -!- SIMILARITY: Belongs to the UPF0144 family.
CC -!- SIMILARITY: Contains 1 HD domain.
CC -!- SIMILARITY: Contains 1 KH domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE001269; AAC65967.1; -.
CC F1R; F71253; F71253.
CC TIGR; TP1018; -.
CC HAMAP; MF_00335; -.
CC InterPro; IPR006674; HD.
CC InterPro; IPR004087; KH dom.
CC InterPro; IPR004088; KH_type_1.
CC InterPro; IPR003607; Mac_puhsphidro.
CC InterPro; IPR006675; Unchar_HD1G.
CC Pfam; PF01966; KH; 1.
CC Pfam; PF00013; KH; 1.
CC SMART; SM00471; HDC; 1.
CC SMART; SM00322; KH; 1.
CC TIGRFAMs; TIGR00277; HD1G; 1.
CC PROSITE; PS50084; KH_TYPE_1; 1.
KW Hypothetical protein; Transmembrane; RNA-binding; Complete proteome.
FT DOMAIN 2 22
FT TRANSMEM 193 261
FT DOMAIN 320 413
FT DOMAIN 320 413
SQ SEQUENCE 504 AA; 57070 MW; D61EEE69B6434745 CRC64;

Query Match 40.0%; Score 38; DB 1; Length 504;
Best Local Similarity 47.8%; Pred. No. 89;
Matches 11; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 2 IAKGRKLV-----VDYDSARHH 18
DB 344 IAKGALLHDVIGKGVETSDRNH 366

RESULT 39
PHR NEUCR
ID PHR NEUCR STANDARD; PRT; 642 AA.
AC P27526;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Deoxyribodipyrimidine photolyase (EC 4.1.99.3) (DNA photolyase)
DE (Photoreactivating enzyme).
DE PHR.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020228; PubMed=1833725;
RA Yajima H., Inoue H., Oikawa A., Yasui A.;
RT "Cloning and functional characterization of a eucaryotic DNA
RT photolyase gene from Neurospora crassa.";
RL Nucleic Acids Res. 19:5359-5362(1991).
CC -!- FUNCTION: This enzyme catalyzes the light-dependent monomerization
CC (300-600 nm) of cyclobutyl pyrimidine dimers (in cis-syn
CC configuration) which are formed between adjacent bases on the
CC same DNA strand, upon exposure to ultraviolet radiation.
CC -!- CATALYTIC ACTIVITY: Cyclobutadipyrimidine (in DNA) = 2 pyrimidine
CC residues (in DNA).

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CC -!- COPACTOR: Contains 2 chromophores: a reduced flavin (FADH2) and a
CC 5,10-methylenetetrahydrofolate. Both chromophores are bound by non-
CC covalent interactions.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the DNA photolyase class-1 family.
CC
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CC
CC EMBL; X58713; CAA41549.1; -.
CC F1R; S18667; S18667.
CC DR HSHP; P00914; LDNP.
CC DR InterPro; IPR002081; DNA photolyase 1.
CC DR InterPro; IPR006050; DNA photolyase N.
CC DR InterPro; IPR005101; FAD_binding_7.
CC DR InterPro; IPR005051; FAD_binding_N.
CC DR Pfam; PF00875; DNA photolyase; 1.
CC DR Pfam; PF03441; FAD_binding_7; 1.
CC DR PRINTS; P00147; DNAPHOTLYASE.
CC DR PRODOM; PD004390; FAD binding N; 1.
CC DR PROSITE; PS00394; DNA_PHOTOLYASES_1_1; 1.
CC DR PROSITE; PS00691; DNA_PHOTOLYASES_1_2; 1.
KW Lyase; Chromophore; Flavoprotein; FAD; DNA repair; DNA-binding.
SQ SEQUENCE 642 AA; 73076 MW; 05B1A56B69F77EDC CRC64;

Query Match 40.0%; Score 38; DB 1; Length 642;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 AKGRKLVYDSARHH 18
DB 339 APEGKLRDDEKARYH 354

RESULT 40
NADO THEER
ID NADO THEER STANDARD; PRT; 651 AA.
AC P32382;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH oxidase (EC 1.-.-.-).
OS Thermoanaerobacter brockii (Thermoanaerobium brockii).
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=29323;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=RT8.G4;
RC MEDLINE=93363637; PubMed=8357835;
RX Liu X.-L., Scopes R.K.;
RT "Cloning, sequencing and expression of the gene encoding NADH oxidase
RT from the extreme anaerobic thermophile Thermoanaerobium brockii.";
RL Biochim. Biophys. Acta 1174:187-190(1993).
CC -!- FUNCTION: Reduces a range of alternative electron acceptors.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COPACTOR: FAD; contains 2 FAD molecules per subunit.
CC -!- SUBUNIT: Homohexamer.
CC -!- PTM: The N-terminus is blocked.
CC
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DR EMBL: X67220; CAA47660.1; -.
DR F1R; S35705; S35706.
DR InterPro; IPR000759; Admrx_reductase.
DR InterPro; IPR001327; FAD pyr_redox.
DR InterPro; IPR003009; FNN enzyme.
DR InterPro; IPR000205; NAD BS.
DR InterPro; IPR001155; Oxidored_FNN.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR000103; Pyridine_redox_2.
DR InterPro; IPR000594; Thif_domain.
DR Pfam; PF00724; oxidored_FNN; 1.
DR Pfam; PF00070; Pyr_redox; 1.
DR PRINTS; PRO0419; ADXRDTASE.
DR PRINTS; PRO0368; FADPNR.
DR PRINTS; PRO0411; ENDRDTASEI.
DR PRINTS; PRO0469; ENDRDTASEII.
DR Oxidoreductase; NAD; FAD; Flavoprotein; Iron-sulfur; 4Fe-4S.
KW METAL 344 344
FT METAL 347 347
FT METAL 351 351
FT METAL 364 364
FT METAL 387 413
FT NP BIND 515 542
FT NP_BIND 515 542
FT SEQUENCE 651 AA; 71306 MW; F2282A24DA817439 CRC64;
Query Match 40.0%; Score 38; DB 1; Length 651;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 3 AKRGKLVYDVSARH 17
DB 405 AKRGHVILYERKQH 419
|||||:::|:|
|||||:::|:|

RESULT 41
STC2 STAAU STANDARD; PRT; 715 AA.
AC F17855;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Staphylocoagulase precursor.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=BB;
RX MEDLINE=88139269; PubMed=3481366;
RA Kaide S., Miyata T., Yoshizawa Y., Kawabata S., Morita T.,
RA Igarashi H., Iwanaga S.;
RT "Nucleotide sequence of the staphylocoagulase gene: its unique COOH-terminal 8 tandem repeats."
RL J. Biochem. 102:1177-1186(1987).
CC -!- FUNCTION: STAPHYLOCOAGULASE IS AN EXTRACELLULAR PROTEIN WHICH SPECIFICALLY FORMS A COMPLEX WITH HUMAN PROTHROMBIN. THIS COMPLEX NAMED STAPHYLOTHROMBIN CAN CLOT FIBRINOGEN WITHOUT ANY PROTEOLYTIC CLEAVAGE OF PROTHROMBIN.
CC -!- DOMAIN: THE C-TERMINAL TANDEM REPEATS ARE NOT REQUIRED FOR THE PROCOAGULANT ACTIVITY.
CC -!- SIMILARITY: TO THE STAPHYLOCOAGULASE FROM STRAIN 213.
CC -----
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CC -----
DR EMBL: D00184; BAA00126.1; -.
DR F1R; A41511; A41511.
DR InterPro; IPR001443; Staphylocoagulase.
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DR Pfam; PF04022; Staphylocoagulase; 8.
DR PROSITE; PS00429; STAPHYLOCOAGULASE; 8.
KW Prothrombin activator; Repeat; Signal.
FT SIGNAL 1 26
FT CHAIN 27 715 STAPHYLOCOAGULASE.
FT DOMAIN 495 710 8 X 27 AA TANDEM REPEATS.
FT SEQUENCE 715 AA; 80100 MW; 46ABC9567AF5F128 CRC64;
Query Match 40.0%; Score 38; DB 1; Length 715;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 9 LVDYDSARHH 18
DB 264 ITSVDSSKHH 273
|||||:::|:|
|||||:::|:|

RESULT 42
SECA MYCSM
ID SECA MYCSM STANDARD; PRT; 957 AA.
AC P71533;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Preprotein translocase SECA subunit.
OS SECA.
GN Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown A.B., Jacobs W.R.;
RT "Conservation of the general secretory pathway: isolation and characterization of SecA homologues from Mycobacterium bovis BCG and M. smegmatis."
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in protein export. Interacts with the secY/secE subunits. SecA has a central role in coupling the hydrolysis of ATP to the transfer of pre-secretory periplasmic and outer membrane proteins across the membrane (By similarity).
CC -!- SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secA, secB, secD, secE, secF, secG and secY (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of membrane (By similarity).
CC -!- SIMILARITY: Belongs to the secA family.
CC -----
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CC -----
DR EMBL: U66081; AAB06754.1; -.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000185; SecA.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF01043; SecA_protein; 1.
DR PRINTS; PRO0906; SECA.
DR TIGRfams; TIGR00963; secA; 1.
DR PROSITE; PS01312; SECA; 1.
KW Protein transport; ATP-binding; Membrane; Translocation; Transport.
FT NP_BIND 98 105 ATP (POTENTIAL).
FT SEQUENCE 957 AA; 107001 MW; AD208569A22BA32E CRC64;
Query Match 40.0%; Score 38; DB 1; Length 957;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 RIAKRGKLVYDVA 15
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DR EMBL; U66362; -; NOT_ANNOTATED_CDS.
DR PIR; G01946; G01946.
DR HSP; P29476; 1QAV.
DR Genew; HGNC:7872; NOS1.
DR MIM; 163731.
DR GO; GO:0005624; Cmembrane fraction; TAS.
DR GO; GO:0004517; Finitric-oxide synthase activity; TAS.
DR GO; GO:0006936; Pmuscle contraction; TAS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN cyt reductase.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxid_FAD/NAD(P).
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR Pfam; PF00595; PDZ; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; PFNCR.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; 1.
DR PROSITE; PS50106; PDZ; 1.
DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
KW Alternative splicing; Multigene family.
FT DOMAIN 17 99 PDZ.
FT DOMAIN 163 245 NNOS-INHIBITING PROTEIN (PIN)-BINDING.
FT DOMAIN 760 940 FLAVODOXIN-LIKE.
FT METAL 420 420 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT DOMAIN 730 750 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 886 917 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 1032 1043 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 1175 1185 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 1250 1268 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1348 1363 NADP (ADP PART) (BY SIMILARITY).
FT VARSPIC 1 336 Missing (in isoform 3).
FT VARSPIC 285 407 /FTID=VSP 003571.
FT FTID=VSP 003571.
FT PFTSQKPTKNGSKPCPKFLKYNKTEVVLDTLHLKS
FT TLETCYIKGSIHPSQSHARPEDVTKGQFLPLAKEF
FT IDQYSSIKRFGSKAMERLEEVNKEIDTSTYQLKDELI
FT -> MKRLRTGFGVGRSHNHPPOENSPORMAAPSVH
FT ASSRRTGLRWFSLTPSTLAHWKRDALSTSAWAPSVH
FT SMOGILKTSACKDSSLSPKSLINTHQLKDLAPKPTWK
FT WKR (in isoform 4).
FT /FTID=VSP 003572.
FT Missing (in isoform 4).
FT /FTID=VSP 003573.
FT Missing (in isoform 2).
FT /FTID=VSP 003574.
FT K -> E (IN REF. 4).
FT LAPRPG -> WQAPR (IN REF. 3 AND 4).
FT QP -> HR (IN REF. 3).
FT V -> L (IN REF. 3).
FT G -> A (IN REF. 3).
FT Y -> I (IN REF. 3).
FT WKR (IN ISOFORM 4).
FT 1434 AA; 160970 MW; 99235793B953BF37 CRC64;
SQ SEQUENCE 1434 AA; 160970 MW; 99235793B953BF37 CRC64;

Query Match 40.0%; Score 38; DB 1; Length 1434;
Best Local Similarity 62.5%; Pred. No. 2.8e-02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 2 IAKRGKRLVD--YDSA 15
Db 65 LAVNGEPLVDLSYDSA 80
: ||| ||| |||
: ||| ||| |||

RESULT 44
NOS1_RABIT
ID NOS1_RABIT
AC O19132;

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DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Nitric-oxide synthase, brain (EC 1.14.13.39) (NOS, type I) (Neuronal
DE NOS) (N-NOS) (nNOS) (Constitutive NOS) (NC-NOS) (bNOS).
GN NOS1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Jeong Y., Yim J.;
RT "Molecular cloning of a cDNA encoding a constitutive nitric oxide
RT synthase from rabbit brain.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
CC with diverse functions throughout the body. In the brain and
CC peripheral nervous system, NO displays many properties of a
CC neurotransmitter.
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme (By similarity).
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin. Inhibited by
CC n-Nos-inhibiting protein (PIN) which may prevent the dimerization
CC of the protein (By similarity).
CC -!- SUBUNIT: Homodimer. Forms a ternary complex with CAPON and RASD1.
CC -!- INTERACTS WITH DLGA (By similarity).
CC -!- SUBCELLULAR LOCATION: In skeletal muscle, it is localized beneath
CC the sarcolemma of fast-twitch muscle fiber by associating with the
CC dystrophin glycoprotein complex (By similarity).
CC -!- DOMAIN: The PDZ domain in the N-terminal part of the neuronal
CC isoform participates in protein-protein interaction, and is
CC responsible for targeting nNOS to synaptic membranes in muscles
CC (By similarity).
CC -!- SIMILARITY: Belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -!- SIMILARITY: Contains 1 PDZ/DRH domain.
CC -----
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CC -----
DR EMBL; U91584; AAB68663.1; -.
DR HSP; P29476; 1QAV.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN cyt reductase.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxid_FAD/NAD(P).
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR Pfam; PF00595; PDZ; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; PFNCR.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; 1.
DR PROSITE; PS50106; PDZ; 1.
DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
KW Multigene family.
FT DOMAIN 17 99 PDZ.

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FT DOMAIN 164 246 NNOS-INHIBITING PROTEIN (PIN)-BINDING (BY
FT SIMILARITY)
FT FT 761 941 FLAVODOXIN-LIKE.
FT FT 421 421 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT FT 731 751 CALMODULIN-BINDING (POTENTIAL).
FT FT 887 918 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT FT NP_BIND 1033 1044 FAD (ADP PART) (BY SIMILARITY).
FT FT NP_BIND 1176 1186 FAD (FLAVIN PART) (BY SIMILARITY).
FT FT NP_BIND 1251 1269 NADP (RIBOSE PART) (BY SIMILARITY).
FT FT NP_BIND 1349 1364 NADP (ADP PART) (BY SIMILARITY).
FT SEQUENCE 1435 AA; 160864 MW; 3ED87ECDD93A7A5A CRC64;

Query Match 40.0%; Score 38; DB 1; Length 1435;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 2 IAKGRKLVLD--YDSA 15
DB 65 LAVNGRPLVDLSYDSA 80

RESULT 45
KKK1 YEAST
ID KKK1 YEAST STANDARD; PRT; 1518 AA.
AC P34244;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable serine/threonine-protein kinase YKL101W (EC 2.7.1.-).
GN YKL101W OR YKL453.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=94078677; PubMed=8256524;
RA Fallier C., Valens M., Puzos V., Fukuhara H., Cheret G., Sor F.,
RA Boletoin-Fukuhara M.;
RT "DNA sequence analysis of a 17 kb fragment of yeast chromosome XI
RT physically localizes the MRB1 gene and reveals eight new open reading
RT frames, including a homologue of the KIN1/KIN2 and SNF1 protein
RT kinases.";
RL Yeast 9:1149-1155(1993).
CC -! SIMILARITY: Belongs to the Ser/Thr family of protein kinases. NIM1
CC subfamily.
CC -----
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CC -----
CC EMBL; X71133; CAA50456.1; -
CC DR EMBL; Z28101; CAA81941.1; -
CC DR FIR; S37928; S37928.
CC DR HSSP; Q63450; 1A06.
CC DR GerMOnline; 139857; -.
CC DR SGD; S0001584; HSL1.
CC DR GO; GO:0005935; C:bud neck; IDA.
CC DR GO; GO:0005940; C:septin ring; IDA.
CC DR GO; GO:0004672; P:protein kinase activity; IDA.
CC DR GO; GO:0000086; P:G2/M transition of mitotic cell cycle; IGI.
CC DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
CC DR GO; GO:0000074; P:regulation of cell cycle; IMP.
CC DR GO; GO:0000135; P:septin checkpoint; IGI.
CC DR InterPro; IPR000719; Prot kinase.
CC DR InterPro; IPR008271; Ser_thr_kinase.
CC DR InterPro; IPR002290; Ser_thr_kinase.
CC DR InterPro; IPR001245; Tyr_kinase.

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DR PFAM: PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding. 81 369 PROTEIN_KINASE.
FT DOMAIN 81 369
FT NP_BIND 87 95 ATP (BY SIMILARITY).
FT BINDING 110 110 ATP (BY SIMILARITY).
FT ACT_SITE 239 239 BY SIMILARITY.
SQ SEQUENCE 1518 AA; 169592 MW; 803F84F7531241DD CRC64;

Query Match 40.0%; Score 38; DB 1; Length 1518;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRGRKLVLDYD 13
DB 1451 KFGKRVVEYD 1460

RESULT 46
SPCA HUMAN
ID SPCA HUMAN STANDARD; PRT; 2418 AA.
AC P02549; O15514;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Spectrin alpha chain, erythrocyte (Srythroid alpha-spectrin).
GN SPTA1 OR SPTA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=90170949; PubMed=1689726;
RA Sahr K.E., Laurila P., Kotula L., Scarpa A.L., Coupal E., Leto T.L.,
RA Linnenbach A.J., Winkelmann J.C., Speicher D.W., Marchesi V.T.,
RA Curtis P.J., Forget B.G.;
RT "The complete cDNA and polypeptide sequences of human erythroid
RT alpha-spectrin.";
RL J. Biol. Chem. 265:4434-4443(1990).
RN [2]
RP SEQUENCE OF 7-533 FROM N.A., AND VARIANTS EL2 PRO-260; PRO-261 AND
RP PRO-471.
RX MEDLINE=90009318; PubMed=2794061;
RA Sahr K.E., Tobe T., Scarpa A., Laughinghouse K., Marchesi S.L.,
RA Agre P., Linnenbach A.J., Marchesi V.T., Forget B.G.;
RT "Sequence and exon-intron organization of the DNA encoding the alpha
RT I domain of human spectrin. Application to the study of mutations
RT causing hereditary elliptocytosis.";
RL J. Clin. Invest. 84:1243-1252(1989).
RN [3]
RP SEQUENCE OF 7-601.
RX MEDLINE=84087888; PubMed=6654896;
RA Speicher D.W., Davis G., Marchesi V.T.;
RT "Structure of human erythrocyte spectrin. II. The sequence of the
RT alpha-I domain.";
RL J. Biol. Chem. 258:14938-14947(1983).
RN [4]
RP SEQUENCE OF 7-125.
RX MEDLINE=84087887; PubMed=6654895;
RA Speicher D.W., Davis G., Yurchenco P.D., Marchesi V.T.;
RT "Structure of human erythrocyte spectrin. I. Isolation of the alpha-I
RT domain and its cyanogen bromide peptides.";
RL J. Biol. Chem. 258:14931-14937(1983).
RN [5]
RP SEQUENCE OF 320-450 FROM N.A.
RX MEDLINE=86205962; PubMed=3458204;

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RA Linnenbach A.J., Speicher D.W., Marchesi V.T., Forget B.G.;
 RT "Cloning of a portion of the chromosomal gene for human erythrocyte
 alpha-spectrin by using a synthetic gene fragment."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2397-2401(1986).
 RN [6]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=84295638; PubMed=6472478;
 RA Speicher D.W., Marchesi V.T.;
 RT "Erythrocyte spectrin is comprised of many homologous triple helical
 segments."
 RL Nature 311:177-180(1984).
 RN [7]
 RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 2407-2418.
 RX MEDLINE=97001215; PubMed=8844207;
 RA Maillet P., Alloisio N., Morle L., Delaunay J.;
 RT "Spectrin mutations in hereditary elliptocytosis and hereditary
 spherocytosis."
 RL Hum. Mutat. 8:97-107(1996).
 RN [9]
 RP VARIANT EL2 SER-24.
 RX MEDLINE=94289716; PubMed=8018926;
 RA Parquet N., Devaux I., Boulanger L., Galand C., Boivin P.,
 Lecomte M.-C., Dhermy D., Garbarz M.;
 RT "Identification of three novel spectrin alpha I/74 mutations in
 hereditary elliptocytosis: further support for a triple-stranded
 folding unit model of the spectrin heterodimer contact site."
 RL Blood 84:303-308(1994).
 RN [10]
 RP VARIANTS EL2 CYS-28; HIS-28; LEU-28 AND SER-28.
 RX MEDLINE=91358728; PubMed=1679439;
 RA Coetzer T.L., Sahr K., Pechal J., Blacklock H., Peterson L., Koler R.,
 Doyle J., Manaster J., Palek J.;
 RT "Four different mutations in codon 28 of alpha spectrin are
 associated with structurally and functionally abnormal spectrin alpha
 I/74 in hereditary elliptocytosis."
 RL J. Clin. Invest. 88:743-749(1991).
 RN [11]
 RP VARIANT EL2 SER-28, AND VARIANT HPP ARG-48.
 RX MEDLINE=91346849; PubMed=1879597;
 RA Floyd P.B., Gallagher P.G., Valentino L.A., Davis M., Marchesi S.L.,
 Forget B.G.;
 RT "Heterogeneity of the molecular basis of hereditary
 pyropoikilocytosis and hereditary elliptocytosis associated with
 increased levels of the spectrin alpha I/74-kilodalton tryptic
 peptide."
 RL Blood 78:1364-1372(1991).
 RN [12]
 RP VARIANT EL2 SER-45.
 RX MEDLINE=89323468; PubMed=2568862;
 RA Lecomte M.-C., Garbarz M., Grandchamp B., Feo C., Gautero H.,
 Devaux I., Bourrier O., Galand C., D'Auriol L., Galibert P.,
 Sahr K.E., Forget B.G., Boivin P., Dhermy D.;
 RT "Sp alpha I/78: a mutation of the alpha I spectrin domain in a white
 kindred with HE and HPP phenotypes."
 RL Blood 74:1126-1133(1989).
 RN [13]
 RP VARIANT EL2/HPP PRO-207.
 RX MEDLINE=92176375; PubMed=1541680;
 RA Gallagher P.G., Tse W.T., Coetzer T., Lecomte M.-C., Garbarz M.,
 Zarkowsky H.S., Baruchel A., Ballas S.K., Dhermy D., Palek J.,
 Forget B.G.;
 RT "A common type of the spectrin alpha I 46-50a-kD peptide abnormality
 in hereditary elliptocytosis and pyropoikilocytosis is associated
 with a mutation distant from the proteolytic cleavage site. Evidence
 for the functional importance of the triple helical model of
 spectrin."
 RL J. Clin. Invest. 89:892-898(1992).
 RN [14]
 RP VARIANT VAL-1857.
 RX MEDLINE=93253053; PubMed=8486776;
 RA Wilmette R., Marechal J., Morle L., Baklouti F., Philippe N.,
 Kastally R., Kotula L., Delaunay J., Alloisio N.;
 RT "Low expression allele alpha DELY of red cell spectrin is associated
 with mutations in exon 40 (alpha V/41 polymorphism) and intron 45 and
 with partial skipping of exon 46."
 RL J. Clin. Invest. 91:2091-2096(1993).
 RN [15]
 RP VARIANT EL2 BARCELONA PRO-469.
 RX MEDLINE=93372367; PubMed=8364215;
 RA dalla Venezia N., Alloisio N., Forissier A., Denoroy L., Aymerich M.,
 Vives-Corrons J.L., Besalduch J., Besson I., Delaunay J.;
 RT "Elliptoikilocytosis associated with the alpha 469 His-->Pro
 mutation in spectrin Barcelona (alpha I/50-46b)."
 RL Blood 82:1661-1665(1993).
 RN [16]
 RP VARIANT CAGLIARI GLY-2024.
 RX MEDLINE=94043025; PubMed=8226774;
 RA Sahr K.E., Coetzer T.L., Moy L.S., Derick L.H., Chishti A.H.,
 Jarolim P., Lorenzo F., Miraglia del Giudice E., Iolascon A.,
 Gallanelli R.;
 RT "Spectrin Cagliari: an Ala-->Gly substitution in helix 1 of beta
 spectrin repeat 17 that severely disrupts the structure and self-
 association of the erythrocyte spectrin heterodimer."
 RL J. Biol. Chem. 268:22656-22662(1993).
 RN [17]
 RP VARIANT EL2 CULOZ VAL-46, AND VARIANT EL2 LYON PHE-49.
 RX MEDLINE=90347052; PubMed=2384601;
 RA Morle L., Roux A.-F., Alloisio N., Pothier B., Starck J., Denoroy J.,
 Morle F., Rudigez R.-C., Forget B.G., Delaunay J., Godet J.;
 RT "Two elliptocytogenic alpha I/74 variants of the spectrin alpha I
 domain. Spectrin Culoz (GGT-->GTT; alpha I 40 Gly-->Val) and
 Spectrin Lyon (CTT-->TTT; alpha I 43 Leu-->Phe)."
 RL J. Clin. Invest. 86:548-554(1990).
 RN [18]
 RP VARIANT EL2 JENDOUBA GLU-791.
 RX MEDLINE=92345619; PubMed=1638030;
 RA Alloisio N., Wilmette R., Morle L., Baklouti F., Marechal J.,
 Ducluzeau M.-T., Denoroy L., Feo C., Forget B.G., Kastally R.,
 Delaunay J.;
 RT "Spectrin Jendouba: an alpha II/31 spectrin variant that is
 associated with elliptocytosis and carries a mutation distant from
 the dimer self-association site."
 RL Blood 80:1809-815(1992).
 RN [19]
 RP VARIANT EL2 TUNIS TRP-41.
 RX MEDLINE=89323436; PubMed=2568861;
 RA Morle L., Morle F., Roux A.F., Godet J., Forget B.G., Denoroy L.,
 Garbarz M., Dhermy D., Kastally R., Delaunay J.;
 RT "Spectrin Tunis (Sp alpha I/78), an elliptocytogenic variant, is due
 to the CCG-->TCG codon change (Arg-->Trp) at position 35 of the
 alpha I domain."
 RL Blood 74:828-832(1989).
 RN [20]
 RP VARIANT EL2 GENOVA TRP-34.
 RX MEDLINE=94250920; PubMed=8193371;
 RA Perrotta S., del Giudice E.M., Alloisio N., Sciaratta G., Pinto L.,
 Delaunay J., Cuttillo S., Iolascon A.;
 RT "Wild elliptocytosis associated with the alpha 34 Arg-->Trp mutation
 in spectrin Genova (alpha I/74)."
 RL Blood 83:3346-3349(1994).
 RN [21]
 RP VARIANT EL2 ANASTASIA THR-45.
 RX MEDLINE=95290423; PubMed=7772539;
 RA Perrotta S., Iolascon A., de Angelis F., Pagano L., Colonna G.,
 Cuttillo S., del Giudice E.M.;
 RT "Spectrin Anastasia (alpha I/78): a new spectrin variant (alpha 45
 Arg-->Thr) with moderate elliptocytogenic potential."
 RL Br. J. Haematol. 89:933-936(1995).
 CC -/- FUNCTION: Spectrin is the major constituent of the cytoskeletal
 network underlying the erythrocyte plasma membrane. It associates
 with band 4.1 and actin to form the cytoskeletal superstructure of
 the erythrocyte plasma membrane.

CC -!- SUBUNIT: Composed of nonhomologous chains, alpha and beta, which
 CC aggregate side-to-side in an antiparallel fashion to form dimers,
 CC tetramers, and higher polymers.
 CC -!- DISASE: Defects in SPAL1 are a cause of thesuis-unlinked
 CC elliptocytosis 2 (EL2) (MIM:130600, 182860, 166900).
 CC Elliptocytosis (also known as ovalocytosis) is a genetically
 CC heterogeneous, autosomal dominant hematologic disorder. It is

Query Match 40.0%; Score 38; DB 1; Length 2418;
 Best Local Similarity 63.6%; Pred. No. 4.9e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAGKRLVD 11
 Db 41 RVAERGQKLED 51
 :.:|:|:|

RESULT 47
 PLE1_CRIGR
 ID PLE1_CRIGR STANDARD; PRT; 4473 AA.
 AC Q9J155;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Plectin 1 (PLTN) (PCN) (300-kDa intermediate filament-associated
 DE protein) (IFAP300) (Fragment).
 GN PLE1.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OC NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20334248; PubMed=10873583;
 RA Clubb B.H.; Chou Y.-H.; Herrmann H.; Svitkina T.M.; Borisy G.G.,
 RA Goldman R.D.;
 RT "The 300-kDa intermediate filament-associated protein (IFAP300) is a
 RT hamster plectin ortholog."
 RL Biochem. Biophys. Res. Commun. 273:183-187(2000).
 RN [2]
 RP PHOSPHORYLATION.
 RX MEDLINE=96215219; PubMed=8626512;
 RA Malecz N.; Folner R.; Stadler C.; Wiche G.;
 RT "Identification of plectin as a substrate of p34cdc2 kinase and
 RT mapping of a single phosphorylation site."
 RL J. Biol. Chem. 271:8203-8208(1996).
 CC -!- FUNCTION: Interlinks intermediate filaments with microtubules and
 CC microfilaments and anchors intermediate filaments to desmosomes or
 CC hemidesmosomes. May be involved not only in the crosslinking and
 CC stabilization of cytoskeletal intermediate filaments network, but
 CC also in the regulation of their dynamics.
 CC -!- SUBUNIT: Homodimer or homotetramer.
 CC -!- DOMAIN: The N-terminus interacts with actin, the C-terminus with
 CC vimentin, desmin, GAP, cytokeratins, lamin B; whereas both the N-
 CC and the C-terminus can bind integrin beta-4.
 CC -!- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
 CC INTERMEDIATE FILAMENTS DURING MITOSIS.
 CC -!- SIMILARITY: Contains 1 actin-binding domain.
 CC -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
 CC -!- SIMILARITY: Contains 32 plectrin repeats.
 CC -!- SIMILARITY: Contains 4 spectrin repeats.
 CC -!- SIMILARITY: Belongs to the plakin or cytolinker family.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF260753; AAF70372.1; -.

DR HSP; Q01082; 1BKR.
 DR InterPro; IPR001589; Actbind actnin.
 DR InterPro; IPR001715; Calponin-like.
 DR InterPro; IPR001101; Plectrin repeat.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF00307; CH; 2.
 DR Pfam; PF00681; Plectin; 20.
 DR SMART; SM00033; CH; 2.
 DR SMART; SM00250; PLEC; 34.
 DR PROSITE; PS00019; ACTININ_1; PARTIAL.
 DR PROSITE; PS00020; ACTININ_2; FALSE_NEG.
 DR PROSITE; PS50021; CH; 2.
 KW Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
 KW Phosphorylation.
 FT NON_TER 1
 FT DOMAIN <1 1259
 FT DOMAIN 1260 2544
 FT DOMAIN 2545 4473
 FT DOMAIN <1 192
 FT DOMAIN <1 74
 FT DOMAIN 87 189
 FT REPEAT 449 508
 FT REPEAT 529 613
 FT REPEAT 626 719
 FT REPEAT 1104 1204
 FT DOMAIN 1258 2548
 FT REPEAT 2615 2652
 FT REPEAT 2653 2690
 FT REPEAT 2691 2728
 FT REPEAT 2729 2766
 FT REPEAT 2770 2804
 FT REPEAT 2905 2942
 FT REPEAT 2943 2980
 FT REPEAT 2981 3018
 FT REPEAT 3019 3056
 FT REPEAT 3057 3094
 FT REPEAT 3274 3311
 FT REPEAT 3312 3349
 FT REPEAT 3350 3387
 FT REPEAT 3388 3425
 FT REPEAT 3429 3463
 FT REPEAT 3609 3646
 FT REPEAT 3647 3684
 FT REPEAT 3685 3722
 FT REPEAT 3723 3760
 FT REPEAT 3764 3797
 FT REPEAT 3800 3834
 FT REPEAT 3852 3889
 FT REPEAT 3890 3927
 FT REPEAT 3928 3965
 FT REPEAT 3966 4003
 FT REPEAT 4007 4041
 FT REPEAT 4043 4094
 FT REPEAT 4197 4234
 FT REPEAT 4235 4272
 FT REPEAT 4273 4310
 FT REPEAT 4311 4348
 FT REPEAT 4349 4386
 FT DOMAIN 4039 4089
 FT DOMAIN 4414 4429
 FT MOD_RES 4328 4328
 SQ SEQUENCE 4473 AA; 509015 MW; E144615D361E3484 CRC64;

Query Match 40.0%; Score 38; DB 1; Length 4473;
 Best Local Similarity 57.1%; Pred. No. 9.5e+02;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKRGKLVYDSAR 16
 Db 1739 AKRQRLAEEDAR 1752
 :|:|:|:|

RESULT 48

PLE1_HUMAN
 ID_PLE1_HUMAN STANDARD; PRT; 4684 AA.
 AC Q15149; Q16640;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Plectin 1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HDI).
 GN PLECI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Placenta;
 RX MEDLINE=96210632; PubMed=8633085;
 RA Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche G.;
 RT "Human plectin: organization of the gene, sequence analysis, and
 RT chromosome localization (8q24).";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
 [2]
 SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND DISEASE.
 RX MEDLINE=96312447; PubMed=8698233;
 RA McLean W.H.I., Pulkkinen L., Smith F.J.D., Rugg E.L., Lane E.B.,
 RA Bullrich F., Burgeson R.E., Amato S., Hudson D.B., Owaribe K.,
 RA McGrath J.A., McMillan J.R., Bady R.A.J., Leigh I.M., Christiano A.M.,
 RA Utto J.;
 RT "Loss of plectin causes epidermolysis bullosa with muscular dystrophy:
 RT cDNA cloning and genomic organization.";
 RL Genes Dev. 10:1724-1735(1996).
 [3]
 VARIANT MD-EBS 1003-GLN--ALA-1005 DEL.
 RX MEDLINE=97049959; PubMed=8894687;
 RA Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yacita H.,
 RA Hachisuka H., Nishikawa T., McLean W.H.I., Utto J.;
 RT "Homozygous deletion mutations in the plectin gene (PLECI) in patients
 RT with epidermolysis bullosa simplex associated with late-onset
 RT muscular dystrophy.";
 RL Hum. Mol. Genet. 5:1539-1546(1996).
 [4]
 VARIANT MD-EBS LEU-429 INS.
 RX MEDLINE=21090821; PubMed=11159198;
 RA Bauer J.W., Rouan F., Kofler B., Reznicek G.A., Kornacker I.,
 RA Muss W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G.,
 RA Wiche G., Utto J., Hinthner H.;
 RT "A compound heterozygous one amino-acid insertion/nonsense mutation in
 RT the plectin gene causes epidermolysis bullosa simplex with plectin
 RT deficiency.";
 RL Am. J. Pathol. 158:617-625(2001).
 [5]
 VARIANT EBS1 TRP-2110.
 RX MEDLINE=21841370; PubMed=11851880;
 RA Koss-Harnes D., Hoeyheim F., Anton-Lamprecht I., Gjesti A.,
 RA Joergensen R.S., Jahnson B.L., Olaisen B., Wiche G.,
 RA Gedde-Dahl T. Jr.;
 RT "A site-specific plectin mutation causes dominant epidermolysis
 RT bullosa simplex Ogna: two identical de novo mutations.";
 RL J. Invest. Dermatol. 118:87-93(2002).
 CC -1- FUNCTION: Interlinks intermediate filaments with microtubules and
 CC microfilaments and anchors intermediate filaments to desmosomes or
 CC hemidesmosomes. Could also bind muscle proteins such as actin to
 CC membrane complexes in muscle. May be involved not only in the
 CC crosslinking and stabilization of cytoskeletal intermediate
 CC filaments network, but also in the regulation of their dynamics.
 CC -1- SUBUNIT: Homodimer or homotetramer.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=Q15149-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q15149-2; Sequence=VSP_005030;
 CC Name=3;

CC IsoId=Q15149-3; Sequence=VSP_005030, VSP_005031;
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in
 CC muscle, heart, placenta and spinal cord.
 CC -1- DOMAIN: The N-terminus interacts with actin, the C-terminus with
 CC vimentin, desmin, GFAP, cytokeratins, lamin B; whereas both the N-
 CC and the C-terminus can bind integrin beta-4.
 CC -1- PTM: PHOSPHORYLATED BY CDC2; REGULATES DISSOCIATION FROM
 CC INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
 CC -1- DISEASE: Defects in PLECI are the cause of epidermolysis bullosa
 CC simplex with muscular dystrophy (MD-EBS) [MIM:28670]; an
 CC autosomal recessive disorder characterized by epidermal blister
 CC formation at the level of the hemidesmosome and associated with
 CC late-onset muscular dystrophy.
 CC -1- DISEASE: Defects in PLECI are the cause of epidermolysis bullosa
 CC simplex 1 (EBS1) [MIM:131950]; also called epidermolysis bullosa
 CC simplex Ogna type. EBS1 is an autosomal dominant form of
 CC epidermolysis bullosa simplex differentiated from the more
 CC generalized form of Koebner [MIM:131900] and the localized form of
 CC Weber and Cockayne [MIM:131800] by the occurrence of skin
 CC bruising.
 CC -1- SIMILARITY: Contains 1 actin-binding domain.
 CC -1- SIMILARITY: Contains 2 calponin-homology (CH) domains.
 CC -1- SIMILARITY: Contains 33 plectin repeats.
 CC -1- SIMILARITY: Contains 4 spectrin repeats.
 CC -1- SIMILARITY: Belongs to the plakin or cytolinker family.
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 CC -----
 CC EMBL; Z54367; CAA91196.1; -;
 CC EMBL; U53204; AAB05427.1; -;
 CC EMBL; U53610; AAB05428.1; -;
 CC EMBL; U53609; AAB05428.1; JOINED.
 CC EMBL; X97053; CAA65765.1; -;
 CC FIR; C59404; A59404.
 CC HSP; Q01082; 1BKR.
 CC Genew; HGNC:9069; PLECI.
 CC GK; Q15149; -;
 CC MIM; 601282; -;
 CC MIM; 28670; -;
 CC MIM; 131950; -;
 CC GO; GO:0008307; F:structural constituent of muscle; TAS.
 CC InterPro; IPR001589; Actbind actinin.
 CC InterPro; IPR001715; Calponin-like.
 CC InterPro; IPR001101; Plectin repeat.
 CC InterPro; IPR005326; S10_plectin_N.
 CC InterPro; IPR002017; Spectrin.
 CC Pfam; PF00307; CH; 2.
 CC Pfam; PF00681; Plectin; 19.
 CC Pfam; PF03501; S10_plectin; 1.
 CC ProDom; PD006662; S10_plectin_N; 1.
 CC SMART; SM00033; CH; 2; S10_plectin_N; 1.
 CC SMART; SM00250; PLEC; 34.
 CC PROSITE; PS00019; ACTININ_1; FALSE_NEG.
 CC PROSITE; PS00020; ACTININ_2; FALSE_NEG.
 CC PROSITE; PS0021; CH; 2.
 CC Coiled coil; Repeat; Structural protein; Cytoskeleton; Actin-binding;
 CC Phosphorylation; Alternative splicing; Epidermolysis bullosa;
 CC Disease mutation.
 CC DOMAIN 1 1470 GLOBULAR 1.
 CC DOMAIN 1471 2755 CENTRAL FIBROUS ROD DOMAIN.
 CC DOMAIN 2756 4684 GLOBULAR 2.
 CC DOMAIN 175 400 ACTIN-BINDING.
 CC DOMAIN 179 282 CH 1.
 CC DOMAIN 295 397 CH 2.
 CC REPEAT 645 710 SPECTRIN 1.
 CC REPEAT 740 824 SPECTRIN 2.
 CC REPEAT 837 930 SPECTRIN 3.

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FT REPEAT 1315 1415 SPECTRIN 4.
FT DOMAIN 1469 2756 COILED COIL (POTENTIAL).
FT REPEAT 2826 2863 PLECTIN 1.
FT REPEAT 2864 2901 PLECTIN 2.
FT REPEAT 2902 2939 PLECTIN 3.
FT REPEAT 2940 2977 PLECTIN 4.
FT REPEAT 2981 3015 PLECTIN 5.
FT REPEAT 3116 3153 PLECTIN 6.
FT REPEAT 3154 3191 PLECTIN 7.
FT REPEAT 3192 3229 PLECTIN 8.
FT REPEAT 3230 3267 PLECTIN 9.
FT REPEAT 3268 3305 PLECTIN 10.
FT REPEAT 3306 3343 PLECTIN 11.
FT REPEAT 3485 3522 PLECTIN 12.
FT REPEAT 3523 3560 PLECTIN 13.
FT REPEAT 3561 3598 PLECTIN 14.
FT REPEAT 3599 3636 PLECTIN 15.
FT REPEAT 3640 3674 PLECTIN 16.
FT REPEAT 3820 3857 PLECTIN 17.
FT REPEAT 3858 3895 PLECTIN 18.
FT REPEAT 3896 3933 PLECTIN 19.
FT REPEAT 3934 3971 PLECTIN 20.
FT REPEAT 3975 4008 PLECTIN 21.
FT REPEAT 4063 4100 PLECTIN 22.
FT REPEAT 4101 4138 PLECTIN 23.
FT REPEAT 4139 4176 PLECTIN 24.
FT REPEAT 4177 4214 PLECTIN 25.
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FT REPEAT 4265 4305 PLECTIN 27.
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FT REPEAT 4484 4521 PLECTIN 31.
FT REPEAT 4522 4559 PLECTIN 32.
FT REPEAT 4560 4597 PLECTIN 33.
FT DOMAIN 4625 4640 BINDING TO INTERMEDIATE FILAMENTS
FT MOD_RES 4539 (BY SIMILARITY).
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FT 409 412 PHOSPHORYLATION (BY CDC2)
FT 429 429 (BY SIMILARITY).
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FT 409 412 ROYLHLPPEIVASLQVRVRPVAVMPARPHVQVQGPL
FT 429 429 GSPKRGPLPTPEQLYRKELEEVSPETVPVPAITKTLA
FT 1003 1005 RGPPEAPAT -> WSGDAEVRVSEDSVNGSGSPSPGD
FT 2110 2110 TLPWNIGKTQRRRGSGGNGSVLDPAERAVIRIA (in
FT 409 412 isoform 2 and isoform 3).
FT 429 429 /FTid=VSP 005030.
FT 1003 1005 Missing (in isoform 3).
FT 2110 2110 /FTid=VSP 005031.
FT 409 412 L > LL (in MD-EBS).
FT 429 429 /FTid=VAR_011336.
FT 1003 1005 Missing (in MD-EBS).
FT 2110 2110 /FTid=VAR_011337.
FT 409 412 R -> W (in EBS1).
FT 429 429 /FTid=VAR_015817.

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Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKRGKRLVDYDSAR 16
DB 1950 AKRGKRLVDYDSAR 1963

RESULT 49
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AC P36717;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Minor core protein (Protein V).
GN Human adenovirus type 12.
OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28282;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94076430; PubMed=8254750;
RA Sprengel J., Schmitz B., Heuss-Neitzel D., Zock C., Doerfler W.;
RT "Nucleotide sequence of human adenovirus type 12 DNA: comparative
functional analysis.";
RL J. Virol. 68:379-389(1994).
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X73487; CAAS1888.1; -.
DR PIR; S33939; S33939.
DR InterPro; IPR005608; Adeno_PV.
DR Pfam; PF03910; Adeno_PV; 1.
KW Core protein; Late protein.
SQ SEQUENCE 347 AA; 39369 MW; 3C338F62AA53027 CRC64;

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Matches 8; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

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DB 327 RVVQGRGLI-LPSVRYH 343
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RESULT 50
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AC P44389;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
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GN (RPSO-A OR RPS15-A OR H11328) AND (RPSO-B OR RPS15-B OR H11468).
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kariya A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: This protein is one of the 16S ribosomal RNA binding
proteins (By similarity).
CC -!- SIMILARITY: Belongs to the S15P family of ribosomal proteins.
CC -----
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CC or send an email to license@isb-sib.ch).

CC EMBL; U32812; AAC22973.1; -.
DR EMBL; U32825; AAC23117.1; -.
DR PIR; H64116; H64116.
DR HSSP; P05766; 1A32.
DR TIGR; H11328; -.
DR TIGR; H11468; -.
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DR InterPro; IPR005290; Ribosomal_S15_b.
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DR ProDom; PD157043; RS15_bact; 1.
DR TIGRFAMs; TIGR00952; S15_bact; 1.
DR PROSITE; PS00362; RIBOSOMAL_S15; 1.
KW Ribosomal protein; rRNA-binding; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
SQ SEQUENCE 88 AA; 10064 MW; 563BAD2B8B8A7043 CRC64;

Query Match 38.9%; Score 37; DB 1; Length 88;
Best Local Similarity 59.3%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIAKRGKLVY 12
| : | | | | |
Db 57 RMVSRREKLLDY 68

Search completed: March 4, 2004, 17:44:54
Job time : 17.1935 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:41:21 ; Search time 18.5806 Seconds
(without alignments)
50.013 Million cell updates/sec

Title: US-10-069-540A-2_COPY_138_155

Perfect score: 95
Sequence: 1 RIAKGRKLVDSARHH 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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104 35 36.8 12 3 US-09-060-039-22 Sequence 22, Appl
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106 35 36.8 54 4 US-09-165-422-15 Sequence 15, Appl
107 35 36.8 83 4 US-09-134-000C-4372 Sequence 4372, Ap
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109 35 36.8 139 4 US-09-107-532A-4424 Sequence 4424, Ap
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118 35 36.8 325 4 US-09-540-236-2444 Sequence 2444, Ap
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126 35 36.8 419 4 US-09-252-991A-30457 Sequence 30457, A
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128 35 36.8 458 4 US-09-252-991A-22614 Sequence 22614, A
129 35 36.8 463 4 US-09-252-991A-24757 Sequence 24757, A
130 35 36.8 464 4 US-09-297-468-2 Sequence 2, Appl
131 35 36.8 485 4 US-09-479-645A-2 Sequence 2, Appl
132 35 36.8 485 4 US-09-479-645A-4 Sequence 4, Appl
133 35 36.8 608 4 US-09-489-039A-12785 Sequence 12785, A
134 35 36.8 611 4 US-09-107-532A-4988 Sequence 4988, A
135 35 36.8 640 4 US-09-177-165A-30 Sequence 30, Appl
136 35 36.8 675 1 US-08-386-495-10 Sequence 10, Appl
137 35 36.8 675 5 PCT-US96-02331-10 Sequence 10, Appl
138 35 36.8 699 4 US-09-808-701A-34 Sequence 34, Appl
139 35 36.8 715 4 US-09-808-701A-33 Sequence 33, Appl
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147 35 36.8 895 4 US-09-489-039A-13127 Sequence 13127, A
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149 35 36.8 944 4 US-09-134-000C-5578 Sequence 5578, Ap
150 35 36.8 962 4 US-09-694-777A-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-630-915A-24
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; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TEXT: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-24

Query Match 100.0%; Score 95; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 2; le-08; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIAGKGRKLVYDSARHH 18
DB 104 RIAGKGRKLVYDSARHH 121

RESULT 2
US-08-630-915A-22
; Sequence /22, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-22

Query Match 100.0%; Score 95; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKRGKLVYDVSARHH 18
Db 139 RIAKRGKLVYDVSARHH 156

RESULT 3
US-08-435-454-4
; Sequence 4, Application US/08435454
; Patent No. 5605830
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; APPLICANT: Sakamuro, Daitoku
; TITLE OF INVENTION: Murine and Human C-Myc Interacting
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,454
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-454-4

Query Match 100.0%; Score 95; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKRGKLVYDVSARHH 18
Db 136 RIAKRGKLVYDVSARHH 153

RESULT 4
US-08-652-972A-4

; Sequence 4, Application US/0852972A
; Patent No. 5723581
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; APPLICANT: Sakamuro, Daitoku
; TITLE OF INVENTION: Murine and Human Box-Dependent
; TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,972A
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,454
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-972A-4

Query Match 100.0%; Score 95; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKRGKLVYDVSARHH 18
Db 136 RIAKRGKLVYDVSARHH 153

RESULT 5
US-08-919-145-6
; Sequence 6, Application US/08919145
; Patent No. 5958753
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; TITLE OF INVENTION: Bau, A Bin1 Interacting Protein, and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/919,145
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,482
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST73AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-919-145-6
Query Match 100.0%; Score 95; DB 2; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRGKLVYDYSARHH 18
Db 136 RIAGRGKLVYDYSARHH 153

RESULT 6
US-08-870-126-4
; Sequence 4, Application US/08870126
; Patent No. 6048702
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; APPLICANT: Sakamuro, Daitoku
; TITLE OF INVENTION: Murine and Human Box-Dependent
; TITLE OF INVENTION: MYC-Interacting Protein (Bin1) and Uses Therefor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,126
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/435,454
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,972
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST60CUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
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```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-870-126-4
Query Match 100.0%; Score 95; DB 3; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRGKLVYDYSARHH 18
Db 136 RIAGRGKLVYDYSARHH 153

RESULT 7
US-09-344-889-6
; Sequence 6, Application US/09344889
; Patent No. 6140465
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; TITLE OF INVENTION: Bau, A Bin1 Interacting Protein, and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,145
; FILING DATE:
; APPLICATION NUMBER: US 60/025,482
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST73AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-344-889-6
Query Match 100.0%; Score 95; DB 3; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRGKLVYDYSARHH 18
Db 136 RIAGRGKLVYDYSARHH 153

RESULT 8
US-09-445-247-4
; Sequence 4, Application US/09445247
; Patent No. 6410238
; GENERAL INFORMATION:
; APPLICANT: Wistar Institute of Anatomy & Biology
```


;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

;; NUMBER OF SEQUENCES: 7310

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

;; STREET: 100 Beaver Street

;; CITY: Waltham

;; STATE: Massachusetts

;; COUNTRY: USA

;; ZIP: 02354

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: CD/ROM ISO9660

;; COMPUTER: PC

;; OPERATING SYSTEM: <Unknown>

;; SOFTWARE: ASCII

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/107,532A

;; FILING DATE: 30-Jun-1998

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 60/085,598

;; FILING DATE: 14 May 1998

;; APPLICATION NUMBER: 60/051571

;; FILING DATE: July 2, 1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Ariniello, Pamela Deneke

;; REGISTRATION NUMBER: 40,489

;; REFERENCE/DOCKET NUMBER: GTC-012

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (781)893-5007

;; TELEFAX: (781)893-8277

;; INFORMATION FOR SEQ ID NO: 6889:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 721 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; HYPOTHETICAL: YES

;; ORIGINAL SOURCE:

;; ORGANISM: Enterococcus faecium

;; FEATURE:

;; NAME/KEY: misc feature

;; LOCATION: (B) LOCATION 1...721

;; SEQUENCE DESCRIPTION: SEQ ID NO: 6889:

US-09-107-532A-6889

Query Match 44.2%; Score 42; DB 4; Length 721;

Best Local Similarity 46.2%; Pred. No. 52;

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 5 RGRKLVYDSARH 17

Db 90 RGKALDFQARH 102

RESULT 12

US-09-252-991A-28840

Sequence 28840, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28840

LENGTH: 1219

TYPE: PRT

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28840

Query Match 44.2%; Score 42; DB 4; Length 1219;

Best Local Similarity 63.6%; Pred. No. 94;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KLVYDSARH 18

Db 107 KLGDFQARH 117

RESULT 13

US-09-107-532A-3726

Sequence 3726, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3726:

SEQUENCE CHARACTERISTICS:

LENGTH: 298 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...298

SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

US-09-107-532A-3726

Query Match 42.6%; Score 40.5; DB 4; Length 298;

Best Local Similarity 62.5%; Pred. No. 36;

Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 RIA-KRGRKLVYDSA 15

Db 180 RLAEKHGAKLVYDNA 195

RESULT 14

```

RESULT 16
US-09-847-057-2
; Sequence 2, Application US/09847057
; Patent No. 6509191
; GENERAL INFORMATION:
; APPLICANT: AGRINOMICS, LLC.
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLANT
; FILE REFERENCE: PAGODA
; CURRENT APPLICATION NUMBER: US/09/847,057
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-847-057-2

```

RESULT 19
US-09-252-991A-22623
; Sequence 22623, Application US/09252991A
; Patent No. 6551795

```
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22623
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22623

Query Match      40.0%; Score 38; DB 4; Length 258;
Best Local Similarity 45.0%; Pred. No. 82;
Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY      1 RIAGRGKLV--DYDSARHH 18
        |||||
Db      56 RRQRRGRPLGDRSAGRHH 75

RESULT 20
US-09-134-001C-3158
; Sequence 3158, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3158
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3158

Query Match      40.0%; Score 38; DB 4; Length 344;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      6 GRKLVYDSA 15
        |||||
Db      10 GKXMDYKSA 19

RESULT 21
US-09-252-991A-30366
; Sequence 30366, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
```

```
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30366
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30366

Query Match      40.0%; Score 38; DB 4; Length 421;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      2 IAKRGKLVYDSARH 17
        |||||
Db      207 VAAAGRLVDAHQQRH 222

RESULT 22
US-09-489-039A-13646
; Sequence 13646, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13646
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13646

Query Match      40.0%; Score 38; DB 4; Length 476;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      1 RIAGRGKLVYDSARHH 18
        |||||
Db      216 RYLRRFSVLDSPDSLRRH 233

RESULT 23
US-09-252-991A-19960
; Sequence 19960, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19960
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19960

Query Match      40.0%; Score 38; DB 4; Length 489;
Best Local Similarity 33.3%; Pred. No. 1.7e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      1 RIAGRGKLVYDSARHH 18
        |||||
```

Db 195 QVVGEAGAEIDVDEAVHH 212

RESULT 24

US-08-419-078-2
; Sequence 2, Application US/08419078
; Patent No. 5587306
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,078
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0552
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 566 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; LIBRARY: NO. 5587306
; CLONE: 9118
; US-08-419-078-2

Query Match 40.0%; Score 38; DB 1; Length 566;
Best Local Similarity 43.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT 25

US-08-726-883-2
; Sequence 2, Application US/08726883
; Patent No. 5676946
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT 26

US-08-272-255-7
; Sequence 7, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
; APPLICANT: Cashmore, Anthony R.
; APPLICANT: Ahmad, Margaret
; APPLICANT: Lin, Chentao
; TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
; TITLE OF INVENTION: Using the Same
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT 27

US-08-726-883-2
; Sequence 2, Application US/08726883
; Patent No. 5676946
; GENERAL INFORMATION:
; APPLICANT: HAWKINS, PHILLIP R.
; APPLICANT: SEILHAMER, JEFFREY J.
; TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 HILLVIEW AVENUE
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,883
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/419,078
; FILING DATE: 10-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: LUTHER, BARBARA J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF0030 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-855-0572
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 566 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; LIBRARY: NO. 5676946
; CLONE: 9118
; US-08-726-883-2

Query Match 40.0%; Score 38; DB 1; Length 566;
Best Local Similarity 43.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT '26

US-08-272-255-7
; Sequence 7, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
; APPLICANT: Cashmore, Anthony R.
; APPLICANT: Ahmad, Margaret
; APPLICANT: Lin, Chentao
; TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
; TITLE OF INVENTION: Using the Same
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT '26

US-08-272-255-7
; Sequence 7, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
; APPLICANT: Cashmore, Anthony R.
; APPLICANT: Ahmad, Margaret
; APPLICANT: Lin, Chentao
; TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
; TITLE OF INVENTION: Using the Same
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT '26

US-08-272-255-7
; Sequence 7, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
; APPLICANT: Cashmore, Anthony R.
; APPLICANT: Ahmad, Margaret
; APPLICANT: Lin, Chentao
; TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
; TITLE OF INVENTION: Using the Same
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT '26

US-08-272-255-7
; Sequence 7, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
; APPLICANT: Cashmore, Anthony R.
; APPLICANT: Ahmad, Margaret
; APPLICANT: Lin, Chentao
; TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
; TITLE OF INVENTION: Using the Same
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT '26

US-08-272-255-7
; Sequence 7, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
; APPLICANT: Cashmore, Anthony R.
; APPLICANT: Ahmad, Margaret
; APPLICANT: Lin, Chentao
; TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
; TITLE OF INVENTION: Using the Same
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT '26

US-08-272-255-7
; Sequence 7, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
; APPLICANT: Cashmore, Anthony R.
; APPLICANT: Ahmad, Margaret
; APPLICANT: Lin, Chentao
; TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
; TITLE OF INVENTION: Using the Same
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,255
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: UPN-1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

Qy 1 RIAKRGKLVYDSAR 16

Db 241 KIFQGESPVYDGG 256

RESULT '26

US-08-272-255-7
; Sequence 7, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
; APPLICANT: Cashmore, Anthony R.
; APPLICANT: Ahmad, Margaret
; APPLICANT: Lin, Chentao
; TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
; TITLE OF INVENTION: Using the Same
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-272-255-7

Query Match 40.0%; Score 38; DB 2; Length 615;
Best Local Similarity 43.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AKRGKLVYDSARH 18
Db 312 APEGKRLRDEKARYH 327

RESULT 27

PCT-US95-08565-7
Sequence 7, Application PC/TUS9508565
GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R.
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08565
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,255
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08565-7

Query Match 40.0%; Score 38; DB 5; Length 615;
Best Local Similarity 43.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AKRGKLVYDSARH 18
Db 312 APEGKRLRDEKARYH 327

RESULT 28

US-09-252-991A-16679
Sequence 16679, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16679
LENGTH: 887
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16679

Query Match 40.0%; Score 38; DB 4; Length 887;
Best Local Similarity 47.1%; Pred. No. 3.2e+02;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 IAKRGKLVYDSARH 18
Db 253 LADRGASGVDQDDPROH 269

RESULT 29

US-09-252-991A-22792
Sequence 22792, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22792
LENGTH: 990
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22792

Query Match 40.0%; Score 38; DB 4; Length 990;
Best Local Similarity 46.2%; Pred. No. 3.6e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 5 RGKLVYDSARH 17
Db 205 RGKLVNWDTKLH 217

RESULT 30

US-08-365-486A-21
Sequence 21, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates

```
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1433 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-486A-21

Query Match 40.0%; Score 38; DB 2; Length 1433;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 2 IAKGRKLVLD--YDSA 15
Db 65 LAVNGRPLVLSYDSA 80

RESULT 31
US-09-123-708-4
; Sequence 4, Application US/09123708
; Patent No. 614687
; GENERAL INFORMATION:
; APPLICANT: SCHRAEDER, Juergen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; FILE REFERENCE: 511169-2003
; CURRENT FILING DATE: 1998-07-28
; EARLIER FILING DATE: 1996-03-01
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-09-123-708-4

Query Match 40.0%; Score 38; DB 3; Length 1433;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 2 IAKGRKLVLD--YDSA 15
Db 65 LAVNGRPLVLSYDSA 80

RESULT 32
US-09-123-624-4
; Sequence 4, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRAEDER, Juergen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR FILING DATE: 4411402.8
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-123-624-4

Query Match 40.0%; Score 38; DB 3; Length 1433;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 2 IAKGRKLVLD--YDSA 15
Db 65 LAVNGRPLVLSYDSA 80

RESULT 33
US-08-880-342-21
; Sequence 21, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
```


; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1433 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-342-21

Query Match 40.0%; Score 38; DB 3; Length 1433;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IAKGRKLVLD--YDSA 15
: |||||
Db 65 LAVNGRPLVLDLYDSA 80

RESULT 34
US-08-365-486A-19
; Sequence 19, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:

; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-486A-19

Query Match 40.0%; Score 38; DB 2; Length 1434;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IAKGRKLVLD--YDSA 15
: |||||
Db 65 LAVNGRPLVLDLYDSA 80

RESULT 35
US-08-880-342-19
; Sequence 19, Application US/08880342
; Patent No. 6216179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.

; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.

; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-342-19

Query Match 40.0%; Score 38; DB 3; Length 1434;
Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IAKGRKLVLD--YDSA 15
: |||||
Db 65 LAVNGRPLVLDLYDSA 80

RESULT 36
US-09-661-258-1
; Sequence 1, Application US/09661258
; Patent No. 6620615
; GENERAL INFORMATION:
; APPLICANT: Stuehr, Dennis J.
; APPLICANT: Adak, Subrata
; TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants
; FILE REFERENCE: 26473/04028
; CURRENT APPLICATION NUMBER: US/09/661,258
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1434
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-661-258-1

Query Match 40.0%; Score 38; DB 4; Length 1434;

Best Local Similarity 62.5%; Pred. No. 5.5e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IAKGRKLVLD--YDSA 15
Db 65 LAVNGRPLVDLSYDSA 80

RESULT 37

US-08-705-625-3
; Sequence 3, Application US/08705625
; Patent No. 5908756
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon H.
; APPLICANT: Jaffrey, Samie R.
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,625
; FILING DATE: 30-AUG-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.57071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1554 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
US-08-705-625-3

Query Match 40.0%; Score 38; DB 2; Length 1554;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IAKGRKLVLD--YDSA 15
Db 65 LAVNGRPLVDLSYDSA 80

RESULT 38

US-09-010-998-6
; Sequence 6, Application US/09010998
; Patent No. 6103872
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon
; APPLICANT: Jaffrey, Samie
; APPLICANT: Snowman, Adele
; APPLICANT: Eliasson, Mikael
; APPLICANT: Cohen, No. 6103872m
; TITLE OF INVENTION: CAPON, a protein that binds
; TITLE OF INVENTION: neuronal nitric oxide synthase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,998
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.73424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1554 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6103872e
US-09-010-998-6

Query Match 40.0%; Score 38; DB 3; Length 1554;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IAKGRKLVLD--YDSA 15
Db 65 LAVNGRPLVDLSYDSA 80

RESULT 39

US-09-220-574-3
; Sequence 3, Application US/09220574
; Patent No. 6168926
; GENERAL INFORMATION:
; APPLICANT: Snyder, Solomon H.
; APPLICANT: Jaffrey, Samie R.
; TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
; TITLE OF INVENTION: Oxide Synthase
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,574
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,625
; FILING DATE: 30-AUG-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.57071
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1554 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Rattus norvegicus
 US-09-220-574-3

Query Match 40.0%; Score 38; DB 3; Length 1554;
 Best Local Similarity 62.5%; Pred. No. 6e+02; 3; Indels 2; Gaps 1;
 Matches 10; Conservative 1; Mismatches 3

Qy 2 IAKRGRKLVLD--YDSA 15
 : | | | | |
 Db 65 LAVNGRPLVLSYDSA 80

RESULT 40

US-09-732-210-1412
 ; Sequence 1412, Application US/09732210
 ; Patent No. 6573361
 ; GENERAL INFORMATION:
 ; APPLICANT: Bunkers, Greg J.
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Mittanck, Cindy A.
 ; APPLICANT: Seale, Jeffrey W.
 ; APPLICANT: Wu, Yonnie S.
 ; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 ; FILE REFERENCE: 38-21(15036)B
 ; CURRENT APPLICATION NUMBER: US/09/732,210
 ; CURRENT FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,513
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,340
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 1753
 ; SEQ ID NO 1412
 ; LENGTH: 88
 ; TYPE: PRT
 ; ORGANISM: Haemophilus influenzae
 US-09-732-210-1412

Query Match 38.9%; Score 37; DB 4; Length 88;
 Best Local Similarity 58.3%; Pred. No. 37;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RIAKRGRKLVYD 12
 : | | | | |
 Db 57 RWVSRRLKLDY 68

RESULT 41

US-09-107-532A-5344
 ; Sequence 5344, Application US/09107532A
 ; Patent No. 6583275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 7310
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts

COUNTRY: USA
 ZIP: 02354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Atinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-8277
 TELEFAX: (781)893-5007
 INFORMATION FOR SEQ ID NO: 5344:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 105 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1...105
 SEQUENCE DESCRIPTION: SEQ ID NO: 5344:
 US-09-107-532A-5344

Query Match 38.9%; Score 37; DB 4; Length 105;
 Best Local Similarity 46.7%; Pred. No. 45;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 4 KRGRKLVYDSARH 18
 : | | | | |
 Db 29 KKNTKLCPHDSNRH 43

RESULT 42

US-09-732-210-577
 ; Sequence 577, Application US/09732210
 ; Patent No. 6573361
 ; GENERAL INFORMATION:
 ; APPLICANT: Bunkers, Greg J.
 ; APPLICANT: Liang, Jihong
 ; APPLICANT: Mittanck, Cindy A.
 ; APPLICANT: Seale, Jeffrey W.
 ; APPLICANT: Wu, Yonnie S.
 ; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 ; FILE REFERENCE: 38-21(15036)B
 ; CURRENT APPLICATION NUMBER: US/09/732,210
 ; CURRENT FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,513
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: US 60/169,340
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 1753
 ; SEQ ID NO 577
 ; LENGTH: 145
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus carnosus
 US-09-732-210-577

Query Match 38.9%; Score 37; DB 4; Length 145;
 Best Local Similarity 50.0%; Pred. No. 64;

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6: Gaps 1;

1 RIAKRGKLVYDS-----ARH 17

Search completed: March 4, 2004, 17:47:40
Job time : 21.5806 secs

QY 61 YKDLKNFLSAVKVMHSSKRVSETLOEYSSWDGHEELKAIWNNDLWEDYEKLADQ 120
 DB 61 YKDLKNFLSAVKVMHSSKRVSETLOEYSSWDGHEELKAIWNNDLWEDYEKLADQ 120
 QY 121 AVRTMEIYVAQSFSEIKERIAKRGKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 180
 DB 121 AVRTMEIYVAQSFSEIKERIAKRGKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 180
 QY 181 TVPFDLNOELLELPILYNSRIGCYVTIFONISNLRDVFYR 221
 DB 181 TVPFDLNOELLELPILYNSRIGCYVTIFONISNLRDVFYR 221

RESULT 2

Q86VVO ID Q86VVO PRELIMINARY; PRT; 565 AA.
 AC Q86VVO
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Breast cancer associated protein BRAP1.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Beasak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalka U., Smillius D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RE EMBL; BC047686; AAH47686.1; -
 DR GO; GO:0006897; P: endocytosis; IEA.
 DR GO; GO:0007268; P: synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR_dom.
 DR Pfam; PF03114; BAR; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR SMART; SM00721; BAR; 1.
 SQ SEQUENCE 565 AA; 61875 MW; 81D1FB99A7707EA3 CRC64;

Query Match 99.1%; Score 1114.5; DB 4; Length 565;
 Best Local Similarity 99.1%; Pred. No. 2.7e-63;
 Matches 221; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MAEGKAGGAGLFAKQVOKKFSRAQKVLQKLGKAVETKDERPEQSASNFYQQAEHGKL 60
 DB 1 MAEGKAGGAGLFAKQVOKKFSRAQKVLQKLGKAVETKDERPEQSASNFYQQAEHGKL 60

QY 61 YKDLKNFLSAVKVMHSSKRVSETLOEYSSWDGHEELKAIWNNDLWEDYEKLADQ 120
 DB 61 YKDLKNFLSAVKVMHSSKRVSETLOEYSSWDGHEELKAIWNNDLWEDYEKLADQ 120
 QY 121 AVRTMEIYVAQSFSEIKERIAKRGKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 179
 DB 121 AVRTMEIYVAQSFSEIKERIAKRGKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 180
 QY 180 QTVFEDLNOELLELPILYNSRIGCYVTIFONISNLRDVFYR 221
 DB 181 QTVFEDLNOELLELPILYNSRIGCYVTIFONISNLRDVFYR 222

RESULT 3

Q9UBWS ID Q9UBWS PRELIMINARY; PRT; 565 AA.
 AC Q9UBWS
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Breast cancer associated protein BRAP1.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miki Y., Saito H.;
 RT "Genomic structure and chromosome location of the BRAP1 gene.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB032710; BAA88125.1; JOINED.
 DR EMBL; AB032699; BAA88125.1; JOINED.
 DR EMBL; AB032700; BAA88125.1; JOINED.
 DR EMBL; AB032701; BAA88125.1; JOINED.
 DR EMBL; AB032702; BAA88125.1; JOINED.
 DR EMBL; AB032703; BAA88125.1; JOINED.
 DR EMBL; AB032704; BAA88125.1; JOINED.
 DR EMBL; AB032705; BAA88125.1; JOINED.
 DR EMBL; AB032706; BAA88125.1; JOINED.
 DR EMBL; AB032707; BAA88125.1; JOINED.
 DR EMBL; AB032708; BAA88125.1; JOINED.
 DR EMBL; AB032709; BAA88125.1; JOINED.
 DR EMBL; AB032698; BAA88108.1; -
 DR Genew; HGNC:1053; BINZ.
 DR GO; GO:0006897; P: endocytosis; IEA.
 DR GO; GO:0007268; P: synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR_dom.
 DR Pfam; PF03114; BAR; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR SMART; SM00721; BAR; 1.
 SQ SEQUENCE 565 AA; 61902 MW; 28D1FB89A7779860 CRC64;

Query Match 98.8%; Score 1111.5; DB 4; Length 565;
 Best Local Similarity 99.1%; Pred. No. 4.2e-63;
 Matches 220; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MAEGKAGGAGLFAKQVOKKFSRAQKVLQKLGKAVETKDERPEQSASNFYQQAEHGKL 60
 DB 1 MAEGKAGGAGLFAKQVOKKFSRAQKVLQKLGKAVETKDERPEQSASNFYQQAEHGKL 60

QY 61 YKDLKNFLSAVKVMHSSKRVSETLOEYSSWDGHEELKAIWNNDLWEDYEKLADQ 120
 DB 61 YKDLKNFLSAVKVMHSSKRVSETLOEYSSWDGHEELKAIWNNDLWEDYEKLADQ 120
 QY 121 AVRTMEIYVAQSFSEIKERIAKRGKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 179
 DB 121 AVRTMEIYVAQSFSEIKERIAKRGKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 180
 QY 180 QTVFEDLNOELLELPILYNSRIGCYVTIFONISNLRDVFYR 221

Db 181 QTVFEDLNQELLELPILYNSRIGCYVTIFQNISLNRDVFYR 222

RESULT 4

ID Q80313 PRELIMINARY; PRT; 524 AA.
AC Q80313;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to bridging integrator 2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044473; AAH44473.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
DR SEQ SEQUENCE 524 AA; 59280 MW; F4A2988732D153FF CRC64;

Query Match 69.8%; Score 782.5; DB 13; Length 524;

Best Local Similarity 65.7%; Pred. No. 3.7e-42;

Matches 151; Conservative 34; Mismatches 36; Indels 9; Gaps 2;

QY 1 MARGK-----AGGAAGLFAKOVKFSRAQEKVLOKLGAVETKDERFEQASNFYQ 52
DB 1 MADGKLGTVGNIGAGILAKRFQSNRAQEKVLOKLGKMTKDEQFEESANLNK 60
QY 53 QQAEGHKLKOLKNFLSVKVMHSSKRVSETLQRIYSSEVDGHEELKAIYVNNDLLED 112
DB 61 QQTGDLRLYKDYKAYNAVKVMHSSKRLSQTLDIYEPDWHGVEDLTVINESDILLND 120
QY 113 YEEKLADQAVRTMEIYVAQFSIKERIAKGRKLVYDSARHLEAVQNA-KDEAKTAK 171
DB 121 YEEKLNDQVVRTMENTAQFDVKERAKGRKLVYDSARHLEAVQNA-KDEAKTAK 180
QY 172 ABEFNKAQTVFEDLNQELLELPILYNSRIGCYVTIFQNISLNRDVFYR 221
DB 181 ABEFNKAQEVFEDINKLEELPVLVYQSRISCYVTMFQNISLNRDVFYK 230

RESULT 5

ID Q9BTH3 PRELIMINARY; PRT; 439 AA.
AC Q9BTH3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Similar to bridging integrator 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,

RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) System Donor
vector.";

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -P- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR EMBL; BC004101; AAH04101.1; -.
DR EMBL; BT006865; AAP35511.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR InterPro; IPR000875; Cectropin.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRODOM; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00268; CECTROPIN; 1.
DR PROSITE; PS00002; SH3; 1.
KW SH3 domain.

SEQ SEQUENCE 439 AA; 48286 MW; 350E428C8E198136 CRC64;

Query Match 60.7%; Score 683; DB 4; Length 439;

Best Local Similarity 61.0%; Pred. No. 6.7e-36;

Matches 136; Conservative 32; Mismatches 53; Indels 2; Gaps 2;

QY 1 MAE-KGAGAGLFAKOVKFSRAQEKVLOKLGAVETKDERFEQASNFYQQAEGHK 59
DB 1 MAEMSGKGTAGKIASNVQKLTAKQEKVLOKLGKADETKDEQFEQCVQNFNKLTEGR 60
QY 60 LYKDLKNFLSVKVMHSSKRVSETLQRIYSSEVDGHEELKAIYVNNDLLEDYEELAD 119
DB 61 LQKDLRTYLSVKVMHSSKRLNCLQEVYEPDPGRDEANKIANNDDLMDYHQLVD 120
QY 120 QAVRTMEIYVAQFSIKERIAKGRKLVYDSARHLEAVQNA-KDEAKTAKAEEFNK 178
DB 121 QALLTMDTVLGQFPDIKSRIAKGRKLVYDSARHYESLQTAKKDEAKIAKEELIK 180
QY 179 AQTVFEDLNQELLELPILYNSRIGCYVTIFQNISLNRDVFYR 221
DB 181 AOKVFEEMVNDVLOELPSLWNSRVGFYVNTFQSTAGLEENFHK 223

RESULT 6

ID Q8WH9 PRELIMINARY; PRT; 490 AA.
AC Q8WH9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Amphiphysin IIb-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kim K.-C., Kim T.-S., Kang K.-H., Choi K.-H.;
RT "Amphiphysin IIb-1, a novel splicing variant of amphiphysin II,
regulates p73b function through protein-protein interactions.";
RL Oncogene 0:0-0(2002).
DR EMBL; AF411606; AAL38509.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR InterPro; IPR001452; SH3.

DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 SQ SEQUENCE 490 AA; 53167 MW; 8F50F36F7B6E9690 CRC64;

Query Match 60.7%; Score 683; DB 4; Length 490;
 Best Local Similarity 61.0%; Pred. No. 7.6e-36;
 Matches 136; Conservative 32; Mismatches 53; Indels 2; Gaps 2;

QY 1 MAE-KGAGAGLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQASNFYQQQAGHK 59
 DB 1 MAEMSGKGVTAAGKIASNVQKGLTRAQKVLQKLGKADETKDEQFECVQNFKNQLTEGTR 60
 QY 60 LYKDLKNFLSAVKVMHSSKSEVSTLQEIYSSWDGHEELKAIWVNDLLWEDYEKLAD 119
 DB 61 LQKDLRTYLVASVKAMHSEKSKINCELOEVYEPDWPGRDEANKIAENNDLLWMDYHQKJVD 120
 QY 120 QAVRTMEIYVQFSEIKERIAKGRKLVYDYSARHLEAVQNA-KDEAKTAKABEEFNK 178
 DB 121 QALLTMDTYLGQFPDIKSRIAKGRKLVYDYSARHLEAVQNA-KDEAKTAKABEEFNK 180
 QY 179 AQTFVEDLNQELLELPILNSRIGCVYVTFQNISNLRDVYR 221
 DB 181 AQVFEEKNVDLQELPILNSRIGCVYVTFQSIAGLEENFHK 223

RESULT 7
 Q7ZWP5 PRELIMINARY; PRT; 478 AA.

ID Q7ZWP5
 AC Q7ZWP5
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Similar to bridging integrator 1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Barachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 ON NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC046852; AAH46852.1; -.
 DR GO; GO:0006897; P: endocytosis; IEA.
 DR GO; GO:0007268; P: synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR_dom.
 DR InterPro; IPR004452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR PROSITE; PS00452; SH3DOMAIN.
 DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00002; SH3; 1.
 SQ SEQUENCE 478 AA; 53445 MW; 042A1A94D59095A8 CRC64;

Query Match 58.9%; Score 662.5; DB 13; Length 478;
 Best Local Similarity 58.6%; Pred. No. 1.5e-34;
 Matches 130; Conservative 35; Mismatches 56; Indels 1; Gaps 1;

QY 1 MAEKGAGAGLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQASNFYQQQAGHK 60
 DB 1 MAELGKGVSAAGKIASNVQKGLTRAQKVLQKLGKADETKDEQFECVQNFKNQLTEGSK 60
 QY 61 YKDLKNFLSAVKVMHSSKSEVSTLQEIYSSWDGHEELKAIWVNDLLWEDYEKLADQ 120

DB 61 QKDLRAYLATVKAMHEASKKLTCELLDVYEPDWPGRDEETNKIAENNDLLWTDYHQKJVDQ 120
 QY 121 AVRTMEIYVQFSEIKERIAKGRKLVYDYSARHLEAVQNA-KDEAKTAKABEEFNKA 179
 DB 121 ALLTMDTYLGQFPDIKSRIAKGRKLVYDYSARHLEAVQNA-KDEAKTAKABEEFNKA 180
 QY 180 QTVFEDLNQELLELPILNSRIGCVYVTFQNISNLRDVYR 221
 DB 181 QKVFEEKNVDLQELPILNSRIGCVYVTFQSIAGLEENFHK 222

RESULT 8
 Q8BXH2 PRELIMINARY; PRT; 250 AA.

ID Q8BXH2
 AC Q8BXH2
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Similar to MYC box dependent interacting protein 1.
 GN AMPH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The PANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK047144; BAC32971.1; -.
 DR MGD; MGI:103574; Amph.
 DR GO; GO:0006897; P: endocytosis; IEA.
 DR GO; GO:0007268; P: synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR_dom.
 DR Pfam; PF03114; BAR; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR SMART; SM00721; BAR; 1.
 SQ SEQUENCE 250 AA; 29125 MW; 568A3D55CC6C37CE CRC64;

Query Match 55.6%; Score 625.5; DB 11; Length 250;
 Best Local Similarity 55.2%; Pred. No. 1.6e-32;
 Matches 117; Conservative 49; Mismatches 45; Indels 1; Gaps 1;

QY 11 GLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQASNFYQQQAGHKYKDLKNFLSA 70
 DB 7 GIFAQVQKFLNRAQKVLQKLGKADETKDEQFECVQNFKNQLTEGRLGYLAA 66
 QY 71 VKVMHSSKSEVSTLQEIYSSWDGHEELKAIWVNDLLWEDYEKLADQAVRTMEIYVA 130
 DB 67 IKGQEASMKLTESLHEVYEPDWPGRDEAVMVGKCDVLWEDFHQKJVDGSLTLDYVLG 126
 QY 131 QFSEIKERIAKGRKLVYDYSARHLEAVQNA-KDEAKTAKABEEFNKAQTVFEDLNQE 189
 DB 127 QFPDIKNRIAKGRKLVYDYSARHLEAVQNA-KDEAKTAKABEEFNKAQTVFEDLNQE 186
 QY 190 LLELPILNSRIGCVYVTFQNISNLRDVYR 221
 DB 187 LQELPILNSRIGCVYVTFQNVSSLEAKFHK 218

RESULT 9
 Q7TQF7 PRELIMINARY; PRT; 686 AA.

ID Q7TQF7
 AC Q7TQF7
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimutz J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC054718; AAF54718.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 686 AA; 75013 MW; D292E24653A442A5 CRC64;
 Query Match 55.6%; Score 625.5; DB 11; Length 686;
 Best Local Similarity 55.2%; Pred. No. 5.2e-32;
 Matches 117; Conservative 49; Mismatches 45; Indels 1; Gaps 1;
 QY 11 GLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQASNFYQQQAEHGKLYKDLNFLSA 70
 Db 7 GIFAKNVQKLNRAQKVLQKLGKADETKDSQFEYVQNFQKQAEGRQLRELRLGYLAA 66
 QY 71 VKVHSSKRVSTLQETIYSSWDGHEELKAIWNNDLLWEDYEKLADQAVRTMEIYVA 130
 Db 67 IKGMQASMKLTESLHEVYEDWYGRDVKWVGKCDVLWEDFHQKLVGSLLLDTYLG 126
 QY 131 QPSEIKERIAKGRKLVYDSARHLEAVQNAK-KDEAKTAKAEFEFNKAQTVFEDLNQE 189
 Db 127 QFPDIKNRIAKSRKLVYDSARHLEALQSSKRDSSRSKAEFEFQKQKVFEEFNVD 186
 QY 190 LLEELPILNSRIGCVYTFQNISNLRDVFYR 221
 Db 187 LQELFSLNSRRVGFYVNTFNKVSLEAKFKH 218
 RESULT 10
 ID Q8NFL3 PRELIMINARY; PRT; 385 AA.
 AC Q8NFL3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amphiphsin I variant NT2 (fragment).
 GN AMPH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; BC034376; AAF34376.1; --
 DR GO; GO:0007268; P:synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphsin.
 DR InterPro; IPR003017; Amphiphsin_1.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PRO1251; AMPHIPHYSIN.
 DR NCBI_TaxID=9606;
 DR ProDom; PD003208; Amphiphsin_1; 1.

RP SEQUENCE FROM N.A.
 RC MEDLINE=22017878; PubMed=12023042;
 RA Terada Y., Tsutsui K., Sano K., Hosoya O., Ohtsuki H., Tokunaga A.,
 RA Teutsui K.;
 RT "Novel splice variants of amphiphsin I are expressed in retina.";
 RL FEBS Lett. 519:185-190(2002).
 DR EMBL; AF498097; AAM44811.1; --
 DR GO; GO:0006897; P:endocytosis; IEA.
 DR GO; GO:0007268; P:synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphsin.
 DR InterPro; IPR003017; Amphiphsin_1.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR dom.
 DR Pfam; PF03114; BAR; 1.
 DR PRINTS; PRO1251; AMPHIPHYSIN.
 DR ProDom; PD003208; Amphiphsin_1; 1.
 DR SMART; SM00721; BAR; 1.
 FT NON_TER 385 385
 SQ SEQUENCE 385 AA; 43753 MW; 4B9AB0A3136711AA CRC64;
 Query Match 55.2%; Score 620.5; DB 4; Length 385;
 Best Local Similarity 54.7%; Pred. No. 5.6e-32;
 Matches 116; Conservative 49; Mismatches 46; Indels 1; Gaps 1;
 QY 11 GLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQASNFYQQQAEHGKLYKDLNFLSA 70
 Db 7 GIFAKNVQKLNRAQKVLQKLGKADETKDSQFEYVQNFQKQAEGRQLRELRLGYLAA 66
 QY 71 VKVHSSKRVSTLQETIYSSWDGHEELKAIWNNDLLWEDYEKLADQAVRTMEIYVA 130
 Db 67 IKGMQASMKLTESLHEVYEDWYGRDVKWVGKCDVLWEDFHQKLVGSLLLDTYLG 126
 QY 131 QPSEIKERIAKGRKLVYDSARHLEAVQNAK-KDEAKTAKAEFEFNKAQTVFEDLNQE 189
 Db 127 QFPDIKNRIAKSRKLVYDSARHLEALQSSKRDSSRSKAEFEFQKQKVFEEFNVD 186
 QY 190 LLEELPILNSRIGCVYTFQNISNLRDVFYR 221
 Db 187 LQELFSLNSRRVGFYVNTFNKVSLEAKFKH 218
 RESULT 11
 ID Q8N4G0 PRELIMINARY; PRT; 695 AA.
 AC Q8N4G0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amphiphsin (Stiff-Man syndrome with breast cancer 128kd
 DE autoantigen).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; BC034376; AAF34376.1; --
 DR GO; GO:0006897; P:endocytosis; IEA.
 DR GO; GO:0007268; P:synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphsin.
 DR InterPro; IPR003017; Amphiphsin_1.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PRO1251; AMPHIPHYSIN.
 DR NCBI_TaxID=9606;
 DR ProDom; PD003208; Amphiphsin_1; 1.

Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

[4]
RL SEQUENCE FROM N.A.
RN STRAIN=Berkeley;
RC Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Friese E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AE003821; AAF58486.1; -;
DR EMBL; AF171225; AAD46684.1; -;
DR EMBL; AJ242855; CAB45188.1; -;
DR EMBL; AY061278; AAL28846.1; -;
DR HSP; P27986; IPTH.
DR FlyBase; FBgn0027356; Amph.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0007269; P:neurotransmitter secretion; NAS.
DR GO; GO:0008104; P:protein localization; IMP.
DR GO; GO:0006937; P:regulation of muscle contraction; IMP.
DR GO; GO:0045313; P:rhabdomyer membrane biogenesis; IMP.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PRODOM; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
DR SH3 domain.
KW SH3 domain.
SQ SEQUENCE 602 AA; 65901 MW; 86D1D4CB AE1B8F31 CRC64;

Query Match 38.2%; Score 429.5; DB 5; Length 602;

Best Local Similarity 40.1%; Pred. No. 1.4e-19;
Matches 85; Conservative 43; Mismatches 51; Indels 3; Gaps 1;

QY 12 LPKQVQKFFRAQKVLQKLGKAVETKDRFQSASNFYQQQAEHGKLYKDLKFLS 71
DB 8 MLKSVQGHAGRAKEKILQNLGKVDRTADEIFDHLNFRQASANRLQKEFNRYRCV 67
QY 72 KMHSSKRVSETLQELYSSEWDGHEELKALVWNNLLMEDYEKLADQAVRTMEIYV 131
DB 68 RAAQASKTLMDSCVEIYEQWSDYDALQATGASLSLWADFAHKLGDQVLIPLNTYTGQ 127
QY 132 FSEIKERIAKGRKLVYDYSARH---HLEAVQNAKDEAKTAKAEFEFNKAQTVFEDLNQ 188
DB 128 PPMKKCKVEKNRKLIDYDGRHSFQNLQANAKRQDDVKLTGREGLEEARVTEILNT 187
QY 189 ELLELPILYNSRGCVTTFQNISNLRDVFY 220
DB 188 ELHDELPAVDSRLFLVTLNQLTLFATEQVVFH 219

RESULT 14

Q21004
ID Q21004 PRELIMINARY; PRT; 461 AA.
AC Q21004;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F58G6.1 protein.
GN F58G6.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]

RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;

RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RT Science 282:2012-2018 (1998).

CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; Z68217; CAA92465.1; -;
DR PIR; T22946; T22946.
DR WormPep; F58G6.1; CE03428.

DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.

DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR dom.
DR InterPro; IPR001452; SH3.

DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.

DR PRODOM; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.

DR PROSITE; PS00002; SH3; 1.
DR SH3 domain.
SQ SEQUENCE 461 AA; 51910 MW; 771C89E21EF7BEC8 CRC64;

Query Match 36.0%; Score 405; DB 5; Length 461;

Best Local Similarity 39.6%; Pred. No. 3.8e-18;
Matches 84; Conservative 52; Mismatches 74; Indels 2; Gaps 2;

QY 10 AGLPAQVQKFFRAQKVLQKLGKAVETKDRFQSASNFYQQQAEHGKLYKDLKFLS 69
DB 2 ADLFNKLKATNRTKEKLGKAKATQDEVDFDQHANLNKQSKCEKLNKVDKNTSS 61
QY 70 AVKMHSSKRVSETLQELYSSEWDGHEELKALVWNNLLMEDYEKLADQAVRTMEIYV 129
DB 62 ALRTLSSAEQLKRDITRDAYEPDPREHLTAIFNLDIQTNELEKTVCDLDPQVTVQV 121
QY 130 AQFSEIKERIAKGRKLVYDYSARHLEAVQ-NAKQD-EAKTAKAEFEFNKAQTVFEDLN 187
DB 122 NQFPDLKCKIEKGRKLVYDYSAKNSFNSVKASSKNDPKLAKATMELQAEQMYTEMN 181
QY 188 QELLELPILYNSRGCVTTFQNISNLRDVF 219
DB 182 NELLELPVAFDSRITFFVDTLQTLFNANSVY 213

RESULT 15

Q8X0D7
ID Q8X0D7 PRELIMINARY; PRT; 273 AA.
AC Q8X0D7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Probable cytoskeletal binding protein.
GN B14A6.200.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 17:29:55 ; Search time 16.8917 Seconds
(without alignments)
2762.588 Million cell updates/sec

Title: US-10-069-540A-2_COPY_1_221

Perfect score: 1125
Sequence: 1 MARGKAGGAGLFAKQVQKK.....ICQYVIFQNLISLRDVFYR 221

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	689	61.2	434	9	US-09-879-957-22
2	683	60.7	482	15	US-10-116-275-238
3	671.5	59.7	451	14	US-10-123-807-4
4	559.5	49.7	404	9	US-09-879-957-24
5	181.5	16.1	284	15	US-10-369-493-2410
6	179.5	16.0	265	15	US-10-369-493-1519
7	160.5	14.3	452	15	US-10-369-493-3119
8	158.5	14.1	489	15	US-10-369-493-2512
9	155.5	13.8	351	15	US-10-369-493-3387
10	154.5	13.7	482	15	US-10-369-493-1690
11	148.5	13.2	265	15	US-10-369-493-12681
12	144	12.8	237	15	US-10-369-493-2408
13	142.5	12.7	420	15	US-10-369-493-13382
14	139.5	12.4	474	14	US-10-032-585-7847
15	118.5	10.5	650	15	US-10-104-047-3636

16	114.5	10.2	853	15	US-10-320-797-3308
17	113	10.0	1005	15	US-10-369-493-1061
18	113	10.0	1881	14	US-10-032-585-7646
19	112.5	10.0	1138	15	US-10-369-493-5874
20	112.5	10.0	1138	15	US-10-369-493-5875
21	111.5	9.9	1790	15	US-10-369-493-1586
22	111	9.9	600	15	US-10-367-687-16
23	110.5	9.8	1169	15	US-10-369-493-1095
24	110	9.8	1938	14	US-10-171-311-164
25	110	9.8	1945	10	US-09-927-597-2
26	110	9.8	1972	14	US-10-171-311-162
27	110	9.8	1972	15	US-10-341-434-103
28	110	9.8	1979	10	US-09-927-597-4
29	109.5	9.7	944	15	US-10-369-493-1682
30	109.5	9.7	1225	15	US-10-369-493-21875
31	109.5	9.7	2139	9	US-09-727-384-6
32	109.5	9.7	2139	14	US-10-023-219-4
33	109	9.7	402	14	US-10-284-400-6
34	109	9.7	403	14	US-10-284-400-14
35	109	9.7	1170	15	US-10-369-493-21887
36	108.5	9.6	824	15	US-10-108-260A-4573
37	108.5	9.6	1043	15	US-10-310-154-449
38	108.5	9.6	1679	15	US-10-369-493-22080
39	107.5	9.6	936	15	US-10-104-047-2621
40	107.5	9.6	1045	9	US-09-815-242-10617
41	107.5	9.6	1948	14	US-10-032-585-7611
42	107	9.5	860	15	US-10-032-334-166
43	107	9.5	975	14	US-10-080-608A-19
44	107	9.5	975	15	US-10-370-685-108
45	106.5	9.5	1312	15	US-10-369-493-1950

ALIGNMENTS

RESULT 1

US-09-879-957-22
; Sequence 22, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWLES, Dana M.
McCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND USING SAME

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,957

FILING DATE: 13-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,915

FILING DATE: 03-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174

TELECOMMUNICATION INFORMATION:


```

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-879-957-22

Query Match          61.2%; Score 689; DB 9; Length 434;
Best Local Similarity 61.9%; Pred. No. 6.2e-48;
Matches 138; Conservative 30; Mismatches 53; Indels 2; Gaps 2;

QY 1 MAE-GKAGGAGLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQSASNFYQQAEGHK 59
Db 1 MAEWSKGVTAGKIASNVQKLTQAEQKVLQKLGKADETKDEQECVQNFNKLTEGTR 60
QY 60 LYKDLKNFLSAVKVMHSSKRSVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEKLAD 119
Db 61 LQDLRTYLSAYKAKHEASKLSECLQEVYEPWPGRDEANKIAENNDLLWMDYHQKLV 120
QY 120 QAVTMEIYVAQFSEIKERIAKGRKLVYDVSARHLEAVQNA-KDEAKTAKAEFEFNK 178
Db 121 QALLTMDTYLGQFPDIKSRIKGRKLVYDVSARHYESLQTAKKDEAKIAKAEELIK 180
QY 179 AQTVEFDLNOELLELPILYNSRICGVYTFQNISNLRDVFYR 221
Db 181 AQKVFEMVNDLQBELPSLWNSRVGFYNTFQSIAGLEENPHK 223

RESULT 2
US-10-116-275-238
; Sequence 238, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-238

Query Match          60.7%; Score 683; DB 15; Length 482;
Best Local Similarity 61.0%; Pred. No. 2.2e-47;
Matches 136; Conservative 32; Mismatches 53; Indels 2; Gaps 2;

QY 1 MAE-GKAGGAGLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQSASNFYQQAEGHK 59
Db 1 MAEWSKGVTAGKIASNVQKLTQAEQKVLQKLGKADETKDEQECVQNFNKLTEGTR 60
QY 60 LYKDLKNFLSAVKVMHSSKRSVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEKLAD 119
Db 61 LQDLRTYLSAYKAKHEASKLSECLQEVYEPWPGRDEANKIAENNDLLWMDYHQKLV 120
QY 120 QAVTMEIYVAQFSEIKERIAKGRKLVYDVSARHLEAVQNA-KKDEAKTAKAEFEFNK 178
Db 121 QALLTMDTYLGQFPDIKSRIKGRKLVYDVSARHYESLQTAKKDEAKIAKAEELIK 180

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QY 179 AQTVEFDLNOELLELPILYNSRICGVYTFQNISNLRDVFYR 221
Db 181 AQKVFEMVNDLQBELPSLWNSRVGFYNTFQSIAGLEENPHK 223

RESULT 3
US-10-123-807-4
; Sequence 4, Application US/10123807
; Publication No. US20030166021A1
; GENERAL INFORMATION:
; APPLICANT: Wistar Institute of Anatomy & Biology
; Prendergast, George C.
; Sakamuro, Daitoku
; TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/123,807
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/445,247
; FILING DATE: 03-Dec-1999
; APPLICATION NUMBER: US 08/870,126
; FILING DATE: 08-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60DPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5618
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-123-807-4

Query Match          59.7%; Score 671.5; DB 14; Length 451;
Best Local Similarity 61.5%; Pred. No. 1.7e-46;
Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;

QY 10 AGLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQSASNFYQQAEGHKLYKDLKNFLS 69
Db 8 AGKIASNVQKLTQAEQKVLQKLGKADETKDEQECVQNFNKLTEGTRLQDLRTYLA 67
QY 70 AVKVVHESKRSVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEKLADQAVTMEIYV 129
Db 68 SVKAMHEASKLNCECLQEVYEPWPGRDEANKIAENNDLLWMDYHQKLVQALLTMDTYL 127
QY 130 AQFSEIKERIAKGRKLVYDVSARHLEAVQNA-KDEAKTAKAEFEFNKAQTVFEDLNQ 188
Db 128 CQFPDIKSRIKGRKLVYDVSARHYESLQTAKKDEAKIAKAEELIKAQKVFEMV 187
QY 189 ELLELPILYNSRICGVYTFQNISNLRDVFYR 221
Db 188 DQBELPSLWNSRVGFYNTFQSIAGLEENPHK 220

```

RESULT 4

US-03-879-957-24
; Sequence 24, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWLKES, Dana M.
McCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,957

FILING DATE: 13-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,915

FILING DATE: 03-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mirock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 404 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-03-879-957-24

Query Match

Best Local Similarity 49.7%; Score 559.5; DB 9; Length 404;

Matches 107; Conservative 30; Mismatches 43; Indels 1; Gaps 1;

QY 42 RFEGASNFYQQAGHGKLYKDLKFNFLSAVKVMHESKRYSETLQEIYSEWDGHEELKA 101

DB 8 RFEGCVQNFKNQLTEGTRLQKDLRTLYLAVKAMHEASKKLNELQEVYEPDNGRDEANK 67

QY 102 IVMNNDLLWDEYEKLDAQVRTWEIYVAQFSIKERIAKRGKLYDVSARHLEAVQN 161

DB 58 IAEENDDLLWMDYHOKVQDQALLMTDTYLGQFDIKRIAKRGKLYDVSARHLYESLQT 127

QY 162 A-KKDEAKTAAKEEFNKAQTVFEDLNQELLBELPILYNSRIGCYVTTFQNTSNLRDVFY 220

DB 128 AKKDEAKTAAKEELIKAKVPEFNVNDLQELPSLWNSRVGYNTFQSIAGLEENFH 187

QY 221 R 221

DB 188 K 188

RESULT 5

US-10-369-493-2410

; Sequence 2410, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 2410

LENGTH: 284

TYPE: PRT

ORGANISM: Schizosaccharomyces pombe

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(284)

OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-2410

Query Match

Best Local Similarity 16.1%; Score 181.5; DB 15; Length 284;

Matches 51; Conservative 33; Mismatches 87; Indels 13; Gaps 5;

QY 28 VLOKLGKAVETKDERFEQASNFYQQAGHGKLYKDLKFNFLSAVKVMHESKRYSETLQOE 87

DB 37 VMKTHGVERTVDREFETERRRTRTWESAKKLQKAGKGYLDALRAMTASQTRIANTIDA 96

QY 88 IYSEWDGHEELKAIYMNNDLLWEDYEE---KLADQAVRTWEI-----YVAQFSIKERI 139

DB 97 FYGDA--GSKDGVSAVYRQ--VVEDLDADTVKELDGPFRITVLDPISRFCSYFPDINAAI 152

QY 140 AKRGKLYDVSARHLE-AVQNAKQDEAKTAKAEEFNKAQTVFEDLNQELLBELPILY 198

DB 153 TKRNHKLDDHDAVRKVKLVDPKSPNDTTKLPRTKEAMAKEVYETLNNQLVSELPOLI 212

QY 199 NSRI 202

DB 213 ALRV 216

RESULT 6

US-10-369-493-1519

; Sequence 1519, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1519

LENGTH: 265

TYPE: PRT

ORGANISM: Saccharomyces cerevisiae

US-10-369-493-1519

```

Query Match      16.0%; Score 179.5; DB 15; Length 265;
Best Local Similarity 24.1%; Pred. No. 7.9e-07;
Matches 52; Conservative 50; Mismatches 87; Indels 27; Gaps 6;

QY 18 OKKFSRAQEKVLQKLGKAVETKDERFEQSASNFYQQQAEGHKLYKDLKNFLSAVKVMHES 77
Db 7 KKAINRAGHSVIUK-NVTKTIDKEYDWEERYKVLQAGEALQKEAKGFLDSLRAVTAS 64

QY 78 SKRVSETIQEY-SSEW-----DGHEELKAIWNNDLLWEDYEK-----LADQA 121
Db 65 OTTIAEVSINLYDDSKYVAGGYNVGYLQCV-----QDFSETVKQDGLPRTV 116

QY 122 VRTMEIYVAQSEIKERIAKGRKLVYDSARHHL-EAVQNAKDKBAKTAKAEFEFNKAQ 180
Db 117 LDPITKSTFYFEIIEBAKRDHKQDFDAKAKVRLVDPAKDASKLPRAEKELSLAK 176

QY 181 TVFEDLNQELBELFILYNSRIGCVYTFIQNISNL 216
Db 177 DIFENLNQLKTELPLQVLSLRVPYDFDPSFEALIKIQ 212

RESULT 7
US-10-369-493-3119
; Sequence 3119, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3119
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3119

Query Match      14.3%; Score 160.5; DB 15; Length 452;
Best Local Similarity 24.6%; Pred. No. 5.4e-05;
Matches 56; Conservative 39; Mismatches 96; Indels 37; Gaps 6;

QY 23 RAQEKVLQKLGKAVETKDERFEQSASNFYQQQAEGHKLYKDLKNFLSAVKVMHESKRVS 82
Db 1 QAPQPKQKFNLGHTKDPVYIDSERRFQELETFETKRLHDESKKYFEAINGLQHQTEFS 60

QY 83 ETLQEIYS-----SEWDG---HEELKAIWNNDLLWEDYEKLAQQ---- 120
Db 61 KAMTEIYKFIISGRMDDPSLVPHGNYGEGIAACEYEAVV-----KOLQETLAPELEMI 113

QY 121 ---AVRTMEIYVAQSEIKERIAKGRKLVYDSARHHLAEVQNAK-----KDEAKTKAAE 173
Db 114 EAVRIRPANELLDVIVKIRKTAKEHKLLDYDRHRAITKGLQDKORSADKAMWKAE 173

QY 174 EEFNKAQTVFEDLNQELBELFILYNSRIGCVYTFIQNISNL 220
Db 174 NEVEQATQSYNFNDLLKPELALEROFTLOPFOFOSFYWMOLNIFY 221

```

```

: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: APPLICANT: Goldman, Barry S.
: APPLICANT: Chen, Xianfeng
: TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
: TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
: FILE REFERENCE: 38-10(52052)B
: CURRENT APPLICATION NUMBER: US/10/369,493
: CURRENT FILING DATE: 2003-02-28
: PRIOR APPLICATION NUMBER: US 60/360,039
: PRIOR FILING DATE: 2002-02-21
: NUMBER OF SEQ ID NOS: 47374
: SEQ ID NO 2512
: LENGTH: 489
: TYPE: PRT
: ORGANISM: Schizosaccharomyces pombe
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)...(489)
: OTHER INFORMATION: unsure at all Xaa locations
: US-10-369-493-2512

Query Match          14.1%; Score 158.5; DB 15; Length 489;
Best Local Similarity 23.8%; Pred. No. 8.7e-05;
Matches 57; Conservative 39; Mismatches 99; Indels 45; Gaps 7;

QY      15 KQVQKKFSRAQKVLQKLKAVETKDRPFQSSANFYQQQAEGHGLYKDLKNFLSAVKVM 74
DB      4 KGFTKALARTQTLLRSKFNVEGKITKDPYEDAGRRFKSLTEAKKLAEDAKCYTDAINGL 63

QY      75 HESSKGVSETLQEIY-----SSEWDGH-----EELKAIYWNDDLWEDYEK 116
DB      64 LNHQIGFADACIETYP:SGRASDPSEYQEGNAEGTEAAEAYKBIYV-----DLQKN 116

QY      117 LADQAVRTWEIYVAQF-----SETKERIAKGRKLVDDYDSARHLEAVQNAK-- 163
DB      117 LASE-----MDVINTRIYVNTGSELLKIYKVDVKLLKEDHQLDYDRHSFSGFKQEKKDK 172

QY      164 --KDBAKTAAAEFBNKAQTVFDLNOELLEELPILYNSRIGCVYTFIQNISMLR-DVFY 220
DB      173 SLKDEKKLYEATAFEOSSQOYEYNNBMLKEELPKLFALAQSFAPLFOGFFYNNQLNVY 232

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; NAME/KEY: unsure
; LOCATION: (1)..(351)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3387

Query Match 13.8%; Score 155.5; DB 15; Length 351;
Best Local Similarity 21.3%; Pred. No. 0.0001;

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OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-2408

Query Match 12.8%; Score 144; DB 15; Length 237;
Best Local Similarity 26.4%; Pred. No. 0.00052;
Matches 46; Conservative 27; Mismatches 75; Indels 26; Gaps 5;
QY 40 DERFQASNFYQQAEGHKLKLDKNFLSAVKVHSSKRVSETLQEIY--SSEWDG-- 95
DB 1 DREFTERRVRYTWESAAKLOKEAGYLDALRAMTASQTRKANTIDAYGDSKDGVS 60
QY 96 -----HEELKAIWNNDLLWEDYEKLDAQVRT-----MEIYVAQFSEIKERIAKGR 144
DB 61 AYYRQVVEDLDA-----DTVKELDXLXRTTVXGPISRFCSPYPPDINAATKSNH 110
QY 145 KLVDYDSARHLE-AVQNAKDEAKTAKAEFEFNKAQTVFEDLNQELLELPIL 197
DB 111 KLLDHDAMRAKVQKLVDPKSPNDITKLPRTKEAAMAKEVETLNNTXGSELPLQ 164

RESULT 13

US-10-369-493-13382
Sequence 13382, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 13382

LENGTH: 420

TYPE: PRT

ORGANISM: Aspergillus nidulans

NAME/KEY: unsure

LOCATION: (1) (420)

OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-13382

Query Match 12.7%; Score 142.5; DB 15; Length 420;
Best Local Similarity 23.1%; Pred. No. 0.0014;
Matches 58; Conservative 40; Mismatches 104; Indels 49; Gaps 5;

QY 15 KQVQKFSRAQEKVLQKLGKAVETKDRFQASNFYQQAEGHKLKLDKNFLSAV--- 71
DB 4 XGFQKSVIRAPQTPFKARFNIGDNTKDPVYTDARRRFQELEKETKCLHDESKKYFDVAVNGR 63
QY 72 -----KVMHSSKRVSETLQEIYSSSEWDGHEELKAIYWN 105
DB 64 PRPDTFRLHSGXPAXGMLDHOIEFSKAMTELKPISGRASPDPSTVTIEGNEGRACEE 123
QY 106 NDLWEYEEKLADQ-----AVRTMEIYVAQFSEIKERIAKGRKLVYDSARH 154
DB 124 YEVIQDLKEALAPLELMIDSRVSPQAQLLEVIKA-----IRKVAVRDHHKLDYDRHN 179
QY 155 HLEAVONAK---KDEAKTAKAEFEFNKAQTVFEDLNQELLELPILYNSRGCVTFIQ 210
DB 180 TLKKLQDKQKSLKDEKALYKAGDVEQATQETYNLYNDLLKDELPLKFALEAFTRPLFQ 239
QY 211 NISNL-RDVFY 220
DB 240 SFYTMQLNVFY 250

RESULT 14

US-10-032-585-7847
Sequence 7847, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:

APPLICANT: Terry, Roemer D.

APPLICANT: Bo, Jiang

APPLICANT: Charles, Boone

APPLICANT: Howard, Bussey

TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery

FILE REFERENCE: 10182-005-999

CURRENT APPLICATION NUMBER: US/10/032,585

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 8000

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7847

LENGTH: 474

TYPE: PRT

ORGANISM: Candida albicans

US-10-032-585-7847

Query Match 12.4%; Score 139.5; DB 14; Length 474;

Best Local Similarity 21.5%; Pred. No. 0.0029;

Matches 53; Conservative 46; Mismatches 103; Indels 45; Gaps 6;

QY 15 KQVQKFSRAQEKVLQKLGKAVETKDRFQASNFYQQAEGHKLKLDKNFLSAVKVM 74
DB 38 KGFKGVLRAPQTPMRQKFNWGEITQDAVYLDARRFRFKEIEMETKCLSBESKKYFNANVM 97
QY 75 HESSKRVSETLQEIYS-----SEWDGHEELKAIYWN-NDLLWED--- 112
DB 98 LDEQIDFAKAVAEIYKPISGRLSDPSATVPEDNPGGIEASESYQAVVQKLDKTLKPLEL 157
QY 113 YEEKLADQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNAK---KDEAK 168
DB 158 IEKGIIVEPAQELKLIQA-----IRKMSVKRDHKQLDLDRHKRNFSKYESKKERTVQDEK 213
QY 169 TAKAEFEFNKAQTVFEDLNQELLELPIL-----YNSRIGCVYTFIQNIS 213
DB 214 MFSQAQAEVIAQCYDYNDLLKNEPLVLFQMSDFIKPLFVSYFYMLNFIYTLTYRME 273
QY 214 NLRDVFY 220
DB 274 ELKIPYF 280

RESULT 15

US-10-104-047-3636

Sequence 3636, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20030236392A1el full length cDNA

FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3636

LENGTH: 650

TYPE: PRT

ORGANISM: Homo sapiens

US-10-104-047-3636

Query Match 10.5%; Score 118.5; DB 15; Length 650;

Best Local Similarity 21.2%; Pred. No. 0.022;

Matches 40; Conservative 40; Mismatches 76; Indels 33; Gaps 7;

QY 18 QKFSRAQEKVLQKLGKAVETKDRFQASNFYQQAEGHKLKLDKNFLSAVKVMHES 77
DB 277 QBEELREQEKKIRKQEKQKWRQEEFLREQQKMGREQE---EKMWRQSKRLREQEKLREQ 333

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:38:36 ; Search time 42.3871 Seconds
(without alignments)
133.987 Million cell updates/sec

Title: US-10-069-540A-2_COPY_138_155

Perfect score: 95

Sequence: 1 RIAKGRKLVYDSARHH 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	439	4 Q9BTH3	Q9Bth3 homo sapien
2	95	100.0	490	4 Q8WH9	Q8wh9 homo sapien
3	95	100.0	564	4 Q9UKN4	Q9ukn4 homo sapien
4	95	100.0	565	4 Q9UBW5	Q9ubw5 homo sapien
5	95	100.0	565	4 Q86VW0	Q86vw0 homo sapien
6	91	95.8	478	13 Q7ZNP5	Q7znp5 xenopus lae
7	90	94.7	524	13 Q80313	Q80313 brachydanio
8	89	93.7	250	11 Q8BXH2	Q8bxh2 mus musculus
9	89	93.7	385	4 Q8NFL3	Q8nfl3 homo sapien
10	89	93.7	686	11 Q7TQF7	Q7tcf7 mus musculus
11	89	93.7	695	4 Q8N4G0	Q8n4g0 homo sapien
12	69	72.6	461	5 Q21004	Q21004 caenorhabdi
13	62	65.3	602	5 Q51092	Q5y092 drosophila
14	53	55.8	273	3 Q8XOD7	Q8xod7 neurospora
15	53	55.8	414	5 Q8WQ54	Q8wq54 geodia cydo
16	49.5	52.1	130	16 Q8X2J8	Q8x2j8 escherichia

17	48	50.5	169	17	Q9HQS1	Q9hqs1 halobacteri
18	47	49.5	424	10	Q64842	Q64842 arabidopsis
19	47	49.5	425	10	Q39229	Q39229 arabidopsis
20	47	49.5	441	10	Q9LEA1	Q9leal arabidopsis
21	47	49.5	578	10	Q9ZST7	Q9zst7 arabidopsis
22	47	49.5	578	10	Q9ZST6	Q9zst6 arabidopsis
23	47	49.5	578	10	Q9LV77	Q9lv77 arabidopsis
24	47	49.5	578	10	Q9LV77	Q9lv77 arabidopsis
25	46	48.4	1163	16	Q89JES	Q89jes bradyrhizob
26	45.5	47.9	83	16	Q83JK1	Q83jk1 shigella fl
27	45.5	47.9	596	4	Q9HT77	Q9ht77 homo sapien
28	45.5	47.9	742	4	Q8NAO4	Q8nao4 homo sapien
29	45.5	47.9	763	4	Q9ER66	Q9er66 homo sapien
30	45.5	47.9	813	4	Q8NE21	Q8ne21 homo sapien
31	45.5	47.9	836	4	Q8H2F5	Q8h2f5 homo sapien
32	45	47.4	128	9	Q852V9	Q852v9 mycobacteri
33	45	47.4	160	5	Q9UOX9	Q9uox9 leishmania
34	45	47.4	171	11	Q9D7W8	Q9d7w8 mus musculu
35	45	47.4	171	11	Q810A3	Q810a3 mus musculu
36	45	47.4	190	9	Q3ZXL0	Q3zxl0 bacterioph
37	45	47.4	524	16	Q8KD94	Q8kd94 chlorobium
38	44	46.3	263	16	Q7WDT3	Q7wdt3 bordetella
39	44	46.3	263	16	Q7W2T5	Q7w2t5 bordetella
40	44	46.3	297	16	Q7V8X1	Q7v8x1 bordetella
41	44	46.3	524	2	Q8GDV2	Q8gdv2 heliobacill
42	43.5	45.8	282	16	Q8ZN24	Q8zn24 salmonella
43	43.5	45.8	282	16	Q8ZAL1	Q8zal1 salmonella
44	43	45.3	349	16	Q7WFG2	Q7wfg2 bordetella
45	43	45.3	349	16	Q7VTS5	Q7vts5 bordetella
46	43	45.3	413	11	Q8BLU6	Q8blu6 mus musculu
47	43	45.3	819	11	Q8BUT2	Q8but2 mus musculu
48	43	45.3	859	11	Q8BWW6	Q8bww6 mus musculu
49	43	45.3	863	11	Q8BZ98	Q8bz98 mus musculu
50	43	45.3	869	11	Q9OXL9	Q9oxl9 rattus norv
51	42	44.2	130	16	Q8E3D2	Q8e3d2 streptococ
52	42	44.2	130	16	Q8DXR3	Q8dxr3 streptococ
53	42	44.2	252	17	Q28300	Q28300 archaeoglob
54	42	44.2	257	17	Q979L7	Q979l7 thermoplas
55	42	44.2	368	10	Q7XIE8	Q7xie8 oryza sativ
56	42	44.2	463	16	Q53770	Q53770 mycobacteri
57	42	44.2	463	16	Q7U1R1	Q7u1r1 mycobacteri
58	42	44.2	487	16	Q988V2	Q988v2 rhizobium l
59	42	44.2	578	16	Q8E4E2	Q8e4e2 coxiella bu
60	42	44.2	652	12	Q91AX4	Q91ax4 human papil
61	42	44.2	756	2	Q8KLH2	Q8klh2 rhizobium e
62	42	44.2	1193	16	Q9HZE5	Q9hze5 pseudomonas
63	42	44.2	1289	2	Q93IR7	Q93ir7 salmonella
64	42	44.2	1289	16	Q8ZRL2	Q8zrl2 salmonella
65	42	44.2	1957	5	Q04010	Q04010 onchocerca
66	41.5	43.7	181	10	Q940D5	Q940d5 cucumis mel
67	41.5	43.7	341	5	Q9UAM1	Q9uam1 leptomonas
68	41.5	43.7	361	5	Q96425	Q96425 leptomonas
69	41.5	43.7	593	16	Q826F7	Q826f7 streptomyc
70	41.5	43.7	731	10	Q39547	Q39547 cucumis mel
71	41.5	43.7	763	11	Q92299	Q92299 mus musculu
72	41.5	43.7	813	11	Q8C9X6	Q8c9x6 mus musculu
73	41	43.2	196	5	Q9XZT2	Q9xzt2 drosophila
74	41	43.2	196	5	Q9W588	Q9w588 drosophila
75	41	43.2	234	2	Q52596	Q52596 agrobacteri
76	41	43.2	237	16	Q8G353	Q8g353 mycobacteri
77	41	43.2	237	16	Q77231	Q77231 mycobacteri
78	41	43.2	338	5	Q18341	Q18341 bombyx mori
79	41	43.2	402	5	Q22968	Q22968 caenorhabdi
80	41	43.2	407	17	Q58864	Q58864 pyrococcus
81	41	43.2	457	16	Q7VHM6	Q7vhw6 helicobacte
82	41	43.2	469	16	Q8RAM6	Q8ram6 thermococ
83	41	43.2	469	16	Q8PVE1	Q8pve1 methanocarc
84	41	43.2	626	12	Q9DIH5	Q9dih5 human papil
85	41	43.2	629	10	Q987M1	Q987m1 oryza sativ
86	41	43.2	933	16	Q83GL1	Q83gl1 tropheryma
87	41	43.2	939	16	Q83HL6	Q83hl6 tropheryma
88	41	43.2	985	5	Q01590	Q01590 caenorhabdi
89	41	43.2	1001	2	Q9JP94	Q9jp94 rhodocyclu


```

90 41 43.2 1490 10 Q7XV99
91 41 43.2 1571 10 Q8S6M8
92 40.5 42.6 306 16 Q8XA42
93 40.5 42.6 306 16 Q8FF21
94 40.5 42.6 306 16 Q83K34
95 40.5 42.6 315 16 Q83714
96 40.5 42.6 408 16 Q8UC94
97 40.5 42.6 458 16 Q55941
98 40.5 42.6 728 11 Q8X0L5
99 40 42.1 78 16 Q8DBV5
100 40 42.1 89 16 Q87M05
101 40 42.1 161 17 Q8HINO
102 40 42.1 171 4 Q8NSM4
103 40 42.1 171 6 Q9BGT1
104 40 42.1 182 10 Q9SFV0
105 40 42.1 182 10 Q8GX56
106 40 42.1 211 16 Q89RR8
107 40 42.1 284 16 Q32734
108 40 42.1 276 16 Q82A55
109 40 42.1 290 4 Q9BUY3
110 40 42.1 298 16 Q8RCH8
111 40 42.1 305 16 Q8XQV5
112 40 42.1 308 16 Q9PMM8
113 40 42.1 344 5 Q15577
114 40 42.1 344 4 Q8NZS5
115 40 42.1 406 11 Q9CZ03
116 40 42.1 411 17 Q8UIN4
117 40 42.1 426 16 Q67155
118 40 42.1 429 16 Q92RX6
119 40 42.1 440 5 Q9U702
120 40 42.1 440 5 Q96686
121 40 42.1 497 4 Q96114
122 40 42.1 514 16 Q8E9X3
123 40 42.1 516 4 Q9BV14
124 40 42.1 520 5 Q9VJ00
125 40 42.1 523 5 Q86P58
126 40 42.1 651 10 Q9LXA5
127 40 42.1 701 16 Q8DUH3
128 40 42.1 735 5 Q9V7N4
129 40 42.1 751 9 Q8W6H6
130 40 42.1 838 5 Q9U9I9
131 40 42.1 1011 5 Q9Y148
132 40 42.1 1042 10 Q7X8U2
133 40 42.1 1059 5 Q9V3X6
134 40 42.1 1061 10 Q7X8N4
135 39.5 41.6 407 2 Q8V8M8
136 39.5 41.6 407 2 Q8VPC6
137 39 41.1 89 16 Q7WCP9
138 39 41.1 89 16 Q7W569
139 39 41.1 89 16 Q7VZU1
140 39 41.1 97 1 Q93681
141 39 41.1 99 16 Q938S3
142 39 41.1 139 16 Q88D20
143 39 41.1 140 10 Q9FWM1
144 39 41.1 140 10 Q7XDJ8
145 39 41.1 165 10 Q9LMI6
146 39 41.1 176 10 Q9XHV9
147 39 41.1 201 17 Q8U3X7
148 39 41.1 209 5 Q9S5D2
149 39 41.1 219 10 Q22412
150 39 41.1 224 10 Q22411

```

ALIGNMENTS

```

RESULT 1
Q9BTH3 PRELIMINARY; PRT; 439 AA.
AC Q9BTH3 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

```

```

DE Q7XV99 oryza sativ
OS Q86m8 oryza sativ
OC Q8xa42 escherichia
OC Q8ff21 escherichia
OC Q83k34 shigella fl
RN NCB1_TaxID=9606;
RP Q83714 treponema p
RP Q8uc94 agrobacteri
RC Q55941 synchocyst
RA Q8X0L5 mus musculu
RL Q8dbw5 vibrio vuln
RN Q87m05 vibrio para
RP Q8hino thermoplasm
RA Q8nsm4 homo sapien
RA Q9bgt1 macaca fasc
RA Q8sfv0 arabisopsis
RA Q8gx56 arabisopsis
RT Q89rr8 bradyrhizob
RT Q32734 agrobacteri
RT Q82a55 streptomyce
RT Q9buy3 homo sapien
DR Q8rch8 thermocanaer
DR Q8xqv5 ralstonia s
DR Q9pmm8 campylobact
DR Q15577 atacus atl
DR Q8nzs5 homo sapien
DR Q9cz03 mus musculu
DR Q8uln4 pyrococcus
DR Q67155 aquifex aeo
DR Q92rx6 rhizobium m
DR Q9vj02 drosophila
DR Q96686 drosophila
DR Q96114 homo sapien
DR Q8e9x3 shewanella
DR Q9bv14 homo sapien
DR Q9vj00 drosophila
DR Q86p58 drosophila
DR Q9lxa5 arabisopsis
DR Q8duh3 streptococc
DR Q9vtn4 drosophila
DR Q8w6h6 sinorhizobi
DR Q9u9i9 caenorhabi
DR Q9y148 drosophila
DR Q7x8u2 oryza sativ
DR Q9v3x6 drosophila
DR Q7x8n4 oryza sativ
DR Q8vrm8 escherichia
DR Q8vpc6 escherichia
DR Q7wcp9 bordetella
DR Q7w569 bordetella
DR Q7vzu1 bordetella
DR Q93681 sulfolobus
DR Q938s3 staphylococ
DR Q88d20 pseudomonas
DR Q9fwml oryza sativ
DR Q7xdj8 oryza sativ
DR Q9lmi6 arabisopsis
DR Q9xhv9 oryza sativ
DR Q8u3x7 pyrococcus
DR Q9s5d2 drosophila
DR Q22412 zea mays (m
DR Q22411 zea mays (m

Similar to bridging integrator 1.
Homo sapiens (human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
NCBI_TaxID=9606;
TISSUE=Pancreas;
Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
Phelan M., Farmer A.;
"Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector."
Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
-/- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; BC004101; AA04101.1; -.
EMBL; BT006865; AAP35511.1; -.
GO; GO:0005897; P: endocytosis; IEA.
GO; GO:0007268; P: synaptic transmission; IEA.
InterPro; IPR003005; Amphiphysin.
InterPro; IPR006632; BAR.
InterPro; IPR000418; BAR dom.
InterPro; IPR000875; Cdcropin.
InterPro; IPR001452; SH3.
Pfam; PF03114; BAR; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR01251; AMPHIPHYSIN.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
SMART; SM00721; BAR; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS00268; CECROPIN; 1.
PROSITE; PS50002; SH3; 1.
SH3 domain.
KW SH3 domain.
SQ
SEQUENCE 439 AA; 48286 MW; 350428C8E198136 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 2,1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAGKGRKLVYDSARHH 18
DB 139 RIAGKGRKLVYDSARHH 156
|||||
|||||

RESULT 2
Q8WVH9 PRELIMINARY; PRT; 490 AA.
AC Q8WVH9
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Amphiphysin Iib-1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kim K.-C., Kim T.-S., Kang K.-H., Choi K.-H.;
RT "Amphiphysin Iib-1, a novel splicing variant of amphiphysin II,
regulates p73b function through protein-protein interactions."
RL Oncogene 0:0-0(2002).
DR EMBL; AF411606; AAL38509.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.

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DR InterPro; IPR004148; BAR_dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00019; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYYSIN.
 DR PRODOM; PD000066; SH3; 1.
 DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 SQ SEQUENCE 490 AA; 53167 MW; 8F50F36F7B6E9690 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 490;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAKGRKLVYDSARHH 18
 |||||
 Db 139 RIAKGRKLVYDSARHH 156

RESULT 3

Q9UKN4 PRELIMINARY; PRT; 564 AA.
 AC Q9UKN4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Bridging integrator-2.
 GN BIN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RZ MEDLINE=20366138; PubMed=10903846;
 RA Ge K., Prendergast G.C.;
 RT "Bin2", a Functionally Nonredundant Member of the BAR Adaptor Gene Family.
 RL Genomics 67:210-220(2000).
 DR EMBL; AF146531; AAD54227.1; -.
 DR GO; GO:0006897; P: endocytosis; IEA.
 DR GO; GO:0007268; P: synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR_dom.
 DR Pfam; PF03114; BAR; 1.
 DR PRINTS; PR01251; AMPHIPHYYSIN.
 DR SMART; SM00721; BAR; 1.
 SQ SEQUENCE 564 AA; 61747 MW; 3CB3791A56CE53CB CRC64;

Query Match 100.0%; Score 95; DB 4; Length 564;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAKGRKLVYDSARHH 18
 |||||
 Db 138 RIAKGRKLVYDSARHH 155

RESULT 4

Q9UBW5 PRELIMINARY; PRT; 565 AA.
 AC Q9UBW5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Breast cancer associated protein BRAP1.
 GN BRAP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Miki Y., Saito H.;
 RT "Genomic structure and chromosome location of the BRAP1 gene."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB032710; BAA88125.1; -.
 DR EMBL; AB032699; BAA88125.1; JOINED.
 DR EMBL; AB032700; BAA88125.1; JOINED.
 DR EMBL; AB032701; BAA88125.1; JOINED.
 DR EMBL; AB032702; BAA88125.1; JOINED.
 DR EMBL; AB032703; BAA88125.1; JOINED.
 DR EMBL; AB032704; BAA88125.1; JOINED.
 DR EMBL; AB032705; BAA88125.1; JOINED.
 DR EMBL; AB032706; BAA88125.1; JOINED.
 DR EMBL; AB032707; BAA88125.1; JOINED.
 DR EMBL; AB032708; BAA88125.1; JOINED.
 DR EMBL; AB032709; BAA88125.1; JOINED.
 DR EMBL; AB032698; BAA88108.1; -.
 DR Genew; HGNC:1053; BIN2.
 DR GO; GO:0006897; P: endocytosis; IEA.
 DR GO; GO:0007268; P: synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR_dom.
 DR Pfam; PF03114; BAR; 1.
 DR PRINTS; PR01251; AMPHIPHYYSIN.
 DR SMART; SM00721; BAR; 1.
 SQ SEQUENCE 565 AA; 61902 MW; 28D1FB89A7779860 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 565;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAKGRKLVYDSARHH 18
 |||||
 Db 138 RIAKGRKLVYDSARHH 155

RESULT 5

Q86VV0 PRELIMINARY; PRT; 565 AA.
 ID Q86VV0;
 AC Q86VV0;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Breast cancer associated protein BRAP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RN RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047686; AAH47686.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR. dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 565 AA; 61875 MW; B1D1FB99A7707EA3 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
DB 138 RIAKGRKLVYDSARHH 155

RESULT 6
Q7ZWPS PRELIMINARY; PRT; 478 AA.
ID Q7ZWPS
AC Q7ZWPS
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DE Similar to bridging integrator 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN TISSUE=Embryo;
RP SEQUENCE FROM N.A.
RA Klein S.; Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046852; AAH46852.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR. dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
SQ SEQUENCE 478 AA; 53445 MW; 042A1A94D59095A8 CRC64;

Query Match 95.8%; Score 91; DB 13; Length 478;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
DB 138 RIAKGRKLVYDSARHH 155

RESULT 7
ID Q80313 PRELIMINARY; PRT; 524 AA.
AC Q80313
DT 01-JUN-2003 (Tremblrel. 24, Created)

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DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to bridging integrator 2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
CX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044473; AAH44473.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR. dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 524 AA; 59280 MW; F4A2988732D153FF CRC64;

Query Match 94.7%; Score 90; DB 13; Length 524;
Best Local Similarity 88.9%; Pred. No. 1.7e-06;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
DB 146 RIAKGRKLVYDSARHH 163

RESULT 8
Q8BXH2 PRELIMINARY; PRT; 250 AA.
ID Q8BXH2
AC Q8BXH2
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to MYC box dependent interacting protein 1.
GN AMPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).
DR EMBL; AK047144; BAC32971.1; -.
DR MGD; MGI:103574; Amph.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR. dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 250 AA; 29125 MW; 568A3D55CC6C37CE CRC64;

Query Match 93.7%; Score 89; DB 11; Length 250;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
DB 134 RIAKGRKLVYDSARHH 151

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RESULT 9
Q8NFL3 PRELIMINARY; PRT; 385 AA.
AC Q8NFL3;
ID Q8NFL3;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Amphiphsin I variant NT2 (Fragment).
GN AMPH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22017878; PubMed=12023042;
RA Terada Y., Tsutsui K., Sano K., Hosoya O., Ohtsuki H., Tokunaga A.,
RA Tsutsui K.;
RT "Novel splice variants of amphiphsin I are expressed in retina.";
RL FEBS Lett. 519:185-190(2002).
DR EMBL, AF498097; AM44811.1; -.
DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphsin.
DR InterPro; IPR003017; Amphiphsin_1.
DR InterPro; IPR006632; BAR.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR ProDom; PD003208; Amphiphsin_1; 1.
DR SMART; SM00721; BAR; 1.
FT NON TER 385
SQ SEQUENCE 385 AA; 43753 MW; 4B9AB0A3136711AA CRC64;

Query Match 93.7%; Score 89; DB 4; Length 385;
Best Local Similarity 94.4%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSARHH 18
DB 134 RIAGRSRKLVDYDSARHH 151

RESULT 10
Q7TOF7 PRELIMINARY; PRT; 686 AA.
AC Q7TOF7;
ID Q7TOF7;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieff P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Matak J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

Query Match 93.7%; Score 89; DB 4; Length 686;
Best Local Similarity 94.4%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSARHH 18
DB 134 RIAGRSRKLVDYDSARHH 151

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC054718; AAHS4718.1; -.
KW Hypothetical protein.
SQ SEQUENCE 686 AA; 75013 MW; D292E24653A442A5 CRC64;

Query Match 93.7%; Score 89; DB 11; Length 686;
Best Local Similarity 94.4%; Pred. No. 3.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSARHH 18
DB 134 RIAGRSRKLVDYDSARHH 151

RESULT 11
Q8N4G0 PRELIMINARY; PRT; 695 AA.
AC Q8N4G0;
ID Q8N4G0;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Amphiphsin (Stiff-Man syndrome with breast cancer 128kD
DE autoantigen).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Brain, and Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL, BC034376; AAH34376.1; -.
DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphsin.
DR InterPro; IPR003017; Amphiphsin_1.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR InterPro; IPR001452; SH3_dom.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD003208; Amphiphsin_1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 695 AA; 76229 MW; 4FC92EE8B028BBFE CRC64;

Query Match 93.7%; Score 89; DB 4; Length 695;
Best Local Similarity 94.4%; Pred. No. 3.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIAGRGKLVYDSARHH 18
DB 134 RIAGRSRKLVDYDSARHH 151

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RESULT 12
Q21004 Q21004 PRELIMINARY; PRT; 461 AA.
AC Q21004;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F58G6.1 protein.
GN F58G6.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; Z68217; CAA92465.1; -
DR PIR; T22946; T22946.
DR WormPep; F58G6.1; CE03428.
DR DR GO; GO:0006897; P: endocytosis; IEA.
DR DR GO; GO:0007268; P: synaptic transmission; IEA.
DR DR InterPro; IPR003005; Amphiphysin.
DR DR InterPro; IPR004148; BAR.
DR DR InterPro; IPR001452; SH3.
DR DR Pfam; PF03114; BAR; 1.
DR DR Pfam; PF00018; SH3; 1.
DR DR PRINTS; PR01251; AMPHIPHYSIN.
DR DR ProDom; PD000066; SH3; 1.
DR DR SMART; SM00721; BAR; 1.
DR DR SMART; SM00326; SH3; 1.
DR DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 461 AA; 51910 MW; 771C89E21EF7BEC8 CRC64;

Query Match 72.6%; Score 69; DB 5; Length 461;
Best Local Similarity 76.5%; Pred. No. 0.0049;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RIAGKRGKLVYDSARH 17
Db 130 KIEKRGKLVYDSAKN 146
:|||||:
:|||||:

RESULT 13
Q9Y092 Q9Y092 PRELIMINARY; PRT; 602 AA.
AC Q9Y092;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amphiphysin protein (LD19810P).
GN AMPH OR CG8604.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Adams M.D.; Celniker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RX MEDLINE=20196006; PubMed=107311132;
RA

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Anatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Wandell M.D., Zhang Q., Chen L.X.,
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Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Auril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Balew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=20076404; PubMed=10607911;
RX Razaq A., Su Y., Mehren J.E., Mizuguchi K., Jackson A.P., Gay N.J.,
O'Kane C.J.;
RT "Characterization of the gene for Drosophila amphiphysin.";
RL Gene 241:167-174(2000).
[3]
RN SEQUENCE FROM N.A.
RP Zhang Y.Q., Xue H., Broadie K.S.;
RT "Dissecting the functions of amphiphysin.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkley;
RC Stapleton M., Brokstein P., Horg L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Murgall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AE003821; AAF58486.1; -
DR EMBL; AF171225; AAD46684.1; -
DR EMBL; AJ242855; CAB45188.1; -
DR EMBL; AY061278; AAL28826.1; -
DR HSP; P27986; IPTT.
DR FlyBase; FBgn0027356; Amph.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0045202; C:synaptic junction; IDA.
DR GO; GO:0007269; P:neurotransmitter secretion; NAS.
DR GO; GO:0008104; P:protein localization; IMP.
DR GO; GO:0006937; P:regulation of muscle contraction; IMP.
DR GO; GO:0045313; P:ribosome membrane biogenesis; IMP.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.

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DR InterPro; IPR004148; BAR_dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00002; SH3; 1.
 KW SH3 domain.
 SQ SEQUENCE 602 AA; 65901 MW; 86D1D4CBAE1B8F31 CRC64;

Query Match 55.3%; Score 62; DB 5; Length 602;
 Best Local Similarity 58.8%; Pred. No. 0.099;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIAGRGKLVVDYDSARH 17
 :: |||::|||::|||
 Db 134 KVEKNRKLIDYDGRH 150

RESULT 14

Q8XOD7 PRELIMINARY; PRT; 273 AA.
 ID Q8XOD7
 AC Q8XOD7
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Probable cytoskeletal binding protein.
 GN B14A6.200.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AL670007; CAD21322.1; -
 DR GO; GO:0006897; P: endocytosis; IEA.
 DR GO; GO:0007268; P: synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR Pfam; PF03114; BAR; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR SMART; SM00721; BAR; 1.
 SQ SEQUENCE 273 AA; 31319 MW; 4B7D99DB7385A3B6 CRC64;

Query Match 55.8%; Score 53; DB 3; Length 273;
 Best Local Similarity 66.7%; Pred. No. 1.3;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAKRGKLVVDYDSAR 16
 |||::|||::|||
 Db 144 IKRGHKLIDYDALR 158

RESULT 15

Q8WQ54 PRELIMINARY; PRT; 414 AA.
 ID Q8WQ54
 AC Q8WQ54
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Putative aggregation factor.
 GN GEOCVAF.

OS Geodia cydonium (Sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Astrophorida; Geodiidae; Geodia.
 OX NCBI_TaxID=6047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schuetze J., Kraak A., Diehl-Seifert B., Mueller W.B.G.;
 RT "Cloning and Expression of the Putative Aggregation Factor from the
 RT Marine Sponge Geodia cydonium."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ311598; CAC83970.1; -
 DR GO; GO:0006897; P: endocytosis; IEA.
 DR GO; GO:0007268; P: synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR Pfam; PF03114; BAR; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR SMART; SM00721; BAR; 1.
 SQ SEQUENCE 414 AA; 46558 MW; 90CABDAB20152310 CRC64;

Query Match 55.8%; Score 53; DB 5; Length 414;
 Best Local Similarity 68.8%; Pred. No. 2.1;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RIAGRGKLVVDYDSAR 16
 |||::|||::|||
 Db 145 RIQKRRKQVDYDLRR 160

RESULT 16

Q8X2J8 PRELIMINARY; PRT; 130 AA.
 ID Q8X2J8
 AC Q8X2J8
 DT 01-MAR-2002 (TREMELrel. 20, Created)
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Hypothetical protein ECs3934.
 GN ECS3934.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12."
 RL DNA Res. 8:11-22(2001).
 DR EMBL; AF002564; BAB37357.1; -
 DR FIR; F91120; F91120.
 KW Hypothetical protein.
 SQ SEQUENCE 130 AA; 14577 MW; 913D2BD3FEE113F CRC64;

Query Match 52.1%; Score 49.5; DB 16; Length 130;
 Best Local Similarity 58.8%; Pred. No. 2.3;
 Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 5 RGRKLV---YDSARHH 18
 |||::|||::|||
 Db 84 RGRGLIECKGYDEARH 100

RESULT 17

Q9HQ51 PRELIMINARY; PRT; 169 AA.
 ID Q9HQ51
 AC Q9HQ51
 DT 01-MAR-2001 (TREMELrel. 16, Created)

DR	GO	GO:0004713	F:protein-tyrosine kinase activity; IEA.
DR	GO	GO:0016740	F:transferase activity; IEA.
DR	GO	GO:0006468	F:protein amino acid phosphorylation; IEA.
DR	InterPro	IPR000719	; Ser Thr kinase.
DR	InterPro	IPR008271	; Ser Thr pkin_AS.
DR	InterPro	IPR001245	; Tyr_pkinase.
DR	Pfam	PF00069	; pkinase; 1.
DR	PRINTS	PR00109	; TYRKINASE.
DR	ProDom	PD000001	; Prot kinase; 1.
DR	PROSITE	PS00011	; PROTEIN_KINASE_DOM; 1.
DR	PROSITE	PS00108	; PROTEIN_KINASE_ST; 1.
KW	KW		Hypothetical protein; ATP-binding; Kinase;
KW	KW		Serine/threonine-protein kinase; Transferrase.
SQ	SEQUENCE	424 AA	; 48086 MW; C1DD63702089307 CRC64;
Query Match		49.5%;	Score 47; DB 10; Length 424
Best Local Similarity		53.3%;	Pred. No. 22;
Matches	8;	Conservative	2; Mismatches 5; Indels
QY	4	KEGKLVVDYSARHH	18
		:	
Db	382	KEGKFPVDINKFRH	396
		:	
RESULT	19		
Q39229		PRELIMINARY;	PRT; 425 AA.
ID	Q39229		
AC	Q39229		
DT	01-NOV-1996	(TrEMBLrel. 01, Created)	
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
GN	Serine/threonine protein kinase.		
DE	ARSK1.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Embryophyta; Tracheopsida; Magnoliophyta; Eudicotyledons; Core eudicotyledons; Brassicales; Brassicaceae; Arabidopsi.		
OX	NCBI_TaxID=3702;		
XP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Columbia;		
RX	MEDLINE=95384198; PubMed=7655506;		
RA	Hwang I.; Goodman H.M.;		
RT	"An Arabidopsis thaliana root-specific kinase homolog is involved in dehydration, ABA, and NaCl.";		
RL	Plant J. 8:37-43 (1995).		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES; 122302; AA81538.1; ...		
DR	GO	GO:0005524	F:ATP binding; IEA.
DR	GO	GO:0004674	F:protein serine/threonine kinase activity; IEA.
DR	GO	GO:0004713	F:protein-tyrosine kinase activity; IEA.
DR	GO	GO:0016740	F:transferase activity; IEA.
DR	GO	GO:0006468	F:protein amino acid phosphorylation; IEA.
DR	InterPro	IPR000719	; Prot kinase.
DR	InterPro	IPR008271	; Ser Thr pkin_AS.
DR	InterPro	IPR001245	; Tyr_pkinase.
DR	Pfam	PF00069	; pkinase; 1.
DR	PRINTS	PR00109	; TYRKINASE.
DR	ProDom	PD000001	; Prot kinase; 1.
DR	PROSITE	PS00011	; PROTEIN_KINASE_DOM; 1.
DR	PROSITE	PS00108	; PROTEIN_KINASE_ST; 1.
KW	KW		ATP-binding; Kinase; Serine/threonine-protein kinase; Transferrase.
SQ	SEQUENCE	425 AA	; 48311 MW; 77998E7606EC94E CRC64;
Query Match		49.5%;	Score 47; DB 10; Length 425;
Best Local Similarity		53.3%;	Pred. No. 22;
Matches	8;	Conservative	2; Mismatches 5; Indels
QY	4	KEGKLVVDYSARHH	18
		:	
Db	383	KEGKFPVDINKFRH	397
		:	


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RESULT 20
Q9LEA1 ID Q9LEA1 PRELIMINARY; PRT; 441 AA.
AC Q9LEA1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Asparagine synthetase (ASN3) (Fragment) (Fragment).
GN T31P16 230.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Zimmermann W., Gruenisen A., Wambutt R., Kalicki J.,
RA Wohldmann P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL356332; CAB92065.1; -.
DR HSSP; P22106; 1CT9.
DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.
DR InterPro; IPR001962; Asn_synthase.
DR Pfam; PF00733; Asn_synthase; 1.
FT NON_TER
SQ SEQUENCE 441 AA; 49619 MW; 7C0B9FCD15D536EA CRC64;

Query Match 49.5%; Score 47; DB 10; Length 441;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KGRKLVYDYSARHH 18
DB 139 KAGREVADYLGTRHH 153

RESULT 21
Q9ZST7 ID Q9ZST7 PRELIMINARY; PRT; 578 AA.
AC Q9ZST7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Asparagine synthetase.
GN ASN3
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99097830; PubMed=9881155;
RA Lam H.M., Hsieh M.H., Coruzzi G.;
RL "Reciprocal regulation of distinct asparagine synthetase genes by
RL light and metabolites in Arabidopsis thaliana.";
RL Plant J. 16:345-353(1998).
DR EMBL; AF095452; AAC72836.1; -.
DR HSSP; P22106; 1CT9.
DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001962; Asn_synthase.
DR InterPro; IPR006426; Asn_synth_AEB.
DR Pfam; PF00733; Asn_synthase; 1.
DR TIGRfams; TIGR01536; asn_synth_AEB; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
SQ SEQUENCE 578 AA; 65077 MW; D05B73C63BF3B663 CRC64;

Query Match 49.5%; Score 47; DB 10; Length 578;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KGRKLVYDYSARHH 18
DB 276 KAGREVADYLGTRHH 290

RESULT 22
Q9ZST6 ID Q9ZST6 PRELIMINARY; PRT; 578 AA.
AC Q9ZST6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Asparagine synthetase.
GN ASN2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99097830; PubMed=9881155;
RA Lam H.M., Hsieh M.H., Coruzzi G.;
RL "Reciprocal regulation of distinct asparagine synthetase genes by
RL light and metabolites in Arabidopsis thaliana.";
RL Plant J. 16:345-353(1998).
DR EMBL; AF095453; AAC72837.1; -.
DR HSSP; P22106; 1CT9.
DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001962; Asn_synthase.
DR InterPro; IPR006426; Asn_synth_AEB.
DR Pfam; PF00733; Asn_synthase; 1.
DR TIGRfams; TIGR01536; asn_synth_AEB; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
SQ SEQUENCE 578 AA; 65077 MW; D05B73C63BF3B663 CRC64;

Query Match 49.5%; Score 47; DB 10; Length 578;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KGRKLVYDYSARHH 18
DB 276 KAGREVADYLGTRHH 290

RESULT 23
Q9LV77 ID Q9LV77 PRELIMINARY; PRT; 578 AA.
AC Q9LV77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Asparagine synthetase (AT5G5010/MXK3 25).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

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DR Pfam; PF00310; GATase 2; 1.
DR TIGRfams; TIGR01536; asn_synth_AEB; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
SQ SEQUENCE 578 AA; 65223 MW; 5BEDF2C7A04636BD CRC64;

Query Match 49.5%; Score 47; DB 10; Length 578;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KGRKLVYDYSARHH 18
DB 276 KAGREVADYLGTRHH 290

RESULT 22
Q9ZST6 ID Q9ZST6 PRELIMINARY; PRT; 578 AA.
AC Q9ZST6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Asparagine synthetase.
GN ASN2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99097830; PubMed=9881155;
RA Lam H.M., Hsieh M.H., Coruzzi G.;
RL "Reciprocal regulation of distinct asparagine synthetase genes by
RL light and metabolites in Arabidopsis thaliana.";
RL Plant J. 16:345-353(1998).
DR EMBL; AF095453; AAC72837.1; -.
DR HSSP; P22106; 1CT9.
DR GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing) . . . ; IEA.
DR GO; GO:0006529; P:asparagine biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001962; Asn_synthase.
DR InterPro; IPR006426; Asn_synth_AEB.
DR Pfam; PF00733; Asn_synthase; 1.
DR TIGRfams; TIGR01536; asn_synth_AEB; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
SQ SEQUENCE 578 AA; 65077 MW; D05B73C63BF3B663 CRC64;

Query Match 49.5%; Score 47; DB 10; Length 578;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KGRKLVYDYSARHH 18
DB 276 KAGREVADYLGTRHH 290

RESULT 23
Q9LV77 ID Q9LV77 PRELIMINARY; PRT; 578 AA.
AC Q9LV77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Asparagine synthetase (AT5G5010/MXK3 25).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

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Mayer K.F.X.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
[2]
SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
[3]
SEQUENCE FROM N.A.
Yanada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C., Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"Arabidopsis Full Length cDNA Clones";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
[4]
SEQUENCE FROM N.A.
Yanada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C., Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"Arabidopsis Open Reading Frame (ORF) Clones";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL360334; CAB96680.1; -
EMBL; BT003929; ANO41976.1; -
EMBL; BT005014; AAO50547.1; -
PIR; T50812; T50812.
HSSP; P22106; 1CT9.
GO; GO:0004066; F:asparagine synthase (glutamine-hydrolyzing). . . ; IEA.
GO; GO:0006529; P:asparagine biosynthesis; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001962; Asn_synthase.
InterPro; IPR006426; Asn_synth_AEB.
InterPro; IPR000583; Glutase_2.
Pfam; PF00733; Asn_synthase; 1.
Pfam; PF00310; Glutase_2; 1.
TIGRFAMs; TIGR01536; asn_synth_AEB; 1.
PROSITE; PS00443; GLUTASE_TYPE-II; 1.
SEQUENCE 578 AA; 65227 MW; 2CF8FE216BDD83E CRC64;

Query Match 49.5%; Score 47; DB 10; Length 578;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY ' 4 KRGRKVLVDYSARHH 18
|||::|||
DB 276 KAGREVADYLGTRRH 290

RESULT 25
Q89JES PRELIMINARY; PRT; 1163 AA.
AC Q89JES;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE B115338 protein.
GN B115338.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiaceae;
OX NCBI_taxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.

OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nunes D.N., Dias-Neto E., Brentani R.R., Camargo A.A.;
 RT "Cloning and characterization of two human homologs of the enhancer of
 RT polycomb gene (EPC1) from Drosophila."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF286905; AAK60501.1; -.
 SQ SEQUENCE 763 AA; 85219 MW; 588D375F40151D03 CRC64;

 Query Match 47.9%; Score 45.5; DB 4; Length 763;
 Best Local Similarity 43.5%; Pred. No. 74;
 Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

 QY 1 RIAKRGKLV-----DYDSARHH 18
 : : : : :
 Db 408 RVGRGRLVLLDRAHSDYDSVFHH 430
 : : : : :

 RESULT 30
 Q8NE21 PRELIMINARY; PRT; 813 AA.
 ID Q8NE21
 AC Q8NE21
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DE Similar to enhancer of polycomb 1.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Testis;
 RA Strausberg R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC036529; AAK36529.1; -.
 SQ SEQUENCE 813 AA; 90893 MW; 1A7DE9D14C291D11 CRC64;

 Query Match 47.9%; Score 45.5; DB 4; Length 813;
 Best Local Similarity 43.5%; Pred. No. 79;
 Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

 QY 1 RIAKRGKLV-----DYDSARHH 18
 : : : : :
 Db 458 RVGRGRLVLLDRAHSDYDSVFHH 480
 : : : : :

 RESULT 31
 Q9H2F5 PRELIMINARY; PRT; 836 AA.
 ID Q9H2F5
 AC Q9H2F5
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DE Enhancer of polycomb.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20564312; PubMed=10976108;
 RA Shimono Y., Murakami H., Hasegawa Y., Takahashi M.;
 RT "RET Finger Protein Is a Transcriptional Repressor and Interacts with
 RT Enhancer of Polycomb That Has Dual Transcriptional Functions."
 RL J. Biol. Chem. 275:39411-39419 (2000).
 DR EMBL; AF277374; AAG41402.1; -.
 DR Genew; HGNC:19876; EPC1.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0016563; F:transcriptional activator activity; TAS.
 DR GO; GO:0016564; F:transcriptional repressor activity; IDA.
 DR GO; GO:0006350; P:transcription; TAS.

SQ SEQUENCE 836 AA; 93463 MW; E9E89699E73336B5 CRC64;

 Query Match 47.9%; Score 45.5; DB 4; Length 836;
 Best Local Similarity 43.5%; Pred. No. 81;
 Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

 QY 1 RIAKRGKLV-----DYDSARHH 18
 : : : : :
 Db 458 RVGRGRLVLLDRAHSDYDSVFHH 480
 : : : : :

 RESULT 32
 Q852V9 PRELIMINARY; PRT; 128 AA.
 ID Q852V9
 AC Q852V9
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Gp246.
 GN 246.
 OS Mycobacteriophage Bx1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
 OC NCBI_TaxID=205877;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22592660; PubMed=12705866;
 RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
 RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
 RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
 RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
 RA Hatfull G.F.;
 RT "Origins of highly mosaic mycobacteriophage genomes."
 RL Cell 113:171-182 (2003).
 DR EMBL; AY129337; AAN16878.1; -.
 SQ SEQUENCE 128 AA; 14386 MW; 1A48FD39E58CBA70 CRC64;

 Query Match 47.4%; Score 45; DB 9; Length 128;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 QY 6 GRKLVYDSARH 17
 : : : : :
 Db 101 GRKLVYDSGTN 112
 : : : : :

 RESULT 33
 Q9UOX9 PRELIMINARY; PRT; 160 AA.
 ID Q9UOX9
 AC Q9UOX9
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN L7171.04.
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OC NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RA Tosato V., Bruschi C.V., Ivens A.C., Murphy L., Quail M.,
 RA Rajandream M.A., Barrell B.G.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Friedlin;
 RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome."
 RL Genome Res. 8:135-145 (1998).
 DR EMBL; AL133435; CAB62807.1; -.
 KW Hypothetical protein.

Qy 1 RIAKRGKLVYDYSAAHH 18
| | : : | | | |
Db 98 RTTYRDGAVIEDSAAHH 115

RESULT 37

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Q8KD94
ID O8KD94 PRELIMINARY; PRT; 524 AA.
AC O8KD94
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Type III restriction system endonuclease, putative.
GN CT1160.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=1203901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Niernan W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AB012877; AA072393.1; -.
DR TIGR; CT1160; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004519; F:endonuclease activity; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR002296; N12N6_mtfase.
DR InterPro; IPR002052; N6_MTFASE.
DR PRINTS; PR00507; N12N6_MTFASE.
DR PROSITE; PS00092; N6_MTFASE; 1.
DR KW Endonuclease; Complete proteome.
SQ SEQUENCE 524 AA; 59223 MW; A3F705751D3ABAA7 CRC64;

Query Match 47.4%; Score 45; DB 16; Length 524;
Best Local Similarity 69.2%; Pred. No. 60;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRGRKLVYDSAR 16
DB 266 KRIRKLVYENQA 278

RESULT 38
Q7WDT3 PRELIMINARY; PRT; 263 AA.
AC Q7WDT3
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Arac family regulatory protein.
GN BA904.
OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640436; CAE39597.1; -.
DR KW Complete proteome.
SQ SEQUENCE 263 AA; 29173 MW; 143B129BB0E436B0 CRC64;

Query Match 46.3%; Score 44; DB 16; Length 263;
Best Local Similarity 46.7%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRGRKLVYDSARHH 18
DB 8 RAGHEVVDYDHPGHH 22

RESULT 40
Q7VSK1 PRELIMINARY; PRT; 297 AA.
AC Q7VSK1
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Arac family regulatory protein.
GN BP3798.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.

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OX NCBI_TaxID=520;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Tohana I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=2287954; PubMed=12310271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger C.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL: BX640422; CAB4053.1; -.
KW Complete proteome.
SQ SEQUENCE 297 AA; 32461 MW; 5A452C5DFC948D23 CRC64;

Query Match 46.3%; Score 44; DB 16; Length 297;
Best Local Similarity 46.7%; Pred. No. 47;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 KRGKRLVDYDSARH 18
DB : : : : :
42 RAGHEVVDYDHPGHH 56

RESULT 41
Q8GDV2 PRELIMINARY; PRT; 524 AA.
ID Q8GDV2
AC Q8GDV2;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Cobyic acid synthase (fragment).
OS Helicobacter mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;
OC Helicobacteriaceae.
OX NCBI_TaxID=28064;
RN [1]
RN SEQUENCE FROM N.A.
RC MEDLINE=22337798; PubMed=12446909;
RA Raymond J., Zhaxybayeva O., Gogarten J.P., Gerdes S.Y.,
RA Blankenship R.E.;
RT "Whole-genome analysis of photosynthetic prokaryotes.";
RL Science 298:1616-1620(2002).
RN [2]
RN SEQUENCE FROM N.A.
RA Liolios K.G., Chu L., Ostrovskaya O., Mendenbaeva N., Koukharenko V.,
RA Gerdes S., Kyripides N., Overbeek R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AY142870; RAN87474.1; -.
DR GO: GO:0003824; F: catalytic activity; IEA.
DR GO: GO:0042242; P: cobyric acid a,C-diamide synthase activity; IEA.
DR GO: GO:0002336; P: vitamin B12 biosynthesis; IEA.
DR InterPro: IPR002596; CblA_P.
DR InterPro: IPR004459; COBQ_synth.
DR Pfam: PF01656; CblA; 1.
DR TIGRFAMs: TIGR00313; cobQ; 1.
FT NON_TER 524
SQ SEQUENCE 524 AA; 56649 MW; 52B9B5770880660A CRC64;

Query Match 46.3%; Score 44; DB 2; Length 524;
Best Local Similarity 30.0%; Pred. No. 88;
Matches 12; Conservative 2; Mismatches 4; Indels 22; Gaps 1;

QY 1 RIAGRGKLVLDY-----DSARH 18
DB : : : : :
418 RIRGGEELVDYDGDVADGVIGSYLHGFDNDLSLHH 457

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RESULT 42
Q8ZN24 PRELIMINARY; PRT; 282 AA.
ID Q8ZN24
AC Q8ZN24;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative ABC superfamily (Membrane) transport protein.
DE YFHH OR STM2572.
GN Salmonella typhimurium.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
DR EMBL: AE008817; AAL21466.1; -.
DR GO: GO:0005523; F: sugar binding; IEA.
DR GO: GO:0003700; P: transcription factor activity; IEA.
DR GO: GO:0005975; P: carbohydrate metabolism; IEA.
DR GO: GO:0006355; P: regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR00281; HTH_RpIR.
DR InterPro: IPR001347; SIS.
DR Pfam: PF01418; HTH_6; 1.
DR Pfam: PF01380; SIS; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 282 AA; 30925 MW; 170726A1AF825 CRC64;

Query Match 45.8%; Score 43.5; DB 16; Length 282;
Best Local Similarity 47.6%; Pred. No. 54;
Matches 10; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 2 IAKRGKLVLDY-----DSARH 17
DB : : : : :
14 LAQSDRLADYLLAQPDTH 34

RESULT 43
Q824L1 PRELIMINARY; PRT; 282 AA.
ID Q824L1
AC Q824L1;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative transcriptional regulator.
GN YFHH OR STY2818 OR T0285.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;

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DR InterPro; IPR002110; ANK.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00023; ank; 7.
DR SMART; SM00248; ANK; 7.
DR PROSITE; PS50088; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
DR KW Hypothetical protein.
FT NON_TER 413
SQ SEQUENCE 413 AA; 45852 MW; 25CB3EBAF8F92796 CRC64;

Query Match          45.3%; Score 43; DB 11; Length 413;
Best Local Similarity 47.1%; Pred. No. 1e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      2 IAKGRKLVDYDSARHH 18
       :|:::||:||||
Db       204 ILERGGEVNDNRHH 220

RESULT 47
QBUT2    PRELIMINARY; PRT; 819 AA.
ID QBUT2
AC QBUT2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Dyanin 3.
GN 9630020E24RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP RFP
RA The FANTOM Consortium,
RA STRAIN=C57BL/6J; TISSUE=Cerebellum;
RE MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.";
RRL Nature 420:563-573(2002).
RRL EMBL; AK082698; BAC38575.1; -.
RDL MGD; MG1_2444162; 9630020E24RIK.
GDI GO; GO:0003924; F:GTPase activity; IEA.
DDR InterPro; IPR001401; Dynamain.
DDR InterPro; IPR000375; Dynamain_central.
DDR InterPro; IPR003130; GED.
DDR InterPro; IPR001849; PH.
DDR Pfam; PF00350; dynamin; 1.
DDR Pfam; PF01031; dynamin_2; 1.
DDR Pfam; PF02212; GED; 1.
DDR Pfam; PF00169; PH; 1.
DDR PRINTS; PR00195; DYNAMIN.
DDR SMART; SM00053; DYNG; 1.
DDR SMART; SM00302; GED; 1.
DDR SMART; SM00233; PH; 1.
DDR PROSITE; PS00410; DYNAMIN; 1.
DDR PROSITE; PS50003; PH DOMAIN; 1.
SQ SEQUENCE 819 AA; 92863 MW; E32BFA2E01B3192A CRC64;

Query Match          45.3%; Score 43; DB 11; Length 819;
Best Local Similarity 46.2%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      5 GRKRLVDYDSARH 17
       :|::||:|
Db       87 KGKKFTDFEVRR 99

RESULT 48
QB8BW6    PRELIMINARY; PRT; 859 AA.
ID QB8W6
AC QB8W6;

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DR InterPro; IPR003130; GED.
DR InterPro; IPR001849; PH.
DR Pfam; PF00350; dynamin_1.
DR Pfam; PF01031; dynamin_2; 1.
DR Pfam; PF02212; GED; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00195; DYNAMIN.
DR SMART; SMO053; DYNG; 1.
DR SMART; SMO0302; GED; 1.
DR SMART; SMO0233; PH; 1.
DR PROSITE; PS00410; DYNAMIN; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
SQ SEQUENCE 863 AA; 97190 MW; 8BDBB091CB10D264 CRC64;

Query Match 45.3%; Score 43; DB 11; Length 863;
Best Local Similarity 46.2%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 RGRKLVYDSARH 17
:|:|:|:|
Db 87 KGKFTDFDEVTH 99

RESULT 50

Q9QXL9 PRELIMINARY; PRT; 869 AA.
AC Q9QXL9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dynamilin il1bb isoform.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96355732; PubMed=9752097;
RA Cook T., Mesa K., Urrutia R.;
RT "Three dynamin-encoding genes are differentially expressed in
developing rat brain."
RL J. Neurochem. 67:927-931(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Cook T., Mesa K., Urrutia R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AF201839; AAF07848.1; -.
DR HSSP; Q05193; LDYN.
DR GO; GO:0003924; F:GTPase activity; IEA.
DR InterPro; IPR001401; Dynamlin.
DR InterPro; IPR000375; Dynamlin_central.
DR InterPro; IPR003130; GED.
DR InterPro; IPR001849; PH.
DR Pfam; PF00350; dynamin; 1.
DR Pfam; PF01031; dynamin_2; 1.
DR Pfam; PF02212; GED; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00195; DYNAMIN.
DR SMART; SMO053; DYNG; 1.
DR SMART; SMO0302; GED; 1.
DR SMART; SMO0233; PH; 1.
DR PROSITE; PS00410; DYNAMIN; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
SQ SEQUENCE 869 AA; 97914 MW; 00B41E41E5425BAD CRC64;

Query Match 45.3%; Score 43; DB 11; Length 869;
Best Local Similarity 46.2%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 RGRKLVYDSARH 17

Db 87 KGKFTDFDEVTH 99

Search completed: March 4, 2004, 17:46:25
Job time : 49.3871 secs

CC proteins are also useful for diagnosing or treating conditions associated
 CC with inappropriate expression of Bin2, e.g. liver cancer, breast cancer,
 CC hepatocarcinoma, myeloid and lymphoid leukemias or blood disorders. The
 CC peptides, nucleic acid sequences or anti-Bin2 antibodies are useful for
 CC diagnosing inappropriate expression of Bin2. Bin2 is also useful for
 CC treating disorders associated with excessive Bin1 levels, e.g. liver,
 CC colorectal, prostate or breast cancers, epithelia cell cancers, melanoma,
 CC or hyperplastic disease states
 XX
 SQ Sequence 564 AA;

Query Match 100.0%; Score 1125; DB 4; Length 564;
 Best Local Similarity 100.0%; Pred. No. 3e-85;
 Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAEGKAGAGLPAKQVKQKFSRAQKQKGLKAVETKDERFQSASNFYQQAEGHKL 60
 DB 1 MAEGKAGAGLPAKQVKQKFSRAQKQKGLKAVETKDERFQSASNFYQQAEGHKL 60
 QY 61 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEKLADQ 120
 DB 61 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEKLADQ 120
 QY 121 AVRTWEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNAKKDEAKTAKAEFEFNKA 180
 DB 121 AVRTWEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNAKKDEAKTAKAEFEFNKA 180
 QY 181 TVFEDLNQELLELPILYNSRIGCYVTIFQNISNLRDVFYR 221
 DB 181 TVFEDLNQELLELPILYNSRIGCYVTIFQNISNLRDVFYR 221

RESULT 2
 ABG13005
 ID ABG13005 standard; protein; 414 AA.

XX AC ABG13005;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #12996.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

XX WO200175067-A2.
 XX
 PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.
 XX
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS77192.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 43364; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC

CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 414 AA;

Query Match 99.1%; Score 1114.5; DB 4; Length 414;
 Best Local Similarity 99.5%; Pred. No. 1.5e-84;
 Matches 221; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MAEGKAGAGLPAKQVKQKFSRAQKQKGLKAVETKDERFQSASNFYQQAEGHKL 60
 DB 1 MAEGKAGAGLPAKQVKQKFSRAQKQKGLKAVETKDERFQSASNFYQQAEGHKL 60
 QY 61 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEKLADQ 120
 DB 61 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEKLADQ 120
 QY 121 AVRTWEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKA 179
 DB 121 AVRTWEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNAKKDEAKTAKAEFEFNKA 180
 QY 180 QTVFEDLNQELLELPILYNSRIGCYVTIFQNISNLRDVFYR 221
 DB 181 QTVFEDLNQELLELPILYNSRIGCYVTIFQNISNLRDVFYR 222

RESULT 3

ABG20887

ID ABG20887 standard; protein; 594 AA.

XX AC ABG20887;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #20878.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS85074.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 51246; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 594 AA;

Query Match 98.8%; Score 1111.5; DB 4; Length 594;
Best Local Similarity 99.1%; Pred. No. 4.3e-84;
Matches 220; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MAEGKAGGAGLFAKQVQKFSRAQEKVLQKLGKAVETKDERFEQSANFYQQQAEHKL 60
Db |||||
QY 61 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWNNDLLWEDYEELADQ 120
Db |||||
QY 90 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWNNDLLWEDYEELADQ 149
QY 121 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 179
Db |||||
QY 150 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNAKDEAKTAKAEFEFNKA 209
QY 180 QTVFEDLNQELLELPILYNSRIGCVYTFIFONISNLRDVFYR 221
Db |||||
QY 210 QTVFEDLNQELLELPILYNSRIGCVYTFIFONISNLRDVFYR 251

RESULT 4

ABG20324

ID ABG20324 standard; protein; 594 AA.

AC ABG20324;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #20315.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

OS WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.

XX Dmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS84511.

XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.

PS Claim 20; SEQ ID NO 50693; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 594 AA;

Query Match 98.8%; Score 1111.5; DB 4; Length 594;
Best Local Similarity 99.1%; Pred. No. 4.3e-84;
Matches 220; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MAEGKAGGAGLFAKQVQKFSRAQEKVLQKLGKAVETKDERFEQSANFYQQQAEHKL 60
Db |||||
QY 30 MAEGKAGGAGLFAKQVQKFSRAQEKVLQKLGKAVETKDERFEQSANFYQQQAEHKL 89
QY 61 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWNNDLLWEDYEELADQ 120
Db |||||
QY 90 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWNNDLLWEDYEELADQ 149
QY 121 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 179
Db |||||
QY 150 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNAKDEAKTAKAEFEFNKA 209
QY 180 QTVFEDLNQELLELPILYNSRIGCVYTFIFONISNLRDVFYR 221
Db |||||
QY 210 QTVFEDLNQELLELPILYNSRIGCVYTFIFONISNLRDVFYR 251

RESULT 5

ABG22457

ID ABG22457 standard; protein; 594 AA.

XX AC ABG22457;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22448.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Dmanac RT, Liu C, Tang YT;

PI WPI; 2001-639362/73.

XX N-PSDB; AAS86644.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 52816; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 594 AA;

Query Match 98.2%; Score 1104.5; DB 4; Length 594;
Best Local Similarity 98.6%; Pred. No. 1.6e-83;
Matches 219; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MAEGKAGGAGLFAKQVQKFSRAQKVLQKLGKAVETKDERPEQSASNFYQQAEHKL 60

Db 30 MAEGKAGGAGLFAKQVQKFSRAQKVLQKLGKAVETKDERPEQSASNFYQQAEHKL 89

QY 61 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWVNNDLWEDYEKLADQ 120

Db 90 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWVNNDLWEDYEKLADQ 149

QY 121 AVRTMEIYVQFSEIKERIAKRGKLVDSARHHEAVQNA-KDEAKTAKAEFEFNA 179

Db 150 AVRTMEIYVQFSEIKERIAKRGKLVDSARHHEAVQNA-KDEAKTAKAEFEFNA 209

QY 180 QTFPEDLNQELLEPLIYNSRIGCVYTFQNISNLRDVFYR 221

Db 210 QTFPEDLNQELLEPLIYNSRIGCVYTFQNISNLRDVFYR 251

RESULT 6

ABG21411

ID ABG21411 standard; protein; 572 AA.

XX AC ABG21411;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #21402.

XX Human; chromosome mapping; gene mapping; gene therapy; forensics;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Dmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS85598.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 51770; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 572 AA;

Query Match 97.0%; Score 1091.5; DB 4; Length 572;
Best Local Similarity 98.2%; Pred. No. 1.9e-82;
Matches 218; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MAEGKAGGAGLFAKQVQKFSRAQKVLQKLGKAVETKDERPEQSASNFYQQAEHKL 60

Db 8 MAEGKAGGAGLFAKQVQKFSRAQKVLQKLGKAVETKDERPEQSASNFYQQAEHKL 67

QY 61 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWVNNDLWEDYEKLADQ 120

Db 68 YKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWVNNDLWEDYEKLADQ 127

QY 121 AVRTMEIYVAFSEIKERIAKRGKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKA 179
 DB 128 AVRTMEIYVAFSEIKERIAKRGKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKA 187
 QY 180 QTVFEDLNQELLELPILYNSRIGCYVTIFQNTISNLRDVFYR 221
 DB 188 QTVFEDLNQELLELPILYNSRIGCYVTIFQNTISNLRDVFYR 229

RESULT 7

ABG20886
 ID ABG20886 standard; protein; 960 AA.

XX AC ABG20886;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #20877.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX FN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS85073.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 51245; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 960 AA;

Query Match 74.1%; Score 833.5; DB 4; Length 960;
 Best Local Similarity 93.9%; Pred. No. 1.2e-60;

Matches 168; Conservative 3; Mismatches 5; Indels 3; Gaps 2;
 QY 46 SASNF--YQQAEGHKLKXDLNFKLSAVKVMHESKRVSETLQEIYSSWDGHEELKAIV 103
 DB 144 SAFHFFIYKCRABGHKLKXDLNFKLSAVKVMHESKRVSETLQFIYSEWYGHLELKAIV 203
 QY 104 WNDLLWEDYEKKLDAQVRTMEIYVAFSEIKERIAKRGKLVYDSARHLEAVQNA- 162
 DB 204 WNDLLWEDYEKKLDAQVRTMEIYVAFSEIKERIAKRGKLVYDSARHLEAVQNA 263
 QY 163 KDEAKTAKAEFEFNKAQTVFEDLNQELLELPILYNSRIGCYVTIFQNTISNLRDVFYR 221
 DB 264 KDEAKTAKAEFEFNKAQTVFEDLNQELLELPILYNSRIGCYVTIFQNTISNLRDVFYR 322

RESULT 8

ABG20323

ID ABG20323 standard; protein; 960 AA.

XX AC ABG20323;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #20314.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX FN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS84510.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 50682; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 960 AA;

Query Match 74.1%; Score 833.5; DB 4; Length 960;

Best Local Similarity 93.9%; Pred. No. 1.2e-60;

Matches 168; Conservative 3; Mismatches 5; Indels 3; Gaps 2;

QY 46 SASNF--YQQAEGHKLYKDLKNFLSAVKVMHSSKRVSETLQFIYSSWDGHEELKATV 103

DB 144 SAFFHYIKRAEGHKLYKDLKNFLSAVKVMHSSKRVSETLQFIYSEWYGHLELKAIV 203

QY 104 WNDLLMEDYBEKLAQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA- 162

DB 204 WNDLLMEDYBEKLAQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA- 263

QY 163 KQDAKTAKEEFNKATQVFEDLNQELLELPILYNSRIGCYVTIFQNISLRDVFYR 221

DB 264 KQDAKTAKEEFNKATQVFEDLNQELLELPILYNSRIGCYVTIFQNISLRDVFYR 322

RESULT 9

ABG22456

ID ABG22456 standard; protein; 425 AA.

XX AC ABG22456;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #22447.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX DR N-PSDB; RAS86643.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

PS Claim 20; SEQ ID NO 52815; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABC0010-ABG3037; represent novel human diagnostic

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 425 AA;

Query Match 68.3%; Score 768.5; DB 4; Length 425;

Best Local Similarity 90.1%; Pred. No. 1.1e-55;

Matches 155; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 51 YQQAEGHKLYKDLKNFLSAVKVMHSSKRVSETLQFIYSSWDGHEELKATV 110

DB 10 FTQAEGHKLYKDLKNFLSAVKVMHSSKRVSETLQFIYSEWYGHLELKAIV 69

QY 111 EDYEEKLAQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KXDEAKT 169

DB 70 EDYEEKLAQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KXDEAKT 129

QY 170 AKAESEFNKAQTVFEDLNQELLELPILYNSRIGCYVTIFQNISLRDVFYR 221

DB 130 AKAESEFNKAQTVFEDLNQELLELPILYNSRIGCYVTIFQNISLRDVFYR 181

RESULT 10

AAW05391

ID AAW05391 standard; protein; 434 AA.

XX AC AAW05391;

DT 18-FEB-1998 (first entry)

DE Mouse SH3p9 protein.

XX Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;

XX cellular signalling element; cellular structural element; malignancy;

XX protein identification; functional domain; protein screening;

XX cellular signal transduction process.

XX Mus musculus.

XX Key Location/Qualifiers

XX Misc-difference 433

XX /note= "encoded by CTA"

XX W09631625-A1.

XX 10-OCT-1996.

XX 04-APR-1996; 96WO-US004454.

XX 07-APR-1995; 95US-00417872.

XX 03-APR-1996; 96US-00630915.

XX (CYTO-). CYTOGEN CORP.

XX (UNYC-) UNIV NORTH CAROLINA.

XX Sparks AB, Hoffman N, Kay BK, Fowlkes DM, McConnell SJ;

XX WPI; 1996-465045/46.

XX N-PSDB; AAT39791.

XX Identifying polypeptide(s) having specific functional domain (esp. SH3

XX domain) - comprises detecting selective binding to recognition unit,

XX regardless of sequence homology.

XX Claim 54; Fig 35; 174pp; English.

XX AAW05386-W05403 represent novel human and mouse Src-homology region 3

XX (SH3) domain containing proteins that can be used in the method of the

CC invention. SH3 domain containing proteins play a role in signalling and
 CC structural elements of cells. The method of the invention is for
 CC identifying polypeptides containing functional domains of interest
 CC (especially SH3 domains). The method comprises contacting a multivalent
 CC recognition unit (RU) complex with a number of peptides and identifying
 CC polypeptides having a selective binding affinity for the RU complex. The
 CC method is based on functional similarities and does not rely on sequence
 CC similarities. Prior methods only gave limited success for identifying
 CC proteins which contain an SH3 domain due to the minimal sequence homology
 CC among known SH3 proteins. It has been found that small peptide RUS in
 CC multivalent form have reduced specificity for a given functional domain
 CC compared to monomer RUS. Multivalent RU complexes are particularly suited
 CC to screening for polypeptides containing functional domains that are
 CC similar to, but not identical in sequence to, the original target
 CC functional domain. The new method enables proteins having a common
 CC function to be identified. Identification of novel SH3 proteins will be
 CC useful for a better understanding of cell growth, malignancy, signal
 CC transduction processes, etc. New candidate drugs can be identified, and
 CC their specificities (e.g. pharmacological activities) can be assessed
 CC using the method of the invention
 XX
 XX SQ Sequence 434 AA;

Query Match 61.2%; Score 688; DB 2; Length 434;
 Best Local Similarity 61.9%; Pred. No. 5.7e-49;
 Matches 138; Conservative 30; Mismatches 53; Indels 2; Gaps 2;
 QY 1 MAE-GRAGGAGLPAKQVKFSPRAQEKVLQKLGKAVETKDERPEQSASNYQQAGHGK 59
 Db 1 MAEMGSKGVYTAGKIASNVQKKLTRAQEKVLQKLGKADETKDEQPCQVQNFNKLTEGTR 60
 QY 60 LYKDLKNFLSAVKVMHSSKEVSETLQETYSSEWDGHEELKAIWNNDLLWEDYEELKAD 119
 Db 61 LQKDLRTYLASVKAMHEASKLSECLQEVYEPFPGDEANKIAENNDLLWMDYHQLVD 120
 QY 120 QAVRTMEIYVAQPSSEIKERIAKRGKLVYDSDARHLEAVQNA-KKDEAKTAKAEFEFNK 178
 Db 121 QALLTMDTYLGGFPDPIKSIKRIAKRGKLVYDSDARHLYESLQTKACKDEAKIAKEEELIK 180
 QY 179 AQTVPEDLNQELLEPLIYNSRIGCVYTFQNISNLRDVFYR 221
 Db 181 AOKVPEEMNVDLQELPSLWNSRVGFYVNTFQSIAGLEENFHK 223

RESULT 11
 AAB62101
 ID AAB62101 standard; protein; 252 AA.
 AC AAB62101;
 DT 29-MAY-2001 (first entry)
 XX Bar domain of Bin1 protein.
 DE
 XX Bridging integrator-2 protein; Bin2; cancer; leukemia; blood disorder;
 KW hyperplastic disease; cytostatic; cell growth regulator; Bin1;
 KW chromosome 4q22.1.
 XX Homo sapiens.
 OS
 XX WO200116158-A2.
 PN
 XX
 PD 08-MAR-2001.
 XX
 XX 30-AUG-2000; 2000WO-US023723.
 XX
 XX 31-AUG-1999; 99US-0151554P.
 XX
 XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 PA
 XX Prendergast GC, Ge K;
 PI WPI; 2001-235087/24.
 DR

XX
 PT New bridging integrator-2 (Bin2) protein and nucleic acid molecules,
 PT useful for regulating cell growth, and for diagnosing or treating
 PT conditions associated with inappropriate expression of Bin2, e.g. cancers
 PT or hepatocarcinoma.
 XX
 PS Example 3; Fig 2; 62pp; English.
 XX
 CC The invention provides a human bridging integrator-2 (Bin2) protein. The
 CC protein can be expressed by standard recombinant methodology. The Bin2
 CC proteins or peptides are useful in regulating cell growth, cell survival,
 CC differentiation, endocytosis and actin organization. These peptides or
 CC proteins are also useful for diagnosing or treating conditions associated
 CC with inappropriate expression of Bin2, e.g. liver cancer, breast cancer,
 CC hepatocarcinoma, myeloid and lymphoid leukemias or blood disorders. The
 CC peptides, nucleic acid sequences or anti-Bin2 antibodies are useful for
 CC diagnosing inappropriate expression of Bin2. Bin2 is also useful for
 CC treating disorders associated with excessive Bin1 levels, e.g. liver,
 CC colorectal, prostate or breast cancers, epithelia cell cancers, melanoma,
 CC or hyperplastic disease states. The present sequence represents the Bar
 CC domain of Bin1 used in homology studies with Bin2 protein
 XX
 XX SQ Sequence 252 AA;

Query Match 60.7%; Score 683; DB 4; Length 252;
 Best Local Similarity 61.0%; Pred. No. 7.6e-49;
 Matches 136; Conservative 32; Mismatches 53; Indels 2; Gaps 2;
 QY 1 MAE-GRAGGAGLPAKQVKFSPRAQEKVLQKLGKAVETKDERPEQSASNYQQAGHGK 59
 Db 1 MAEMGSKGVYTAGKIASNVQKKLTRAQEKVLQKLGKADETKDEQPCQVQNFNKLTEGTR 60
 QY 60 LYKDLKNFLSAVKVMHSSKEVSETLQETYSSEWDGHEELKAIWNNDLLWEDYEELKAD 119
 Db 61 LQKDLRTYLASVKAMHEASKLSECLQEVYEPFPGDEANKIAENNDLLWMDYHQLVD 120
 QY 120 QAVRTMEIYVAQPSSEIKERIAKRGKLVYDSDARHLEAVQNA-KKDEAKTAKAEFEFNK 178
 Db 121 QALLTMDTYLGGFPDPIKSIKRIAKRGKLVYDSDARHLYESLQTKACKDEAKIAKEEELIK 180
 QY 179 AQTVPEDLNQELLEPLIYNSRIGCVYTFQNISNLRDVFYR 221
 Db 181 AOKVPEEMNVDLQELPSLWNSRVGFYVNTFQSIAGLEENFHK 223

RESULT 12
 ABU89771
 ID ABU89771 standard; protein; 482 AA.
 AC ABU89771;
 DT 10-JUL-2003 (first entry)
 XX
 XX Protein differentially expressed in cardiovascular disease #65.
 DE
 XX Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
 KW myocardial infarction; cardiast; antiarteriosclerotic; antianginal;
 KW gene therapy; differential gene expression.
 XX
 OS Homo sapiens.
 XX
 XX WO2003031650-A2.
 PN
 XX
 PD 17-APR-2003.
 XX
 XX 02-OCT-2002; 2002WO-EP011034.
 XX
 XX 08-OCT-2001; 2001GB-00024145.
 XX
 XX (FARB) BAYER AG.
 PA
 XX Munnes M, Gehrman M, Wick M, Schmitz G;
 PI
 XX


```

AC AAW47295;
XX
DT 01-JUN-1998 (first entry)
XX
DE DE
DE DE
XX Human Binl.
XX
KW Human; Box-dependent myc-interacting protein; Binl; treatment; cancer;
KW hyperplastic disease; neurodegenerative disease; antibody; diagnosis.
XX
XX Homo sapiens.
OS
XX US5723581-A.
XX
XX 03-MAR-1998.
XX
XX 24-MAY-1996; 96US-00652972.
XX
XX 05-MAY-1995; 95US-00435454.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Sakamuro D, Prendergast GC;
XX
XX WPI; 1998-178541/16.
XX N-PSDB; AAV15692.
XX
XX Box-dependent myc-interacting protein Binl - useful for, e.g. treating
XX diseases associated with inadequate Binl levels such as colon cancer.
XX
XX Claim 1; Col 25-30; 32pp; English.
XX
XX The present sequence is human Box-dependent myc-interacting protein Binl,
XX which can be used to treat diseases associated with inadequate Binl
XX levels, e.g. liver, colon or breast cancer or hyperplastic diseases, or
XX diseases where Binl activity needs to be inhibited, e.g.
XX neurodegenerative diseases, or to raise antibodies for diagnostic
XX purposes
XX
XX Sequence 451 AA;
XX
Query Match 59.7%; Score 671.5; DB 2; Length 451;
Best Local Similarity 61.5%; Pred. No. 1.4e-47;
Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;
QY 10 AGLFAKQVQKFRAGAEKVLQKLGKAVETKDRFQASNFYQQAEGHKLYKDLKNFLS 69
DB 8 AGKIASNVQKLTFAQAEKVLQKLGKADETKDEQFCQVQNFKLTGTRLQKDLRTYLA 67
QY 70 AVKVMHSSKRVSETLOEIIYSSEWDGHEELKAIYVNNDDLWEDYEEKLADQAVRTMEIYV 129
DB 68 SVKAMHEASKKLNCEQLQEVTEPDPWGRDEANKIAENNDLLWMDYHQKLVQALLTMDTYL 127
QY 130 AQPSEIKERIAKGRKLVYDVSARHLEAVQNA-KDEAKTAKAEFEFNKAQTVFEDLNQ 188
DB 128 GQFPDIKRIAKGRKLVYDVSARHYESLSQTAKKDEAKIAKAEELIKAKQVFEENVV 187
QY 189 ELLEELPILYNSRIGCYVTIFQNISNLRDVFYR 221
DB 188 DLOEELPSLWNSRVGFYNTFQSIAGLEENFHK 220
RESULT 15
AAB36881
ID AAB36881 standard; protein; 451 AA.
XX
XX AAB36881;
XX
XX 22-FEB-2001 (first entry)
XX
XX Human Binl protein.
XX
XX Human; BIN1-associated U1-specific; Bau; cancer; gene therapy.
XX

```

```

OS Homo sapiens.
XX
XX US6140465-A.
XX
XX 31-OCT-2000.
XX
XX 29-JUN-1999; 99US-00344889.
XX
XX 29-AUG-1996; 96US-0025482P.
XX
XX 27-AUG-1997; 97US-00919145.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Prendergast GC;
XX
XX WPI; 1998-207038/18.
XX N-PSDB; AAC68498.
XX
XX New isolated BIN1-associated U1-specific protein - which acts as a tumour
XX suppressor, used to develop products for treating e.g. cancers, hyper-
XX plastic disease states or degenerative diseases.
XX
XX Disclosure; Fig 3; 22pp; English.
XX
XX The present invention relates to mammalian BIN1-associated U1-specific
XX (Bau) protein. The Bau protein is useful in the detection, diagnosis and
XX treatment of cancers or other disorders associated with inappropriate
XX BIN1 levels and/or deregulation, deficiency or amplification of the c-Myc
XX oncogenes. The proteins are also useful as antigens for the development
XX of anti-Bau antisera and antibodies to Bau, or to a desired fragment of
XX the Bau protein, as diagnostic reagents, in gene therapy, and in
XX screening and developing chemical compounds or proteins which may be used
XX for the treatment of cancers characterized by Bau or BIN1, which regulate
XX inappropriate MYC levels
XX
XX Sequence 451 AA;
XX
Query Match 59.7%; Score 671.5; DB 2; Length 451;
Best Local Similarity 61.5%; Pred. No. 1.4e-47;
Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;
QY 10 AGLFAKQVQKFRAGAEKVLQKLGKAVETKDRFQASNFYQQAEGHKLYKDLKNFLS 69
DB 8 AGKIASNVQKLTFAQAEKVLQKLGKADETKDEQFCQVQNFKLTGTRLQKDLRTYLA 67
QY 70 AVKVMHSSKRVSETLOEIIYSSEWDGHEELKAIYVNNDDLWEDYEEKLADQAVRTMEIYV 129
DB 68 SVKAMHEASKKLNCEQLQEVTEPDPWGRDEANKIAENNDLLWMDYHQKLVQALLTMDTYL 127
QY 130 AQPSEIKERIAKGRKLVYDVSARHLEAVQNA-KDEAKTAKAEFEFNKAQTVFEDLNQ 188
DB 128 GQFPDIKRIAKGRKLVYDVSARHYESLSQTAKKDEAKIAKAEELIKAKQVFEENVV 187
QY 189 ELLEELPILYNSRIGCYVTIFQNISNLRDVFYR 221
DB 188 DLOEELPSLWNSRVGFYNTFQSIAGLEENFHK 220
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:46:32 ; Search time 31.9355 Seconds
(without alignments)
119.014 Million cell updates/sec

Title: US-10-069-540A-2_COPY_138_155

Perfect score: 95

Sequence: 1 RIAGKGRKLVDYDSARHH 18

Scoring table: BLOSUM62

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Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

Published Applications AA:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	404	9	US-09-879-957-24
2	95	100.0	434	9	US-09-879-957-22
3	95	100.0	451	14	US-10-123-807-4
4	95	100.0	482	15	US-10-116-275-238
5	50	52.6	351	15	US-10-369-493-3387
6	47	49.5	745	15	US-10-369-493-12681
7	45.5	47.9	742	15	US-10-104-047-2962
8	43	45.3	237	15	US-10-369-493-2408
9	43	45.3	284	15	US-10-369-493-2410
10	42	44.2	634	9	US-09-731-221-78
11	42	44.2	906	13	US-10-060-230-19
12	42	44.2	906	13	US-10-060-230-20
13	42	44.2	906	13	US-10-060-230-21
14	42	44.2	906	13	US-10-060-230-22
15	41.5	43.7	593	14	US-10-156-761-14765

16	41	43.2	90	14	US-10-203-081-4	Sequence 4, Appli
17	41	43.2	237	14	US-10-080-170-500	Sequence 500, App
18	41	43.2	657	15	US-10-369-493-12857	Sequence 12857, A
19	41	43.2	771	14	US-10-128-714-3280	Sequence 3280, Ap
20	41	43.2	905	14	US-10-128-714-8280	Sequence 8280, Ap
21	40.5	42.6	511	15	US-10-259-194A-180	Sequence 180, App
22	40	42.1	276	14	US-10-156-761-13731	Sequence 13731, A
23	40	42.1	294	9	US-09-927-738-9	Sequence 9, Appli
24	40	42.1	406	14	US-10-405-219-125	Sequence 125, App
25	40	42.1	414	9	US-09-925-302-706	Sequence 706, App
26	40	42.1	414	9	US-09-927-738-8	Sequence 8, Appli
27	40	42.1	414	15	US-10-264-049-2843	Sequence 2843, Ap
28	40	42.1	436	15	US-10-262-445-6	Sequence 6, Appli
29	40	42.1	440	10	US-09-932-367A-19	Sequence 19, Appl
30	40	42.1	830	15	US-10-369-493-7014	Sequence 7014, Ap
31	39	41.1	30	14	US-10-029-386-27685	Sequence 27685, A
32	39	41.1	315	14	US-10-306-762-187	Sequence 187, App
33	39	41.1	360	9	US-09-847-057-2	Sequence 2, Appli
34	39	41.1	390	15	US-10-369-493-12646	Sequence 12646, A
35	39	41.1	450	10	US-09-949-029-72	Sequence 72, Appl
36	39	41.1	471	14	US-10-128-714-3080	Sequence 3080, Ap
37	39	41.1	565	14	US-10-128-714-8080	Sequence 8080, Ap
38	38.5	40.5	724	14	US-10-211-962-25	Sequence 25, Appl
39	38	40.0	90	15	US-10-630-590-149	Sequence 149, App
40	38	40.0	225	15	US-10-369-493-20139	Sequence 20139, A
41	38	40.0	306	15	US-10-320-797-3084	Sequence 3084, Ap
42	38	40.0	314	15	US-10-369-493-10341	Sequence 10341, A
43	38	40.0	475	9	US-09-925-301-1263	Sequence 1263, Ap
44	38	40.0	632	14	US-10-128-714-8131	Sequence 8131, Ap
45	38	40.0	715	9	US-09-870-759-86	Sequence 86, Appl
46	38	40.0	715	10	US-09-751-708A-86	Sequence 86, Appl
47	38	40.0	757	15	US-10-369-493-16797	Sequence 16797, A
48	38	40.0	950	9	US-09-815-242-11961	Sequence 11961, A
49	38	40.0	1433	14	US-10-224-249-14	Sequence 14, Appl
50	38	40.0	1518	9	US-09-801-368-152	Sequence 152, App
51	38	40.0	1518	15	US-10-369-493-22243	Sequence 22243, A
52	37.5	39.5	636	15	US-10-369-493-17930	Sequence 17930, A
53	37.5	39.5	1249	15	US-10-369-493-6039	Sequence 6039, Ap
54	37	38.9	81	10	US-09-813-153-115	Sequence 115, App
55	37	38.9	89	9	US-09-815-242-11245	Sequence 11224, A
56	37	38.9	89	9	US-09-815-242-11245	Sequence 11224, A
57	37	38.9	110	14	US-10-156-761-7872	Sequence 7872, Ap
58	37	38.9	114	14	US-10-156-761-11982	Sequence 11982, A
59	37	38.9	145	9	US-09-815-242-5551	Sequence 5551, Ap
60	37	38.9	145	9	US-09-815-242-12237	Sequence 12237, A
61	37	38.9	150	15	US-10-369-493-13196	Sequence 13196, A
62	37	38.9	342	15	US-10-369-493-1467	Sequence 1467, Ap
63	37	38.9	342	15	US-10-369-493-13196	Sequence 13196, A
64	37	38.9	355	10	US-09-882-227-608	Sequence 608, App
65	37	38.9	381	15	US-10-369-493-10515	Sequence 10515, A
66	37	38.9	474	15	US-10-369-493-19396	Sequence 19396, A
67	37	38.9	513	15	US-10-369-493-13196	Sequence 13196, A
68	37	38.9	577	14	US-10-156-761-12668	Sequence 12668, A
69	37	38.9	642	15	US-10-108-260A-4483	Sequence 4483, Ap
70	37	38.9	840	15	US-10-369-493-3233	Sequence 3233, Ap
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72	37	38.9	1277	9	US-09-969-362-3	Sequence 3, Appli
73	36	37.9	89	9	US-09-815-242-10313	Sequence 10313, A
74	36	37.9	89	9	US-09-815-242-11754	Sequence 11754, A
75	36	37.9	89	9	US-09-815-242-13767	Sequence 13767, A
76	36	37.9	130	15	US-10-364-743-83	Sequence 83, Appl
77	36	37.9	170	9	US-09-738-626-5096	Sequence 5096, Ap
78	36	37.9	188	15	US-10-369-493-18256	Sequence 18256, A
79	36	37.9	206	10	US-09-764-891-4189	Sequence 4189, Ap
80	36	37.9	252	15	US-10-369-493-14032	Sequence 14032, A
81	36	37.9	254	14	US-10-441-626-9	Sequence 9, Appli
82	36	37.9	254	14	US-10-441-626-10	Sequence 10, Appl
83	36	37.9	269	15	US-10-264-213-201	Sequence 201, App
84	36	37.9	271	15	US-10-369-493-9095	Sequence 9095, Ap
85	36	37.9	306	15	US-10-369-493-3028	Sequence 3028, Ap
86	36	37.9	317	14	US-10-306-762-230	Sequence 230, App
87	36	37.9	336	15	US-10-369-493-19238	Sequence 19238, A
88	36	37.9	347	14	US-10-156-761-9006	Sequence 9006, Ap

89 Sequence 9212, Ap
90 Sequence 9453, Ap
91 Sequence 9458, Ap
92 Sequence 12394, A
93 Sequence 2049, Ap
94 Sequence 73, Appl
95 Sequence 413, Appl
96 Sequence 122, Appl
97 Sequence 7, Appl
98 Sequence 2271, Ap
99 Sequence 12119, A
100 Sequence 22186, A
101 Sequence 22186, A
102 Sequence 334, Appl
103 Sequence 12465, A
104 Sequence 14716, A
105 Sequence 15197, A
106 Sequence 11426, A
107 Sequence 14391, A
108 Sequence 22152, A
109 Sequence 9875, Ap
110 Sequence 14788, A
111 Sequence 21698, A
112 Sequence 11685, A
113 Sequence 14947, A
114 Sequence 4, Appl
115 Sequence 3149, Ap
116 Sequence 11238, A
117 Sequence 132, Appl
118 Sequence 16805, A
119 Sequence 22294, A
120 Sequence 12, Appl
121 Sequence 7, Appl
122 Sequence 260, Appl
123 Sequence 9148, Ap
124 Sequence 22621, A
125 Sequence 22622, A
126 Sequence 7, Appl
127 Sequence 184, Appl
128 Sequence 6, Appl
129 Sequence 23, Appl
130 Sequence 14, Appl
131 Sequence 5006, Ap
132 Sequence 10948, A
133 Sequence 1978, Ap
134 Sequence 5, Appl
135 Sequence 13344, A
136 Sequence 54, Appl
137 Sequence 8173, Ap
138 Sequence 33747, A
139 Sequence 3953, Ap
140 Sequence 338, Appl
141 Sequence 13, Appl
142 Sequence 1978, Ap
143 Sequence 13, Appl
144 Sequence 336, Appl
145 Sequence 1519, Ap
146 Sequence 85, Appl
147 Sequence 85, Appl
148 Sequence 84, Appl
149 Sequence 84, Appl
150 Sequence 7244, Ap

ALIGNMENTS

RESULT 1
US-09-879-957-24
; Sequence 24, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.

HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWLES, Dana M.
MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-879-957-24
Query Match 100.0%; Score 95; DB 9; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RIAGKGRKLVYDSARHH 18
Db 104 RIAGKGRKLVYDSARHH 121
RESULT 2
US-09-879-957-22
; Sequence 22, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLES, Dana M.
; MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York


```

/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 13-Jun-2001
/ APPLICATION NUMBER: US/09/879,957
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/630,915
/ FILING DATE: 03-APR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 1101-174
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-3090
/ TELEFAX: (212) 869-8864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 434 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-879-957-22

Query Match 100.0%; Score 95; DB 9; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIAKGRKLVYDSARHH 18
Db 139 RIAKGRKLVYDSARHH 156

RESULT 3
US-10-123-807-4
/ Sequence 4, Application US/10123807
/ Publication No. US20030166021A1
/ GENERAL INFORMATION:
/ APPLICANT: Wistar Institute of Anatomy & Biology
/ Prendergast, George C.
/ Sakamuro, Daitoku
/ TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Howson and Howson
/ STREET: Spring House Corporate Cntr, P O Box 457
/ CITY: Spring House
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19477
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/123,807
/ FILING DATE: 16-Apr-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/445,247
/ FILING DATE: 03-Dec-1999
/ APPLICATION NUMBER: US 08/870,126
/ FILING DATE: 06-JUN-1997

```

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bak, Mary E.
/ REGISTRATION NUMBER: 31,215
/ REFERENCE/DOCKET NUMBER: WST60DPCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-540-9200
/ TELEFAX: 215-540-5818
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 451 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-123-807-4

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```

Query Match 100.0%; Score 95; DB 14; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RIAKGRKLVYDSARHH 18
Db 136 RIAKGRKLVYDSARHH 153

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RESULT 4
US-10-116-275-238
/ Sequence 238, Application US/10116275
/ Publication No. US20030211476A1
/ GENERAL INFORMATION:
/ APPLICANT: Elan Pharmaceutical Technology
/ APPLICANT: O'Mahony, Daniel J.
/ APPLICANT: Brayden, David
/ APPLICANT: Byrne, Daragh
/ APPLICANT: Lambkin, Imelda
/ APPLICANT: Higgins, Lisa
/ TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
/ FILE REFERENCE: E1067/20087
/ CURRENT APPLICATION NUMBER: US/10/116,275
/ CURRENT FILING DATE: 2002-10-04
/ NUMBER OF SEQ ID NOS: 349
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 238
/ LENGTH: 482
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-116-275-238

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Query Match 100.0%; Score 95; DB 15; Length 482;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RIAKGRKLVYDSARHH 18
Db 139 RIAKGRKLVYDSARHH 156

```

```

RESULT 5
US-10-369-493-3387
/ Sequence 3387, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28

```

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; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3387
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(351)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3387

Query Match          52.6%; Score 50; DB 15; Length 351;
Best Local Similarity 69.2%; Pred. No. 4.6;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 KRGRKLVYDSAR 16
Db 226 KRGRKLVYDSAR 238

RESULT 6
US-10-369-493-12681
; Sequence 12681, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12681
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(265)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12681

Query Match          49.5%; Score 47; DB 15; Length 265;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IAKGRKLVYDSAR 16
Db 151 IAKGRKLVYDSAR 165

RESULT 7
US-10-104-047-2962
; Sequence 2962, Application US/10104047
; Publication No. US20030233692A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030233692A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2962
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2962

Query Match          47.9%; Score 45.5; DB 15; Length 742;
Best Local Similarity 43.5%; Pred. No. 55;
Matches 10; Conservative 3; Mismatches 5; Indels 5; Gaps 1;

QY 1 RIAGRGKLV-----DYDSARH 18
Db 387 RVGRGRVLLDRAHSDYDSVFH 409

RESULT 8
US-10-369-493-2408
; Sequence 2408, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2408
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(237)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2408

Query Match          45.3%; Score 43; DB 15; Length 237;
Best Local Similarity 53.3%; Pred. No. 42;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IAKGRKLVYDSAR 16
Db 105 IAKGRKLVYDSAR 119

RESULT 9
US-10-369-493-2410
; Sequence 2410, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2410
; LENGTH: 284
; TYPE: PRT
```

; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(284)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2410

Query Match 45.3%; Score 43; DB 15; Length 284;
Best Local Similarity 53.3%; Pred. No. 51;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IAKGRKLVYDSAR 16
Db 152 ITRNKHLLDHDAMR 166

RESULT 10
US-09-731-221-78
; Sequence 78, Application US/09731221
; Patent No. US20020018778A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael
; TITLE OF INVENTION: Passive Desensitization
; FILE REFERENCE: 2002834-0103
; CURRENT APPLICATION NUMBER: US/09/731,221
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 78
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Arachis
; OTHER INFORMATION: Hypogaea
US-09-731-221-78

Query Match 44.2%; Score 42; DB 9; Length 634;
Best Local Similarity 64.3%; Pred. No. 1.7e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKGRKLVYDSAR 16
Db 86 ATRGRQFGDYDDAR 99

RESULT 11
US-10-060-230-19
; Sequence 19, Application US/10060230
; Publication No. US20020173014A1
; GENERAL INFORMATION:
; APPLICANT: HILTUNEN, Kalervo
; TITLE OF INVENTION: A method to control cellular (3R)-hydroxyacyl-CoA
; TITLE OF INVENTION: esters, precursor molecules for polyhydroxyalkanoate
; TITLE OF INVENTION: synthesis in genetically modified organisms
; FILE REFERENCE: 0365-0528P
; CURRENT APPLICATION NUMBER: US/10/060,230
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 19991667
; PRIOR FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Candida tropicalis
US-10-060-230-19

Query Match 44.2%; Score 42; DB 13; Length 906;
Best Local Similarity 46.7%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAKGRKLVYDSAR 16

Db 267 VAKGFSEILDYDSR 281

RESULT 12
US-10-060-230-20
; Sequence 20, Application US/10060230
; Publication No. US20020173014A1
; GENERAL INFORMATION:
; APPLICANT: HILTUNEN, Kalervo
; TITLE OF INVENTION: A method to control cellular (3R)-hydroxyacyl-CoA
; TITLE OF INVENTION: esters, precursor molecules for polyhydroxyalkanoate
; TITLE OF INVENTION: synthesis in genetically modified organisms
; FILE REFERENCE: 0365-0528P
; CURRENT APPLICATION NUMBER: US/10/060,230
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 19991667
; PRIOR FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Candida tropicalis
US-10-060-230-20

Query Match 44.2%; Score 42; DB 13; Length 906;
Best Local Similarity 46.7%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAKGRKLVYDSAR 16
Db 267 VAKGFSEILDYDSR 281

RESULT 13
US-10-060-230-21
; Sequence 21, Application US/10060230
; Publication No. US20020173014A1
; GENERAL INFORMATION:
; APPLICANT: HILTUNEN, Kalervo
; TITLE OF INVENTION: A method to control cellular (3R)-hydroxyacyl-CoA
; TITLE OF INVENTION: esters, precursor molecules for polyhydroxyalkanoate
; TITLE OF INVENTION: synthesis in genetically modified organisms
; FILE REFERENCE: 0365-0528P
; CURRENT APPLICATION NUMBER: US/10/060,230
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 19991667
; PRIOR FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Candida tropicalis
US-10-060-230-21

Query Match 44.2%; Score 42; DB 13; Length 906;
Best Local Similarity 46.7%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAKGRKLVYDSAR 16
Db 267 VAKGFSEILDYDSR 281

RESULT 14
US-10-060-230-22
; Sequence 22, Application US/10060230
; Publication No. US20020173014A1
; GENERAL INFORMATION:
; APPLICANT: HILTUNEN, Kalervo
; TITLE OF INVENTION: A method to control cellular (3R)-hydroxyacyl-CoA

; TITLE OF INVENTION: esters, precursor molecules for polyhydroxyalkanoate
; TITLE OF INVENTION: synthesis in genetically modified organisms
; FILE REFERENCE: 0365-0528P
; CURRENT APPLICATION NUMBER: US/10/060,230
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 19991667
; PRIOR FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 906
; TYPE: PRT
; ORGANISM: Candida tropicalis
US-10-060-230-22

Query Match 44.2%; Score 42; DB 13; Length 906;
Best Local Similarity 46.7%; Pred. No. 2.5e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAKRGKLVYDSAR 16
Db 267 VAKRFSEILDYDSR 281
:||||:||||:|

RESULT 15
US-10-156-761-14765
; Sequence 14765, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14765
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14765

Query Match 43.7%; Score 41.5; DB 14; Length 593;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 8 KLVDYDSARHH 18
Db 514 QLIDYDS-RHH 523
:||||:||||

RESULT 16
US-10-203-081-4
; Sequence 4, Application US/10203081
; Publication No. US20030082527A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Gary K.
; TITLE OF INVENTION: Viral Cell Death Protein and Uses Therefore
; FILE REFERENCE: P03909
; CURRENT APPLICATION NUMBER: US/10/203,081
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

; LENGTH: 90
; TYPE: PRT
; ORGANISM: Snowshoe hare virus
US-10-203-081-4

Query Match 43.2%; Score 41; DB 14; Length 90;
Best Local Similarity 37.5%; Pred. No. 32;
Matches 6; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 RIAKRGKLVYDSAR 16
Db 47 RVSGRQIILNESGR 62
:||||:||||:|

RESULT 17
US-10-080-170-500
; Sequence 500, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; FILE REFERENCE: 03495-0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 500
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-500

Query Match 43.2%; Score 41; DB 14; Length 237;
Best Local Similarity 52.9%; Pred. No. 89;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IAKRGKLVYDSARHH 18
Db 79 LTKRGKALDDILARDH 95
:||||:||||

RESULT 18
US-10-369-493-12857
; Sequence 12857, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12857
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(657)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12857

```
Query Match      43.2%; Score 41; DB 15; Length 657;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches      8; Conservative      3; Mismatches      5; Indels      0; Gaps      0;

Qy      3 AKGRKLVYDSARHH 18
      : || | : |||||
Db      238 SSRGAGLTNVD SARHN 253

RESULT 19
US-10-128-714-3280
; Sequence 3280, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3280
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3280

Query Match      43.2%; Score 41; DB 14; Length 771;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches      8; Conservative      3; Mismatches      5; Indels      0; Gaps      0;

Qy      3 AKGRKLVYDSARHH 18
      : || | : |||||
Db      231 SSRGAGLTNVD SARHN 246

RESULT 20
US-10-128-714-8280
; Sequence 8280, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
```

```
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8280
; LENGTH: 905
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8280
```

```
Query Match      43.2%; Score 41; DB 14; Length 905;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches      8; Conservative      3; Mismatches      5; Indels      0; Gaps      0;
```

```
Qy      3 AKGRKLVYDSARHH 18
      : || | : |||||
Db      362 SSRGAGLTNVD SARHN 377
```

```
RESULT 21
US-10-259-194A-180
; Sequence 180, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghassseman, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 180
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-194A-180
```

```
Query Match      42.6%; Score 40.5; DB 15; Length 511;
Best Local Similarity 53.3%; Pred. No. 2.4e+02;
Matches      8; Conservative      4; Mismatches      2; Indels      1; Gaps      1;
```

```
Qy      4 KGRKLVYDSARHH 18
      : || | : |||||
Db      141 RGAEIDF SARHH 154
```

```
RESULT 22
US-10-156-761-13731
; Sequence 13731, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
```

APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13731
LENGTH: 276
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-13731

Query Match 42.1%; Score 40; DB 14; Length 276;
Best Local Similarity 53.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 RKLVYDSARH 17
Db 83 RELADVDAARH 93

RESULT 23

US-09-927-738-9
Sequence 9, Application US/09927738
Patent No. US20020076799A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongwen
TITLE OF INVENTION: Compositions and Methods of modulating TGF-B signaling
FILE REFERENCE: 17633/1082
CURRENT APPLICATION NUMBER: US/09/927,738
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/119786
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: PCT/US00/03561
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 294
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Clone S1+12 -5 protein
US-09-927-738-9

Query Match 42.1%; Score 40; DB 9; Length 294;
Best Local Similarity 58.3%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGRKLVYDSDA 15
Db 200 RRSRLVDYENA 211

RESULT 24

US-10-205-219-125
Sequence 125, Application US/10205219
Publication No. US20030138603A1
GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Finnick, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

FILE REFERENCE: WL-A-018200
CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 125
LENGTH: 406
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: SNX6
US-10-205-219-125

Query Match 42.1%; Score 40; DB 14; Length 406;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGRKLVYDSDA 15
Db 312 RRSRLVDYENA 323

RESULT 25

US-09-925-302-706
Sequence 706, Application US/09925302
Patent No. US2002004941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 706
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-706

Query Match 42.1%; Score 40; DB 9; Length 414;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGRKLVYDSDA 15
Db 320 RRSRLVDYENA 331

RESULT 26

US-09-927-738-8
Sequence 8, Application US/09927738
Patent No. US20020076799A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongwen
TITLE OF INVENTION: Compositions and Methods of modulating TGF-B signaling
FILE REFERENCE: 17633/1082
CURRENT APPLICATION NUMBER: US/09/927,738
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/119786
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: PCT/US00/03561
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 414

```
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Clone S1-12 -2 protein Sequence
US-09-927-738-8

Query Match          42.1%; Score 40; DB 9; Length 414;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      4 KGRKRLVDYDSA 15
DB      320 RRSRLVDYENA 331

RESULT 27
US-10-264-049-2843
; Sequence 2843, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2843
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2843

Query Match          42.1%; Score 40; DB 15; Length 414;
Best Local Similarity 58.3%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      4 KGRKRLVDYDSA 15
DB      320 RRSRLVDYENA 331

RESULT 28
US-10-262-445-6
; Sequence 6, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Simon
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
```

```
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Curaseq1 version 0.1
; SEQ ID NO 6
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-445-6

Query Match          42.1%; Score 40; DB 15; Length 436;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      4 KGRKRLVDYDSA 15
DB      342 RRSRLVDYENA 353

RESULT 29
US-09-932-367A-19
; Sequence 19, Application US/09932367A
; Publication No. US20030027152A1
; GENERAL INFORMATION:
; APPLICANT: RHODES, Simon J.
; APPLICANT: BRIDWELL, Jeanne L.
; APPLICANT: MEIER, Bradley C.
; APPLICANT: PARKER, Gretchen E.
; APPLICANT: PRICE, Jeffrey R.
; APPLICANT: SHOWALTER, Aaron D.
; APPLICANT: SLOOP, Kyle W.
; TITLE OF INVENTION: GENERATION OF DIAGNOSTIC TOOLS TO ASSAY THE HUMAN
; FILE REFERENCE: LHX3/P-LIM/LIN-3 FACTOR
; CURRENT APPLICATION NUMBER: US/09/932,367A
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/04424
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/121,110
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-932-367A-19

Query Match          42.1%; Score 40; DB 10; Length 440;
Best Local Similarity 77.8%; Pred. No. 2.5e+02;
```


Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 VDYDSARHH 18
|:|:|:|:|
Db 269 VDYDSFSHH 277

RESULT 30

US-10-369-493-7014
; Sequence 7014, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7014
; LENGTH: 830
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-7014

Query Match 42.1%; Score 40; DB 15; Length 830;

Best Local Similarity 46.2%; Pred. No. 4.9e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 KRGKRLVDYDSAR 16
|:|:|:|:|
Db 88 KKGHEFVDFDAVR 100

RESULT 31

US-10-029-386-27685
; Sequence 27685, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27685
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL137071.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
US-10-029-386-27685

Query Match 41.1%; Score 39; DB 14; Length 30;

Best Local Similarity 50.0%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IAKGRKRLVDYDSARH 17
|:|:|:|:|
Db 15 ISKEDRELFLSSQRH 30

RESULT 32

US-10-306-762-187
; Sequence 187, Application US/10306762
; Publication No. US20030187220A1
; GENERAL INFORMATION:
; APPLICANT: Park, Frances
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
; TITLE OF INVENTION: MONONUCLEOTIDE BINDING PROTEIN (FMNBP)
; FILE REFERENCE: 52498-20011.00
; CURRENT APPLICATION NUMBER: US/10/306,762
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US 60/334,132
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 315
; TYPE: PRT
; ORGANISM: D. melanogaster (18859731)
US-10-306-762-187

Query Match 41.1%; Score 39; DB 14; Length 315;

Best Local Similarity 52.9%; Pred. No. 2.5e+02;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IAKGRKRLVDYDSARH 18
|:|:|:|:|
Db 257 IEKYLCLVDYDNAPHN 273

RESULT 33

US-09-847-057-2
; Sequence 2, Application US/09847057
; Patent No. US20020004943A1
; GENERAL INFORMATION:
; APPLICANT: AGRINOMICS, LLC.
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLAN
; FILE REFERENCE: PAGODA
; CURRENT APPLICATION NUMBER: US/09/847,057
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-847-057-2

Query Match 41.1%; Score 39; DB 9; Length 360;

Best Local Similarity 43.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RIAGRKRLVDYDSAR 16
|:|:|:|:|
Db 339 RLTKKSAYLVDFESCR 354

RESULT 34

US-10-369-493-12646
; Sequence 12646, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 12646
 ; LENGTH: 390
 ; TYPE: PRT
 ; ORGANISM: Aspergillus nidulans
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)...(390)
 ; OTHER INFORMATION: unsure at all xaa locations
 ; US-10-369-493-12646

Query Match 41.1%; Score 39; DB 15; Length 390;
 Best Local Similarity 53.8%; Pred. No. 3.2e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GRKLVYDSARHH 18
 Db 16 GRILADFFTRRH 28

RESULT 35

US-09-949-029-72
 ; Sequence 72, Application US/09949029
 ; Publication No. US20030134278A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Karpen, G.H.
 ; APPLICANT: Dobie, K.W.
 ; APPLICANT: Kennedy, C.D.
 ; APPLICANT: Velasco, V.M.
 ; APPLICANT: McGrath, T.L.
 ; APPLICANT: Weko, J.
 ; APPLICANT: Patterson, R.W.

; TITLE OF INVENTION: Identification of chromosome inheritance modifiers in Drosophila
 ; FILE REFERENCE: 1211.015US1
 ; CURRENT APPLICATION NUMBER: US/09/949,029
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/231,178
 ; PRIOR FILING DATE: 2000-09-07
 ; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 72
 ; LENGTH: 450
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-949-029-72

Query Match 41.1%; Score 39; DB 10; Length 450;
 Best Local Similarity 38.9%; Pred. No. 3.7e+02;
 Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RIARKGRKLVYDSARHH 18
 Db 217 KLARYLPLRWPDARH 234

RESULT 36

US-10-128-714-8080
 ; Sequence 3080, Application US/10128714
 ; Publication No. US20030119013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Hu, Wengqi
 ; APPLICANT: Tishkoff, Daniel

; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Eroshtkin, Alexey M
 ; APPLICANT: Lemieux, Sebastien M
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: 10182-018-999
 ; CURRENT APPLICATION NUMBER: US/10/128,714
 ; CURRENT FILING DATE: 2002-04-23
 ; PRIOR APPLICATION NUMBER: US 60/285,697
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 60/287,066
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/295,890
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/303,899
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/316,362
 ; PRIOR FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 8603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3080
 ; LENGTH: 471
 ; TYPE: PRT
 ; ORGANISM: Aspergillus fumigatus
 ; US-10-128-714-3080

Query Match 41.1%; Score 39; DB 14; Length 471;
 Best Local Similarity 50.0%; Pred. No. 3.9e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 RGRKLVYDSARHH 18
 Db 425 RGRKREDKDSREH 438

RESULT 37

US-10-128-714-8080
 ; Sequence 8080, Application US/10128714
 ; Publication No. US20030119013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Hu, Wengqi
 ; APPLICANT: Tishkoff, Daniel
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Eroshtkin, Alexey M
 ; APPLICANT: Lemieux, Sebastien M

; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: 10182-018-999
 ; CURRENT APPLICATION NUMBER: US/10/128,714
 ; CURRENT FILING DATE: 2002-04-23
 ; PRIOR APPLICATION NUMBER: US 60/285,697
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 60/287,066
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/295,890
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/303,899
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/316,362
 ; PRIOR FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 8603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8080
 ; LENGTH: 565
 ; TYPE: PRT
 ; ORGANISM: Aspergillus fumigatus
 ; US-10-128-714-8080

Query Match 41.1%; Score 39; DB 14; Length 565;
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 RGRKLVYDSARHH 18
| | | | | | | | | |
Db 519 RGRKFEDKSKRHH 532

RESULT 38
US-10-211-962-25
; Sequence 25, Application US/10211962
; Publication No. US20030082640A1
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Gotthardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/10/211,962
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/562,737
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 25
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-10-211-962-25

Query Match 40.5%; Score 38.5; DB 14; Length 724;
Best Local Similarity 56.2%; Pred. No. 7.4e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

Qy 4 KRG---RKLVDYDSAR 16
| | | | | | | | | |
Db 428 KRGFVIRKLFYDXTK 443

RESULT 39
US-10-630-590-149
; Sequence 149, Application US/10630590
; Publication No. US20040018487A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter
; APPLICANT: Schweizer, Johannes
; APPLICANT: Diaz-Sarmiento, Chamorro Samoa
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008
; CURRENT APPLICATION NUMBER: US/10/630,590
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 60/269,523
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/710,059
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-630-590-149

Query Match 40.0%; Score 38; DB 15; Length 90;
Best Local Similarity 62.5%; Pred. No. 98;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IAKRGRKLVYDSAR 15
| | | | | | | | | |
Db 55 LAVNGRPLVDSLVSAR 70

RESULT 40
US-10-369-493-20139
; Sequence 20139, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20139
; LENGTH: 225
; TYPE: PRT
; ORGANISM: No. US20030233675A1altoc punctiforme
US-10-369-493-20139

Query Match 40.0%; Score 38; DB 15; Length 225;
Best Local Similarity 56.2%; Pred. No. 2.6e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 AKRGRKLVYDSARHH 18
| | | | | | | | | |
Db 98 AKYGDKLWDTIAKHH 113

RESULT 41
US-10-320-797-3084
; Sequence 3084, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3084
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3084

Query Match 40.0%; Score 38; DB 15; Length 306;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 RGRKLVYDSARHH 18
| | | | | | | | | |
Db 8 RDIQFVDYDNRVRFH 21

RESULT 42

US-10-369-493-10341
 ; Sequence 10341, Application US/10369493
 ; Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Goldman, Barry S.
 APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 10341

LENGTH: 314

TYPE: PRT

ORGANISM: *Cytophaga hutchinsonii*

US-10-369-493-10341

Query Match 40.0%; Score 38; DB 15; Length 314;

Best Local Similarity 66.7%; Pred. No. 3.7e+02;

Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 RKLVDYDSARHH 18

Db 303 RDLVDYTIARKH 314

RESULT 43

US-09-925-301-1263

; Sequence 1263, Application US/09945301

; Patent No. US20020052308A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 1263

LENGTH: 475

TYPE: PRT

ORGANISM: *Homo sapiens*

FEATURE:

NAME/KEY: SITE

LOCATION: (249)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-301-1263

Query Match 40.0%; Score 38; DB 9; Length 475;

Best Local Similarity 43.8%; Pred. No. 5.7e+02;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 RIAKRGKLVYDSAR 16

Db 276 KIFQGESPVYDGR 291

RESULT 44

US-10-128-714-8191

; Sequence 8191, Application US/10128714

; Publication No. US20030119013A1

GENERAL INFORMATION:

APPLICANT: Jiang, Bo

APPLICANT: Hu, Wenqi

APPLICANT: Tishkoff, Daniel

APPLICANT: Zamudio, Carlos

APPLICANT: Eroshkin, Alexey M

APPLICANT: Lemieux, Sebastien M

TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and

; TITLE OF INVENTION: Methods of Use

FILE REFERENCE: 10182-018-999

CURRENT APPLICATION NUMBER: US/10/128,714

CURRENT FILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US 60/285,697

PRIOR FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: US 60/287,066

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: US 60/295,890

PRIOR FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: US 60/303,899

PRIOR FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US 60/316,362

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEQ ID NOS: 8603

SOFTWARE: Patent in version 3.1

SEQ ID NO 8191

LENGTH: 632

TYPE: PRT

ORGANISM: *Aspergillus fumigatus*

US-10-128-714-8191

Query Match 40.0%; Score 38; DB 14; Length 632;

Best Local Similarity 61.5%; Pred. No. 7.8e+02;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AKRGKLVYDSA 15

Db 5 AKPRKLLDDSS 17

RESULT 45

US-09-870-759-86

; Sequence 86, Application US/09870759

; Patent No. US20020177551A1

GENERAL INFORMATION:

APPLICANT: TERMAN, David S

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

FILE REFERENCE: 870759

CURRENT APPLICATION NUMBER: US/09/870,759

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: US 60/208,128

PRIOR FILING DATE: 2000-05-30

NUMBER OF SEQ ID NOS: 166

SOFTWARE: Patent in version 3.1

SEQ ID NO 86

LENGTH: 715

TYPE: PRT

ORGANISM: *Staphylococcus aureus*

US-09-870-759-86

Query Match 40.0%; Score 38; DB 9; Length 715;

Best Local Similarity 50.0%; Pred. No. 8.8e+02;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 LVDYDSARHH 18

Db 264 ITSVDSSKHH 273

RESULT 46

US-09-751-708A-86

; Sequence 86, Application US/09751708A

; Publication No. US20030157113A1

```
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-86

Query Match 40.0%; Score 38; DB 10; Length 715;
Best Local Similarity 50.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 LVDYDSARHH 18
DB 264 ITSYDSSKHH 273
: |||:|
: |||:|

RESULT 47
US-10-369-493-16797
; Sequence 16797, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16797
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-16797

Query Match 40.0%; Score 38; DB 15; Length 757;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 IAKGRKLVYD 13
DB 364 LEKGRRLIGWD 375
: |||:|
: |||:|

RESULT 48
US-09-815-242-11961
; Sequence 11961, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
```

```
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11961
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11961

Query Match 40.0%; Score 38; DB 9; Length 950;
Best Local Similarity 46.2%; Pred. No. 1.2e+03;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 RGRKLVYDSARH 17
DB 165 RGRKLVNWDTKLH 177
: |||:|
: |||:|

RESULT 49
US-10-224-249-14
; Sequence 14, Application US/10224249
; Publication No. US20030087867A1
; GENERAL INFORMATION:
; APPLICANT: Vogels, Ronald V.
; APPLICANT: Verlinden, Stefan F.F.
; TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis
; FILE REFERENCE: 2183-5233US
; CURRENT APPLICATION NUMBER: US/10/224,249
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: PCT/NL00/00482
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: EP 99202263.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/143,101
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CHAIN
; LOCATION: (1)...(1433)
; OTHER INFORMATION: Human nitric oxide synthase
US-10-224-249-14

Query Match 40.0%; Score 38; DB 14; Length 1433;
Best Local Similarity 62.5%; Pred. No. 1.8e+03;
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 2 IAKGRKLVYD--YDSA 15
DB 65 LAVNGRFLVDSYDSA 80
: |||:|
: |||:|

RESULT 50
```

US-09-801-368-152
; Sequence 152, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milns, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 152
; LENGTH: 1518
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-152

Query Match 40.0%; Score 38; DB 9; Length 1518;
Best Local Similarity 70.0%; Pred. No. 2e+03;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRGRKLVVDYD 13
| | | | |
Db 1451 KFGKRVVEYD 1460

Search completed: March 4, 2004, 17:55:17
Job time : 33.9355 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:24:55 ; Search time 23.7096 Seconds
(without alignments)
1228.072 Million cell updates/sec

Title: US-10-069-540A-2
Perfect score: 2855
Sequence: 1 MAEGKAGGAGLFAKQVOKK.....NNLTAPEQPEVSTSENPOL 564

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	816.5	28.6	434	4	US-08-630-915A-22
2	793.5	27.8	451	1	US-08-652-972A-4
3	793.5	27.8	451	3	US-08-870-126-4
4	793.5	27.8	451	4	US-09-445-247-4
5	792	27.7	451	2	US-08-435-454-4
6	792	27.7	451	1	US-08-919-145-6
7	792	27.7	451	3	US-09-344-883-6
8	792	27.7	451	5	PCT-US96-06231A-4
9	675	23.6	404	4	US-08-630-915A-24
10	243	8.5	904	4	US-09-976-594-615
11	207.5	7.3	1324	4	US-09-645-456A-13
12	207.5	7.3	1324	4	US-09-425-324A-13
13	207.5	7.3	1324	4	US-09-645-791-13
14	205	7.2	1353	4	US-09-645-456A-11
15	205	7.2	1353	4	US-09-425-324A-11
16	205	7.2	1353	4	US-09-645-791-11
17	201.5	7.1	1298	4	US-09-645-456A-14
18	201.5	7.1	1298	4	US-09-425-324A-14
19	201.5	7.1	1298	4	US-09-645-791-14
20	199.5	7.0	1297	4	US-09-688-188B-14
21	199.5	7.0	1297	4	US-09-291-417D-14
22	199.5	7.0	1332	4	US-09-645-456A-9
23	199.5	7.0	1332	4	US-09-425-324A-9
24	199.5	7.0	1332	4	US-09-645-791-9
25	198.5	7.0	1231	4	US-08-714-741-41
26	197	6.9	1360	3	US-09-393-569-2
27	197	6.9	1360	4	US-09-579-664B-14

Sequence 34, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 5095, Ap

ALIGNMENTS

RESULT 1
US-08-630-915A-22
; Sequence 22, Application US/08630915A
; Patent No. 5409820

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 FENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STANDARDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-22

Query Match 28.6%; Score 816.5; DB 4; Length 434;
Best Local Similarity 45.1%; Pred. No. 3.3e-47;
Matches 193; Conservative 47; Mismatches 105; Indels 83; Gaps 11;

QY 1 MAE-GRAGGAGLFAKQVOKKSRRAQKVLQKLGKAVETKDRFRPSQASNFYQQAECHK 59
Db 1 MAEMGSGVITAGIASNVOKLTRAQKVLQKLGKADETKDRFQECQVQNFNKLQTEGR 60
QY 60 LYKDLNFKLSAVKVMHSSKRVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEELAD 119
Db 61 LOKDLRYLASVAMHSAKSLSECLQEVYEPENFGDEANKIAENNDLLWMDYHQKLV 120
QY 120 QAVRTMEIYVAQSEIKERIAKGRKLVYDSARHLEAVQNA-KQBAKTAKABEENK 178
Db 121 QALLTMDTYLQGPFDIKSRITAKGRKLVYDSARHLYESLQAKKDEAKIAKABEELIK 180
QY 179 AQTVFEDLNLEELPILVNSRIGCVYVTFONISNLRDVFVREMSKLNHNLXVWSKLE 238
Db 181 AQVFEMVNDLQBELPILVNSRVGFYVNTFQSIAGLEENFKENSKLNQNLNDVLSLE 240
QY 239 KQHSNKVYVYKGLSSSRRLSVLPPVTRATVSSPLTSPTSSTLSKSESESVSATEDL 298
Db 241 KQHSNTFTVKAQPSD-----NAPEKGNKSPSP----- 268
QY 299 APDAAQEDNSSEIKELLEEEIEKEGSEASSSE---EDDPLACNGPAQAQPSPTTERAK 355
Db 269 PPD-----GSPATPEIRVNHPEFA-----SGASPGATIPKSP 302
QY 356 SQEVLPSSTPSPGGALSPGQSSSATE-----VVLRTRTAS-----EGSEQPKKQAS 405
Db 303 SQ-----PAEASEVVGGAQEPGETAASEATSSSLPAVVVETFSATVNGAVEGS-----AG 352
QY 406 IQRTSAPP 413
Db 353 TGRDLPLP 360

RESULT 2

US-08-972A-4
; Sequence 4, Application US/08652972A
; Patent No. 5723581
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; APPLICANT: Sakamuro, Daitoku
; TITLE OF INVENTION: Murine and Human Box-Dependent
; TITLE OF INVENTION: MYC-Interacting Protein (Bin1) and Uses Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,972A
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,454
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60BUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-972A-4

Query Match 27.8%; Score 793.5; DB 1; Length 451;
Best Local Similarity 36.6%; Pred. No. 1.2e-45;
Matches 193; Conservative 66; Mismatches 152; Indels 117; Gaps 11;
QY 10 AGLFAKQVOKKSRRAQKVLQKLGKAVETKDRFRPSQASNFYQQAECHKLYKDLNFKLS 69
Db 8 AKIASNVOKLTRAQKVLQKLGKADETKDRFQECQVQNFNKLQTEGRLOKDLRYLAS 67
QY 70 AVKWHSSKRVSETLQEIYSSSEWDGHEELKAIWVNDLLWEDYEELADQAVRTMEIYV 129
Db 68 SYKAMHSAKSLSECLQEVYEPENFGDEANKIAENNDLLWMDYHQKLVQALLTMDTYL 127
QY 130 AQSIEIKERIAKGRKLVYDSARHLEAVQNA-KQBAKTAKABEENKIAQTVFEDLNQ 188
Db 128 GQFPDIKSRITAKGRKLVYDSARHLYESLQAKKDEAKIAKABEELIKIAQKVFEEMNV 187
QY 189 ELLEELPILVNSRIGCVYVTFONISNLRDVFVREMSKLNHNLXVWSKLEKQHSNKVYV 248
Db 188 DQBELPILVNSRVGFYVNTFQSIAGLEENFKENSKLNQNLNDVLYGLEKQHSNTFTV 247
QY 249 KGLSSSRRLSVLPPVTRATVSSPLTSPTSSTLSKSESESVSATEDLAPDAAQEDN 308
Db 248 K-----AOPRKSILFSLRRKNSDNAPAKGNKSP----- 278
QY 309 SEIKELLEEEIEKEGSEASSSEEDDPLACNGPAQAQPSPTTERAKSQEVLPSSTPS 368
Db 279 -----SPDGSPPATPEIRVNH-----PE 298
QY 369 PGGALSPGQSSSATEVVLRTRTASGSEQPKKQASIQRTSAPPSPRPPPRATASPRPS 428
Db 299 PAGGATPGA-----TLPKSPSPAEASEVAGGTQPAAGAQEPGETAASEAA 344
QY 429 SGNIPS-----SPTASGGSPSPRASLTGT-----TASPRTSLEVSPN 467
Db 345 SSSLPAVVVETFPATVNGTVEGSG--AGRLDLPGRFMFKVQAQHDYATDTDLQKAG 402
QY 468 PEPPEKPVRTPEAKE-----NENIHQNPE-ELCTS--PTLMTSQV 505
Db 403 DIVLVITPQNPBEQDEGLMGVYKESDWNQHKLEKCRGVFFENTERV 450

RESULT 3

US-08-870-126-4
; Sequence 4, Application US/08870126
; Patent No. 6048702
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; APPLICANT: Sakamuro, Daitoku
; TITLE OF INVENTION: Murine and Human Box-Dependent
; TITLE OF INVENTION: MYC-Interacting Protein (Bin1) and Uses Therefor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,126
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/435,454
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,972
; FILING DATE: 24-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST60CUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-870-126-4

Query Match 27.8%; Score 793.5; DB 3; Length 451;
Best Local Similarity 36.6%; Pred. No. 1.2e-45;
Matches 193; Conservative 66; Mismatches 152; Indels 117; Gaps 11;

QY 10 AGLFAQVQKFSRAQKVLQKLGAVETKDERFEQSASNFYQQAGHKLKYLKLNFLS 69
DB 8 AGKIASNVQKLTQAEKVLQKLGKRADETKDEQEQCVQNFKNQLTGTLQKDLRYLA 67
QY 70 AVKWHESKRVSETLOEYISYSEWDGHEELKAIYVNNDLWEDYEELKADQAVRTMEIYV 129
DB 68 SVKAMEASKKLNECLQEVPEDPWGRDEANKIAENNDLLWMDYHOKLVQALLTMDTYL 127
QY 130 AQSFIKRIAKRGKLVYDSARHHLBAVQNA-KDEAKTAKAESEFNKAQTVFEDLNQ 188
DB 128 GQFPDIKSRIAKRGKLVYDSARHHLBAVQNA-KDEAKTAKAESEFNKAQTVFEDLNQ 187
QY 189 ELLELPILYNSRIGCYVTFQNIENLSDVFRMSKLNHLYVMSKLEKQHSNKVYV 248
DB 188 DLQELPLSNRIGCYVTFQNIENLSDVFRMSKLNHLYVMSKLEKQHSNKVYV 247
QY 249 KGLSSSRSLVISPPVTRATVSSPLTSPTSLKSESESVATEDLAPDAAGEDN 308
DB 248 K-----AQRKSKLFSRLRRKNSDNAPAKGNKSP-----278
QY 309 SEIKELLEEEIEKEGSEASSEEDDPLPACNGPAQAQPSPTTTERAKSQEVLPSSTPS 368
DB 279 -----SPPDGSFAATPEIRVNHE-----PE 298
QY 369 PGGALSPSQPSSATEVVLRTTASGEQPKKRASTQRTSAPSRPPPPRATASPRPS 428
DB 299 PAGGATPGA-----TLPKSPQPAEASEVAGGTQPAAGAQEFGETAASEAA 344
QY 429 SGNIPS-----SPTASGGGSPTSFASLTGT-----TASPRTSLEVSPN 467
DB 345 SSSLPAVVVETPPATVNGTVEGGSG--AGRLDLPFGFMFKVQAQHDYATATDDELQKAG 402
QY 468 PEPPEKPVRTPEAKE-----NENIHQNPE-ELCTS--PTLMTSOV 505
DB 403 DVVLVIFPNQPEQDEGLMGVKESDWNQHKLEKRCGVFPENFTERV 450

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RESULT 4
US-09-445-247-4
; Sequence 4, Application US/09445247
; Patent No. 6410238
; GENERAL INFORMATION:
; APPLICANT: Wistar Institute of Anatomy & Biology
; Prendergast, George C.
; Sakamuro, Daitoku
; TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESS: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/445,247
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/870,126
; FILING DATE: 06-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60DPCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-09-445-247-4

Query Match 27.8%; Score 793.5; DB 4; Length 451;
Best Local Similarity 36.6%; Pred. No. 1.2e-45;
Matches 193; Conservative 66; Mismatches 152; Indels 117; Gaps 11;

QY 10 AGLFAQVQKFSRAQKVLQKLGAVETKDERFEQSASNFYQQAGHKLKYLKLNFLS 69
DB 8 AGKIASNVQKLTQAEKVLQKLGKRADETKDEQEQCVQNFKNQLTGTLQKDLRYLA 67
QY 70 AVKWHESKRVSETLOEYISYSEWDGHEELKAIYVNNDLWEDYEELKADQAVRTMEIYV 129
DB 68 SVKAMEASKKLNECLQEVPEDPWGRDEANKIAENNDLLWMDYHOKLVQALLTMDTYL 127
QY 130 AQSFIKRIAKRGKLVYDSARHHLBAVQNA-KDEAKTAKAESEFNKAQTVFEDLNQ 188
DB 128 GQFPDIKSRIAKRGKLVYDSARHHLBAVQNA-KDEAKTAKAESEFNKAQTVFEDLNQ 187
QY 189 ELLELPILYNSRIGCYVTFQNIENLSDVFRMSKLNHLYVMSKLEKQHSNKVYV 248
DB 188 DLQELPLSNRIGCYVTFQNIENLSDVFRMSKLNHLYVMSKLEKQHSNKVYV 247
QY 249 KGLSSSRSLVISPPVTRATVSSPLTSPTSLKSESESVATEDLAPDAAGEDN 308
DB 248 K-----AQRKSKLFSRLRRKNSDNAPAKGNKSP-----278
QY 309 SEIKELLEEEIEKEGSEASSEEDDPLPACNGPAQAQPSPTTTERAKSQEVLPSSTPS 368
DB 279 -----SPPDGSFAATPEIRVNHE-----PE 298
QY 369 PGGALSPSQPSSATEVVLRTTASGEQPKKRASTQRTSAPSRPPPPRATASPRPS 428
DB 299 PAGGATPGA-----TLPKSPQPAEASEVAGGTQPAAGAQEFGETAASEAA 344
QY 429 SGNIPS-----SPTASGGGSPTSFASLTGT-----TASPRTSLEVSPN 467
DB 345 SSSLPAVVVETPPATVNGTVEGGSG--AGRLDLPFGFMFKVQAQHDYATATDDELQKAG 402
QY 468 PEPPEKPVRTPEAKE-----NENIHQNPE-ELCTS--PTLMTSOV 505
DB 403 DVVLVIFPNQPEQDEGLMGVKESDWNQHKLEKRCGVFPENFTERV 450

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Db 326 TOPAAGAQEPGETSASEAASSSLPAVVVTFPATVNCVTEGG-----SGAGRLDLP 377

RESULT 5

US-08-435-454-4
; Sequence 4, Application US/08435454
; Patent No. 5605830
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; APPLICANT: Sakamuro, Daitoku
; TITLE OF INVENTION: Murine and Human C-Myc Interacting
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,454
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-435-454-4

Query Match 27.7%; Score 792; DB 1; Length 451;

Best Local Similarity 44.0%; Pred. No. 1.5e-45;
Matches 184; Conservative 53; Mismatches 119; Indels 62; Gaps 9;

Qy	10	AGLFAKQVQKFSRAQEKVLQKLGKAVETKDERFEQSASFYQQAEGHKLKDLNPLS	69
Db	8	AGKIASNVQKLTFAQEKVLQKLGKADETKDEQFQCVQNFNQLTEGTLQKDLRTYLA	67
Qy	70	AVKMHSSKRVSETLQEIYSEWDGHEELKAIWNNDLLWEDYEKLADQAVRTMETIY	129
Db	68	SVKAMHEASKKLNCEIQEYEPDPWGRDBANKIAENNDLLMDYHQKLVQDALLTMDTYL	127
Qy	130	AQFSEIKERIAKGRKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKAQTVFEDLNQ	188
Db	128	GQPDIKSRIAKGRKLVYDSARHYESLQAKKDKAKIAKEELIKAKQVFEEVNV	187
Qy	189	ELLEELPILYNSRIGCVTIFQNISLRDVFREMSKLNHNLVYFMSKLEKQHSNKVYV	248
Db	188	DLOEELPSLWNSRVGFYVNTFQSIAGLEENFHKMSKLNQNLNDVLVGLKQKHSNTFTV	247
Qy	249	KGLSSSSRSRLVISPVRTATVSPVTSPTSLSKSESSESVATEDLAPDAAQGEDN	308
Db	248	K-----AQPKKSKLFSRLRRKKNSDNAPAKGNKSPS-----	279
Qy	309	SEIKELLEEEIEKEGSEASSSE---EDDPLPACNG-PAQAQPSPTTTERAKSQEVLPS	364
Db	280	-----PPDGSFAATPEIRVNHPEPAGGATPGATLPKSPSPAEASE--VAGG	325
Qy	365	TTSPG---GALSPSQSSSSATEVVLRTTAS-----EGSEQPKKGIORTSAPP	413

RESULT 6

US-08-919-145-6
; Sequence 6, Application US/08919145
; Patent No. 5958753
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; TITLE OF INVENTION: Bau, A Binl Interacting Protein, and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,145
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,482
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST73AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-919-145-6

Query Match 27.7%; Score 792; DB 2; Length 451;

Best Local Similarity 44.0%; Pred. No. 1.5e-45;
Matches 184; Conservative 53; Mismatches 119; Indels 62; Gaps 9;

Qy	10	AGLFAKQVQKFSRAQEKVLQKLGKAVETKDERFEQSASFYQQAEGHKLKDLNPLS	69
Db	8	AGKIASNVQKLTFAQEKVLQKLGKADETKDEQFQCVQNFNQLTEGTLQKDLRTYLA	67
Qy	70	AVKMHSSKRVSETLQEIYSEWDGHEELKAIWNNDLLWEDYEKLADQAVRTMETIY	129
Db	68	SVKAMHEASKKLNCEIQEYEPDPWGRDBANKIAENNDLLMDYHQKLVQDALLTMDTYL	127
Qy	130	AQFSEIKERIAKGRKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKAQTVFEDLNQ	188
Db	128	GQPDIKSRIAKGRKLVYDSARHYESLQAKKDKAKIAKEELIKAKQVFEEVNV	187
Qy	189	ELLEELPILYNSRIGCVTIFQNISLRDVFREMSKLNHNLVYFMSKLEKQHSNKVYV	248
Db	188	DLOEELPSLWNSRVGFYVNTFQSIAGLEENFHKMSKLNQNLNDVLVGLKQKHSNTFTV	247
Qy	249	KGLSSSSRSRLVISPVRTATVSPVTSPTSLSKSESSESVATEDLAPDAAQGEDN	308
Db	248	K-----AQPKKSKLFSRLRRKKNSDNAPAKGNKSPS-----	279
Qy	309	SEIKELLEEEIEKEGSEASSSE---EDDPLPACNG-PAQAQPSPTTTERAKSQEVLPS	364
Db	280	-----PPDGSFAATPEIRVNHPEPAGGATPGATLPKSPSPAEASE--VAGG	325

QY 365 TTPSPG-----GALSPGQPSSTATEVWLRTTAS-----EGSEOPKKRASIQRTSAPP 413
DB 326 TOPAAGAQEPGTSASBAASSLPAVVVETTPATVNGTVEGG-----SGAGRLDLP 377
RESULT 7
US-09-344-889-6
; Sequence 6, Application US/09344889
; Patent No. 6140465
; GENERAL INFORMATION:
; APPLICANT: Prendergast, George C.
; TITLE OF INVENTION: Bau, A Binl Interacting Protein, and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,145
; FILING DATE:
; APPLICATION NUMBER: US 60/025,482
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST73AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-344-889-6
Query Match 27.7%; Score 792; DB 3; Length 451;
Best Local Similarity 44.0%; Pred. No. 1.5e-45;
Matches 184; Conservative 53; Mismatches 119; Indels 62; Gaps 9;
QY 10 AGLFAKQVKFSRAQEKVLQKLGKAVETKDERFQSSNFYQQAEGHKLKDKNPLS 69
DB 8 AGKIASNVQKLTQAEKVLQKLGKAVETKDERFQCVQNFQKLTGTRQLDKLRTYLA 67
QY 70 AVKVMHSSKRVSTLQETIYSSEWDGHEELKAIWNNDDLWEDYEELADQAVRTMEIYV 129
DB 68 SVKAMEASKCLNECLQEVTEPDWPGDEANKIAENNDLLWMDYHOKLVDQALLTMDTYL 127
QY 130 AQPSEIKERIAKGRKLVDDYSARHHLAVQNA-KKDEAKTAAEEFENKCAQVFEEDLNQ 188
DB 128 GQFPDIKSIARIGRKLVDYDSARHHLAVQNA-KKDEAKTAAEEFENKCAQVFEEMNV 187
QY 189 ELLEELPILYNSRICGVYTFQINSLRDVYFREMSKLNHLNLYEVMSKLEKQHSNKVFVY 248
DB 188 DLQELPLSNRSGVGYNTFQISAGLEENFHKMSKLNQNLNDVLVGLKQHSNTFTV 247
QY 249 KGLSSRSRLVISPPVTRATVSSPLTSPTSTSLKSESSESVSATEDLAPDAQGEDN 308

DB 248 K-----AQP RKSKLFSKRLRRKNSDNAPAKGNKSPS----- 279
QY 309 SEIKELLEEEIEKGESEASSE---EDDPLACNG-PAAQSPPTERRAKSOEEVLPS 364
DB 280 -----PPDGSFAATPEIRVNHPEPEAGGATFGATLPKSPSOPAEASE--VAGG 325
QY 365 TTPSPG-----GALSPGQPSSTATEVWLRTTAS-----EGSEOPKKRASIQRTSAPP 413
DB 326 TOPAAGAQEPGTSASBAASSLPAVVVETTPATVNGTVEGG-----SGAGRLDLP 377
RESULT 8
PCT-US96-06231A-4
; Sequence 4, Application PC/TUS9606231A
; GENERAL INFORMATION:
; APPLICANT: Wistar Institute of Anatomy & Biology
; TITLE OF INVENTION: Murine and Human Box-Dependent
; TITLE OF INVENTION: Myc-Interacting Protein (BIN1) and Uses Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06231A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,454
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60APCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-06231A-4
Query Match 27.7%; Score 792; DB 5; Length 451;
Best Local Similarity 44.0%; Pred. No. 1.5e-45;
Matches 184; Conservative 53; Mismatches 119; Indels 62; Gaps 9;
QY 10 AGLFAKQVKFSRAQEKVLQKLGKAVETKDERFQSSNFYQQAEGHKLKDKNPLS 69
DB 8 AGKIASNVQKLTQAEKVLQKLGKAVETKDERFQCVQNFQKLTGTRQLDKLRTYLA 67
QY 70 AVKVMHSSKRVSTLQETIYSSEWDGHEELKAIWNNDDLWEDYEELADQAVRTMEIYV 129
DB 68 SVKAMEASKCLNECLQEVTEPDWPGDEANKIAENNDLLWMDYHOKLVDQALLTMDTYL 127
QY 130 AQPSEIKERIAKGRKLVDDYSARHHLAVQNA-KKDEAKTAAEEFENKCAQVFEEDLNQ 188
DB 128 GQFPDIKSIARIGRKLVDYDSARHHLAVQNA-KKDEAKTAAEEFENKCAQVFEEMNV 187
QY 189 ELLEELPILYNSRICGVYTFQINSLRDVYFREMSKLNHLNLYEVMSKLEKQHSNKVFVY 248
DB 188 DLQELPLSNRSGVGYNTFQISAGLEENFHKMSKLNQNLNDVLVGLKQHSNTFTV 247

QY 249 KGLSSSSRRSLVSPVTRATVTSPTSLKSESESVSATEDLAPDAAGEDN 308
 Db 248 K-----AQRKSKLFSRLRRKNSDNAPAKGNKSPS----- 279
 QY 309 SEIKELLEEEIEKESSESSSE---EDDPLACNG-PAQAQPSPTTTERAKSQEVLPS 364
 Db 280 -----PPDGSPPATPEIRVNHPEPEFAGATGATLPKSPQPAEASE--VAGG 325
 QY 365 TTPSPG---GALSPGQSSSATEVLRTRTAS-----EGSEQPKKASTORTSAPP 413
 Db 326 TQPAAGAQPGETSASEAASSLPAVVVETPPATVNGTVEGG-----SGAGRLDLP 377

RESULT 9

US-08-630-915A-24
 ; Sequence 24, Application US/08630915A
 ; Patent No. 6309820
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: HOFFMAN, No. 6309820h
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: FOWLES, Dana M.
 ; APPLICANT: McCONNELL, Stephen J.
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
 ; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
 ; TITLE OF INVENTION: USING SAME
 ; NUMBER OF SEQUENCES: 227
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/630,915A
 ; FILING DATE: 03-APR-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 1101-174
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 404 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-630-915A-24

Query Match 23.6%; Score 675; DB 4; Length 404;
 Best Local Similarity 34.1%; Pred. No. 9.9e-38;
 Matches 169; Conservative 62; Mismatches 133; Indels 132; Gaps 12;

QY 42 RFEQSNFYQQQAEGHKLKDLNFKLSAVKVMHSSKRVSETLQEIYSSSEWDGHEELKA 101
 Db 8 RFEQCVQNFNKLTEGTRLQDLRTLYASVKAHEASKKLNELQSVYEPDPGRDEANK 67
 QY 102 IVWNDDLLWEDYEKLDAQVTRWEIYVAQFSIKERIAKRGKLVYDSARHLEAVQN 161
 Db 68 IAEENNLLWMDYHOKLVQDQALLTMDTYLGQFPDIKSIKRGKLVYDSARHYESLQT 127
 QY 162 A-KXDEAKTAKAEEFNKAQTVEFDLNQELLELPILYNSRIGCYVTIFQNSLNRDVFY 220

Db 128 AKKQDEAKIAKABEELIKAKQVFEEVMVDLQEBLPSLWNSRVGFYVNTFQSIAGLEENFH 187
 QY 221 REMSKLNENLYEVMKLEKOHSNKVFVVKGLSSSSRRSLVSPVTRATVTSPTSLKSESESV 280
 Db 188 KEMSKLNQNTDNLVGLKQHGNSITVK----- 216
 QY 281 STLKSESESVSATEDLAPDAQEDNSBIKELLEEBEIEKEGSEASSEEDDPLPACN 340
 Db 217 -----AQSNDNAPAK-----GNKSPS----- 232
 QY 341 GPAQAQPSPTTTERAKSQEVLPSSTTPSPGGALSPGQSSSATEVLRTRTASEGSEOP 400
 Db 233 -PPDGSPPATPEIRVNH-----PEPAGATPGA-----TLPKSPSQP 269
 QY 401 KRASIORTSAPPRPPPPPRATASPRSSGNIPS-----SPTASGGSGSPTSPRAS 450
 Db 270 AEASEVAGTQPAAGAQEPGETAASEAASSSLPAVVVETPPATVNGTVEGGSG--AGRLD 327
 QY 451 LGTG-----TASPRISLEVPNPPPEPKPVETPEAKE-----NENIHQNPE 492
 Db 328 LPPGFMFVKVQAQHDYATDTDELQLKAGDVVLVIPPONPEEQBEGMLMGVKSQDWNQHK 387
 QY 493 -ELCTS--PTLMTISQV 505
 Db 388 LEKCRGVFPENFTERV 403

RESULT 10

US-09-976-594-615
 ; Sequence 615, Application US/09976594
 ; Patent No. 6673549
 ; GENERAL INFORMATION:
 ; APPLICANT: Furness, Michael
 ; APPLICANT: Buchbinder, Jenny
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 ; FILE REFERENCE: PA-0041 US
 ; CURRENT APPLICATION NUMBER: US/09/976,594
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,409
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 1143
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 615
 ; LENGTH: 904
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 2789525CD1
 ; US-09-976-594-615

Query Match 8.5%; Score 243; DB 4; Length 904;
 Best Local Similarity 23.4%; Pred. No. 3.4e-08;
 Matches 142; Conservative 90; Mismatches 224; Indels 152; Gaps 28;

QY 6 AGGAAGLFAKQVKKPSRAQKVLQKLGKAVETKDERPEQASNFYQQQAEGHKLKDLK 65
 Db 3 AGFFRGTSAEQ--DNEFSNKKQKLLKQL--KFAECLEKKYDMSKVN----- 44
 QY 66 NELSVMKVMHSSKRVSETLQEIYSSSEWDGHEELKAIWNNDLLWEDYEKLDAQVTRM 125
 Db 45 --LEVIKFW--ITKVVITIL-----GFEDDVI-----EFIFNQLVKNPDS--KMM 85
 QY 126 EYVAQFSIKERIAKRGKLVYDSARHLEAVQNA-----KKDEAKTAKAEEFNKAQT 181
 Db 86 QINLTGFLNGKNAREFMGLWPLLLSAQENIAGISAPLELKKEEIKQRQIEQ--KLASM 144
 QY 182 VFEDLNQELLELPILYNSRIGCYVTIFQNSLNRDVFYREMSKLNENLYEVMKLEKQH 241
 Db 145 KKODEDKD-----KRDKEKESR-----EKRRSR 170
 QY 242 SNKVFVVKGLSSSSRRSLVSPVTRATVTSPTSLKSESESVSATEDLAPD 301

Db 171 SPR--RRKSRSPRR--SSPVRRERKSHRSRPH-----RTKSRSP--AP- 214
 QY 302 AAGGDNSEIKELLEEEIEKEGS--EASSSE-----DPLPACNGPAQAQSPPTT 353
 Db 215 ----EKKEKTELPFESVVKPEPSVOEATSTSDILKVPKPFIEP--PKPEPSKNSKK 267
 QY 354 AKSQEVLPSSTTPSGGALSPGSPSSGATVWLRTTASGSEQ---PKKRASIORTS 410
 Db 268 EKEKTRPRSRSRKSRSTRSPSHTRPRRRHRSRSRVSPPRRSPRRSPRRRT 327
 QY 411 APPSRPPPRATASRP-----SSGNTPSSATSGGSPSPRASLTGTAS--PRISLE 463
 Db 328 PPRMPPPPRHRRSRSPVRRRRSRASLSGSSSSSRSPKPPKRTTSSPPKTRR 387
 QY 464 VSNPPPEPK-----PVRTPAEKENENHNQNPPE-----LCTSTPLMTSOVASEPG 510
 Db 388 LPSASPPRRRRHPSPAPPPKTR--HSPTFQSNTRKSRVSVSPGRTSGKVTXKG 444
 QY 511 EAK-----RNE-----DKONKLISADSGDQQLQVSMVPPENNLTAPPEQEE 555
 Db 445 TEKRESPPAPKPKRVKVELSEBEDXGKMAAADSVQORQYR----RQOQSSSDSGSS 500
 QY 556 VSTSENPO 563
 Db 501 SSEDERP 508

RESULT 11
 US-09-645-456A-13
 ; Sequence 13, Application US/09645456A
 ; Patent No. 6562580
 ; GENERAL INFORMATION:
 ; APPLICANT: FU, C. Alan
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND
 ; FILE REFERENCE: A-68344/RMS/DHR
 ; CURRENT APPLICATION NUMBER: US/09/645,456A
 ; CURRENT FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US/09/425,324
 ; PRIOR FILING DATE: 1999-10-21
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 1324
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic
 US-09-645-456A-13

Query Match 7.3%; Score 207.5; DB 4; Length 1324;
 Best Local Similarity 18.9%; Pred. No. 1.4e-05;
 Matches 113; Conservative 114; Mismatches 257; Indels 115; Gaps 21;
 QY 15 KQVQKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQQAEHGK-----LYK 62
 Db 296 QVRIQLKDHIDRTKKRGEKDETE---YEYSGSEEEENDSGEPSSILNLPGETLRR 352
 QY 63 DLKNFLSAVKVNHSSKRVSETLQEIYSEWDGHEELKAIWNNDLLWEDYEE---KLAD 119
 Db 353 DFLRLQANKERSEALR-----QOLEQQORENEEHKQLLAERQKRIEEOQRRLLEE 407
 QY 120 QAVRTMEIYVAQFSEIKERIAKRGKLVYDSARHLEAVQNAKKBATAKAEFEFNKA 179
 Db 408 QORREKELKQOERQRRHVEEQWRREERRAEHQEYKQLEBEQOERLQRLQOE 467
 QY 180 QTVFDLNLQELLEPLI-----LYNSRIGCVTITFQINSLNLDVYREMSKLN----- 227
 Db 468 RDYLSLQHORQOERQVPEKPLHYKEG--MSPSEKPAWAKEV--EERSRLNRQSSPAMP 523
 QY 120 QAVRTMEIYVAQFSEIKERIAKRGKLVYDSARHLEAVQNAKKBATAKAEFEFNKA 179
 Db 408 QORREKELKQOERQRRHVEEQWRREERRAEHQEYKQLEBEQOERLQRLQOE 467
 QY 180 QTVFDLNLQELLEPLI-----LYNSRIGCVTITFQINSLNLDVYREMSKLN----- 227
 Db 468 RDYLSLQHORQOERQVPEKPLHYKEG--MSPSEKPAWAKEV--EERSRLNRQSSPAMP 523
 QY 228 HNLVEVMSKLEKQHNKVFVVKGLSSSRSLVSPVTRATVSPLTSPSTSLSKS 287

Db 524 HKVANRISDPNLPFRSEFSISGVQ-----PARTPPMLRPV-DQIPLHLVAVKS 571
 QY 288 EESVSATEDLADAAQGEDNSNSEIKELLEEEIEKEGSEASSSEEDDPLFA-----CN 340
 Db 572 QCPALTASQSVHEQPTKLGSGFQALNVTSHRVEMPRQNSDPTSENPLTRIEKDRSS 631
 QY 341 GPAQAQ--PSPPTTERAKSQEVLPSSTTPSGGALSP--SQPSSSATEVVLTRTASEG 396
 Db 632 WLQOEDIPPKVPQRTTTSIPALARKNSPGNSALGPLGSGQPIRASNPDLRRT----- 685
 QY 397 SQOPKKRASIORTSAPPSPPPPRATASPRPSSSGNIPSS--PTASGGGSPSPRASLTGT 455
 Db 686 --EPILSPFORTSSGSS-----SSSTFSSQSPSGGSGQSPGQAGS----- 725
 QY 456 ASPTSLVSP-----NPEPPEKPVRTPEAKENENHNQNPPEL-----CTS 497
 Db 726 -BSTRVRANSKSGSPVLPEPAKVPESRDTTPSRPADLTALAKELRELRIETNR 784
 QY 498 PLMTSQVASPEGAKEKMEKKNKLISADSGDQ--QLQVSMVPPENNLTAPPEQEE 555
 Db 785 PMKVTDYSSSESESESESEEDGE-----SETHDGTVAUSDIPRLIPTGAPGSE 837

RESULT 12
 US-09-425-324A-13
 ; Sequence 13, Application US/09425324A
 ; Patent No. 6562591
 ; GENERAL INFORMATION:
 ; APPLICANT: FU, C. Alan
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND
 ; FILE REFERENCE: A-68344/RMS/DHR
 ; CURRENT APPLICATION NUMBER: US/09/425,324A
 ; CURRENT FILING DATE: 1999-10-21
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 1324
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic
 US-09-425-324A-13

Query Match 7.3%; Score 207.5; DB 4; Length 1324;
 Best Local Similarity 18.9%; Pred. No. 1.4e-05;
 Matches 113; Conservative 114; Mismatches 257; Indels 115; Gaps 21;
 QY 15 KQVQKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQQAEHGK-----LYK 62
 Db 296 QVRIQLKDHIDRTKKRGEKDETE---YEYSGSEEEENDSGEPSSILNLPGETLRR 352
 QY 63 DLKNFLSAVKVNHSSKRVSETLQEIYSEWDGHEELKAIWNNDLLWEDYEE---KLAD 119
 Db 353 DFLRLQANKERSEALR-----QOLEQQORENEEHKQLLAERQKRIEEOQRRLLEE 407
 QY 120 QAVRTMEIYVAQFSEIKERIAKRGKLVYDSARHLEAVQNAKKBATAKAEFEFNKA 179
 Db 408 QORREKELKQOERQRRHVEEQWRREERRAEHQEYKQLEBEQOERLQRLQOE 467
 QY 180 QTVFDLNLQELLEPLI-----LYNSRIGCVTITFQINSLNLDVYREMSKLN----- 227
 Db 468 RDYLSLQHORQOERQVPEKPLHYKEG--MSPSEKPAWAKEV--EERSRLNRQSSPAMP 523
 QY 228 HNLVEVMSKLEKQHNKVFVVKGLSSSRSLVSPVTRATVSPLTSPSTSLSKS 287
 Db 524 HKVANRISDPNLPFRSEFSISGVQ-----PARTPPMLRPV-DQIPLHLVAVKS 571
 QY 288 EESVSATEDLADAAQGEDNSNSEIKELLEEEIEKEGSEASSSEEDDPLFA-----CN 340
 Db 572 QCPALTASQSVHEQPTKLGSGFQALNVTSHRVEMPRQNSDPTSENPLTRIEKDRSS 631
 QY 341 GPAQAQ--PSPPTTERAKSQEVLPSSTTPSGGALSP--SQPSSSATEVVLTRTASEG 396

Db 632 WLRQEDIPPKVQRTTISIPALARKNSPGNSALGRLGSPQIRASNDLRT----- 685
 QY 397 SEQPKKASRTASTAPPPPPRATASPPSSGNIPSS-PTASGGGSPTSRASLTGT 455
 Db 686 --EPILSPLORTSSGSS-----SSSTPSSQPSQSGSQSGS----- 725
 QY 456 ASPRTSLVSP---NPEPPKPVRTPEAKENIHQNPPEL-----CTS 497
 Db 726 -SERTRVANSKSEGSPVLPHEPAKVPKPEESRDITRSPADLTALAKELRELRIETNR 784
 QY 498 PTLMTSQVASEPGEAKMEDKEKONKLISADSSEGD-QLOVSMVPPNNLTAPEPQE 555
 Db 785 PMKVTDYSSSESESESESEDEGE-----SETHDGTVAVSDIPRLIPTGAPGSNEQ 937

RESULT 13

US-09-645-791-13
 ; Sequence 13, Application US/09645791
 ; Patent No. 6569658
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Ying
 ; APPLICANT: Fu, Alan C
 ; APPLICANT: Shen, May
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AN
 ; TITLE OF INVENTION: METHODS OF USE
 ; FILE REFERENCE: A-68344-1/RMS/DHR
 ; CURRENT FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 09/645,791
 ; PRIOR FILING DATE: 1999-10-21
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 1324
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic
 US-09-645-791-13

Query Match 7.3%; Score 207.5; DB 4; Length 1324;
 Best Local Similarity 18.9%; Pred. No. 1.4e-05;
 Matches 113; Conservative 114; Mismatches 257; Indels 115; Gaps 21;
 QY 15 KQVQKFSRAQEKVLQKLGKAVETKDERPEQASNFYQQAGHK-----LYK 62
 Db 296 RQVRIQLKDHIDRTKKRGKEDETE---YEYSGSEEEENDSGSPSSILNLPGESTLRR 352
 QY 63 DLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWNNDLLEDYEE---KLAD 119
 Db 353 DFLRLQANKERSEALR-----QQLQQQRENEEHKQLLAERQKRIEEOQRRLEE 407
 QY 120 QAVTMEIYVAQSEIKERIAKGRKLVYDSARHLEAVONAKKDEAKTAKAEFEFKA 179
 Db 408 QQRREKLRKQERQERHYEEQRRREERRAEHQYKRLQEBQROAERLQRLQKE 467
 QY 180 QTVFEDLNQELLEPLT---LYNSRIGCVTTFONISNLRDVFYREMSKLN----- 227
 Db 468 RYLVLSLQHQEQRPVEKPLHYKEG--MSPSEKPAKAVE--EERSRLNRQSSPAMP 523
 QY 228 HNLVYVMSKLEKQHSNKFVVKVGLSSSSRSLSLVSPPVTRATVSSPLTSPSTLSLKS 287
 Db 524 HKVANRISDPNLPSSSFSISGVQ-----PARTPMLRDV-DPQIPHILVAVKS 571
 QY 288 ESESVSATDLAPDAAGEDNSEIKELLEBEETKEGSEASSEEDDLPLA-----CN 340
 Db 572 QGPALTASQSVHEOPTKGLSGFQALNVTSHRVEMPRQSDPTSENPPLTPIEKFDRSS 631
 QY 341 GPAQAQ--PSPPTTRAKSQBEVLPSSPTSPFGGALSP--SGQSSSATEVLRTRTASEG 396
 Db 632 WLRQEDIPPKVQRTTISIPALARKNSPGNSALGRLGSPQIRASNDLRT----- 685

QY 397 SEQPKKASRTASTAPPPPPRATASPPSSGNIPSS-PTASGGGSPTSRASLTGT 455
 Db 686 --EPILSPLORTSSGSS-----SSSTPSSQPSQSGSQSGS----- 725
 QY 456 ASPRTSLVSP---NPEPPKPVRTPEAKENIHQNPPEL-----CTS 497
 Db 726 -SERTRVANSKSEGSPVLPHEPAKVPKPEESRDITRSPADLTALAKELRELRIETNR 784
 QY 498 PTLMTSQVASEPGEAKMEDKEKONKLISADSSEGD-QLOVSMVPPNNLTAPEPQE 555
 Db 785 PMKVTDYSSSESESESESEDEGE-----SETHDGTVAVSDIPRLIPTGAPGSNEQ 837

RESULT 14

US-09-645-456A-11
 ; Sequence 11, Application US/09645456A
 ; Patent No. 6562580
 ; GENERAL INFORMATION:
 ; APPLICANT: Fu, C. Alan
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AN
 ; TITLE OF INVENTION: METHODS OF USE
 ; FILE REFERENCE: A-68344/RMS/DHR
 ; CURRENT FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US/09/645,456A
 ; PRIOR FILING DATE: 1999-10-21
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 1353
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic
 US-09-645-456A-11

Query Match 7.2%; Score 205; DB 4; Length 1353;
 Best Local Similarity 18.7%; Pred. No. 2.1e-05;
 Matches 119; Conservative 111; Mismatches 247; Indels 158; Gaps 23;
 QY 15 KQVQKFSRAQEKVLQKLGKAVETKDERPEQASNFYQQAGHK-----LYK 62
 Db 296 RQVRIQLKDHIDRTKKRGKEDETE---YEYSGSEEEENDSGSPSSILNLPGESTLRR 352
 QY 63 DLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWNNDLLEDYEEKLADQAV 122
 Db 353 DFLRLQANKERSEALR-----QQLQQQRENEEHKQLL-----AERQKRIEEOKE 400
 QY 123 RTMEIYVAQSEIKERIAKGRKLVYDSARHLEAVONAKKDEAKTAKAEFEF-----N 177
 Db 401 QRRRL-----EQQRREKLRKQERQRRHYEE--QMRREERRRAEHQYIRQLE 452
 QY 178 KAQTVFEDLNQELLEPLTLYNSRIGCVTTFONISNLRDV--FYREMSKLNHNLVYVMS 235
 Db 453 EBOQLEILQQLLHEQALLLEYK-----RKLEEQRAERLQRLQKRDYLVLSLQH 505
 QY 236 KLEQKH-----SNKFVVKVGLSSSSRSLSLVS----- 263
 Db 506 QRCEQRPVEKPKLYHYKEGMSSEKPAKAVEERSRLNRQSSPAMPKVNRISSDNLPL 565
 QY 264 -----PVRTATVSSPLTSPSTLSLKSSESVSATDLAPDAAGEDNSEI 311
 Db 566 PRSEFSISGVQPAKTPPMLREV-DPQIPHILVAVKSQPALTASQSVHEOPTKGLSGFQE 624
 QY 312 KELLEBEETKEGSEASSEEDDLPLA-----CNGPAQAQ--PSPPTTRAKSQBEVLP 362
 Db 625 ALNVTSHRVEMPRQSDPTSENPPLTPIEKFDRSSWLQEBEDIPPKVQRTTISIPALA 684
 QY 363 SSTTSPFGGALSP--SGQSSSATEVLRTRTASEGSEQPKKASRTASTAPPPPPR 420
 Db 685 RKNSPGNSALGRLGSPQIRASNDLRT-----EPILSPLORTSSGSS----- 730
 QY 421 ATASPPSSGNIPSS-PTASGGGSPTSRASLTGTASPTSLVSP-----NPPEPKPV 475

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:31:50 ; Search time 42.3548 Seconds
(without alignments)
86.723 Million cell updates/sec

Title: US-10-069-540A-2_COPY_23_35

Perfect score: 61

Sequence: 1 RAQEKVQLKGR 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

A_Geneseq_29Jan04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	108	5	Abb06161 Human NS
2	61	100.0	137	4	Abg21410 Novel hum
3	61	100.0	252	4	Abg62101 Bar domai
4	61	100.0	414	4	Abg13005 Novel hum
5	61	100.0	434	2	Aaw05391 Mouse SH3
6	61	100.0	451	2	Aaw06602 Human box
7	61	100.0	451	2	Aaw47295 Human Bin
8	61	100.0	451	2	Abg36881 Human Bin
9	61	100.0	451	2	Aaw94504 Human Bin
10	61	100.0	453	6	Abx69631 Human CGD
11	61	100.0	482	6	Abu89771 Protein d
12	61	100.0	564	4	Aab62100 Human bri
13	61	100.0	572	4	Abg21411 Novel hum
14	61	100.0	588	7	Adp45951 Rat Prote
15	61	100.0	588	7	Adg60848 Rat Prote
16	61	100.0	588	7	Adg60840 Rat Prote
17	61	100.0	588	7	Adg60844 Rat Prote
18	61	100.0	588	7	Adg60852 Rat Prote
19	61	100.0	593	7	Adg60842 Human Pro
20	61	100.0	593	7	Adp45953 Human Pro
21	61	100.0	593	7	Adg60850 Human Pro
22	61	100.0	593	7	Adg60846 Human Pro
23	61	100.0	593	7	Adg60854 Human Pro
24	61	100.0	594	4	Abg20887 Novel hum
25	61	100.0	594	4	Abg20324 Novel hum

26	61	100.0	683	7	ADD44887	Add44887 Rat Prote
27	61	100.0	695	5	AAE22091	Aae22091 Human amp
28	61	100.0	695	5	AAU75110	Aau75110 Synaptic
29	61	100.0	695	7	ADD44889	Add44889 Human Pro
30	51	83.6	594	4	ABG22457	Abg22457 Novel hum
31	47	77.0	602	4	ABB63948	Abb63948 Drosophil
32	41	67.2	373	4	AAU03699	Aau03699 Group B S
33	41	67.2	651	5	ABP30317	Abp30317 Streptoco
34	41	67.2	654	5	ABP29732	Abp29732 Streptoco
35	41	67.2	654	5	ABP26469	Abp26469 Streptoco
36	41	67.2	1381	4	ABE57920	Abbe57920 Drosophil
37	40	65.6	284	6	ADB07514	Adb07514 Alloiooco
38	40	65.6	297	6	ADB07516	Adb07516 Alloiooco
39	39	63.9	154	5	AAE15583	Aae15583 Mutated G
40	39	63.9	179	5	AAE15580	Aae15580 Mutated G
41	39	63.9	206	5	AAE15579	Aae15579 Mutated G
42	39	63.9	268	5	AAE15309	Aae15309 Glycine m
43	39	63.9	293	5	AAE15308	Aae15308 Glycine m
44	39	63.9	295	5	AAE15582	Aae15582 Alternati
45	39	63.9	506	3	AAE15620	Aae15620 Streptoco
46	39	63.9	510	4	AAU38014	Aau38014 Streptoco
47	39	63.9	510	4	AAU37881	Aau37881 Streptoco
48	39	63.9	510	6	ABU02157	Abu02157 S. pneumo
49	39	63.9	510	6	ABU46197	Abu46197 Protein e
50	38	62.3	80	4	AAU58951	Aau58951 Propionib
51	38	62.3	80	6	ABM55470	Abm55470 Propionib
52	38	62.3	101	4	AAE94218	Aae94218 Human pro
53	38	62.3	202	3	AAE75719	Aae75719 Neisseria
54	38	62.3	220	6	ABP78753	Abp78753 N. gonorr
55	38	62.3	243	6	ABP78416	Abp78416 N. gonorr
56	38	62.3	244	4	ABG16068	Abg16068 Novel hum
57	38	62.3	268	3	AAU44888	Aau44888 Human laf
58	38	62.3	331	3	AAU44887	Aau44887 Human laf
59	38	62.3	357	5	AAU47581	Aau47581 Drosophil
60	38	62.3	427	2	AAE68607	Aae68607 Dorsalin
61	38	62.3	464	6	ABU43827	Abu43827 Protein e
62	38	62.3	474	3	ABU44560	Abu44560 Virulence
63	38	62.3	474	5	ABP54512	Abp54512 Pasteurel
64	38	62.3	481	6	ABM65091	Abm65091 Phototrab
65	38	62.3	490	6	ADA32995	Ada32995 Acinetoba
66	38	62.3	509	4	ABE71278	Abb71278 Drosophil
67	38	62.3	552	4	ABG62176	Abg62176 Human p60
68	38	62.3	646	4	ABG24969	Abg24969 Novel hum
69	38	62.3	944	4	ABG28794	Abg28794 Novel hum
70	38	62.3	1338	4	ABG25447	Abg25447 Novel hum
71	37	60.7	33	4	ABE37738	Abb37738 Peptide #
72	37	60.7	209	2	AAU29510	Aau29510 Human lun
73	37	60.7	209	3	AAE44458	Aae44458 Human lun
74	37	60.7	209	4	AAE13799	Aae13799 Human lun
75	37	60.7	209	7	ADD66490	Ad66490 Human lun
76	37	60.7	209	7	ABE87744	Ab87744 Human lun
77	37	60.7	378	6	ABU45731	Abu45731 Protein e
78	37	60.7	446	6	ADA56740	Ada56740 Human sec
79	37	60.7	446	6	ADA40587	Ada40587 Human sec
80	37	60.7	446	7	ADB91457	Adb91457 Human sec
81	37	60.7	446	7	ADC74008	Adc74008 Human sec
82	37	60.7	447	2	AAW88693	Aaw88693 Secreted
83	37	60.7	447	4	ABE50460	Ab50460 Human sec
84	37	60.7	447	6	ABO44717	Ab044717 Novel hum
85	37	60.7	447	7	ABO26197	Ab026197 Human pro
86	37	60.7	451	2	AAW63687	Aaw63687 Membrane
87	37	60.7	461	3	AAE66724	Aae66724 Membrane
88	37	60.7	461	3	AAE57941	Aae57941 Human tra
89	37	60.7	461	3	AAE33468	Aae33468 Human PRO
90	37	60.7	461	4	AAE05573	Aae05573 Human PRO
91	37	60.7	461	4	AAE93271	Aae93271 Human PRO
92	37	60.7	461	4	AAE93593	Aae93593 Human PRO
93	37	60.7	461	4	AAU12398	Aau12398 Human PRO
94	37	60.7	461	4	AAU13931	Aau13931 Human PRO
95	37	60.7	461	4	AAE65247	Aae65247 Human PRO
96	37	60.7	461	5	ABB84897	Abb84897 Human PRO
97	37	60.7	461	5	ABE95503	Ab95503 Human ang
98	37	60.7	461	6	ABU58062	Abu58062 Human PRO

DE Novel human diagnostic protein #21401.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX

OS Homo sapiens.
 XX

XX WO200175067-A2.
 XX

XX 11-OCT-2001.
 XX

XX 30-MAR-2001; 2001WO-US008631.
 XX

XX 31-MAR-2000; 2000US-00540217.
 XX

XX 23-AUG-2000; 2000US-00649167.
 XX

XX (HYSE-) HYSEQ INC.
 XX

XX Dmanac RT, Liu C, Tang YT;
 XX

XX WPI; 2001-639362/73.
 XX

XX N-PSDB; AAS85597.
 XX

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX

XX Claim 20; SEQ ID NO 51769; 103pp; English.
 XX

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

XX Sequence 137 AA;
 XX

Query Match 100.0%; Score 61; DB 4; Length 137;
 Best Local Similarity 100.0%; Pred. No. 0.0077;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAQEKVQLKLGKA 13
 |||||
 Db 52 RAQEKVQLKLGKA 64

RESULT 3

ABG62101

ID AAB62101 standard; protein; 252 AA.

XX AAB62101;

XX 29-MAY-2001 (first entry)

XX Bar domain of Binl protein.

KW Bridging integrator-2 protein; Bin2; cancer; leukemia; blood disorder;
 KW hyperplastic disease; cytostatic; cell growth regulator; Binl;
 XX chromosome 4q22.1.

OS Homo sapiens.
 XX

XX WO200116158-A2.
 XX

XX 08-MAR-2001.
 XX

XX 30-AUG-2000; 2000WO-US023723.
 XX

XX 31-AUG-1999; 99US-0151554P.
 XX

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX

XX Prendergast GC, Ge K;
 XX

XX WPI; 2001-235087/24.
 XX

XX New bridging integrator-2 (Bin2) protein and nucleic acid molecules,
 PT useful for regulating cell growth, and for diagnosing or treating
 PT conditions associated with inappropriate expression of Bin2, e.g. cancers
 PT or hepatocarcinoma.
 XX

XX Example 3; Fig 2; 62pp; English.
 XX

XX The invention provides a human bridging integrator-2 (Bin2) protein. The
 CC protein can be expressed by standard recombinant methodology. The Bin2
 CC proteins or peptides are useful in regulating cell growth, cell survival,
 CC differentiation, endocytosis and actin organization. These peptides or
 CC proteins are also useful for diagnosing or treating conditions associated
 CC with inappropriate expression of Bin2, e.g. liver cancer, breast cancer,
 CC hepatocarcinoma, myeloid and lymphoid leukemias or blood disorders. The
 CC peptides, nucleic acid sequences or anti-Bin2 antibodies are useful for
 CC diagnosing inappropriate expression of Bin2. Bin2 is also useful for
 CC treating disorders associated with excessive Binl levels, e.g. liver,
 CC colorectal, prostate or breast cancers, epithelia cell cancers, melanoma,
 CC or hyperplastic disease states. The present sequence represents the Bar
 CC domain of Binl used in homology studies with Bin2 protein
 XX

XX Sequence 252 AA;
 XX

Query Match 100.0%; Score 61; DB 4; Length 252;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAQEKVQLKLGKA 13
 |||||
 Db 24 RAQEKVQLKLGKA 36

RESULT 4

ABG13005

ID ABG13005 standard; protein; 414 AA.

XX AC ABG13005;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #12996.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX

OS Homo sapiens.
 XX

XX WO200175067-A2.
 XX

XX 11-OCT-2001.
 XX

XX 30-MAR-2001; 2001WO-US008631.
 XX

PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 PA (HYSE-) HYSEQ INC.
 XX Dmanac RT, Liu C, Tang YT;
 XX N-PSDB; AAS77192.
 DR WPI; 2001-639362/73.
 XX N-PSDB; AAS77192.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 43364; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 414 AA;
 Query Match 100.0%; Score 61; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGA 13
 DB 23 RAQEKVLQKLGA 35
 RESULT 5
 AAW05391
 ID AAW05391 standard; protein; 434 AA.
 AC AAW05391;
 XX 18-FEB-1998 (first entry)
 DT Mouse SH3P9 protein.
 DE Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
 KW cellular signalling element; cellular structural element; malignancy;
 KW protein identification; functional domain; protein screening;
 KW cellular signal transduction process.
 XX Mus musculus.
 OS Key Location/Qualifiers
 FH Misc-difference 433
 FT /note= "encoded by CTA"
 XX WO9631625-A1.
 XX

PD 10-OCT-1996.
 XX 04-APR-1996; 96WO-US004454.
 XX 07-APR-1995; 95US-00417872.
 PR 03-APR-1996; 96US-00630915.
 XX (CYTO-) CYTOGEN CORP.
 PA (UYN-) UNIV NORTH CAROLINA.
 XX Sparks AB, Hoffman N, Kay BK, Fowlkes DM, McConnell SJ;
 PI WPI; 1996-465045/46.
 XX N-PSDB; AAT39791.
 DR Identifying polypeptide(s) having specific functional domain (esp. SH3
 PT domain) - comprises detecting selective binding to recognition unit,
 PT regardless of sequence homology.
 XX Claim 54; Fig 35; 174pp; English.
 CC AAW05386-W05403 represent novel human and mouse Src-homology region 3
 CC (SH3) domain containing proteins that can be used in the method of the
 CC invention. SH3 domain containing proteins play a role in signalling and
 CC structural elements of cells. The method of the invention is for
 CC identifying polypeptides containing functional domains of interest
 CC (especially SH3 domains). The method comprises contacting a multivalent
 CC recognition unit (RU) complex with a number of peptides and identifying
 CC polypeptides having a selective binding affinity for the RU complex. The
 CC method is based on functional similarities and does not rely on sequence
 CC similarities. Prior methods only gave limited success for identifying
 CC proteins which contain an SH3 domain due to the minimal sequence homology
 CC among known SH3 proteins. It has been found that small peptide RUS in
 CC multivalent form have reduced specificity for a given functional domain
 CC compared to monomer RUS. Multivalent RU complexes are particularly suited
 CC to screening for polypeptides containing functional domains that are
 CC similar to, but not identical in sequence to, the original target
 CC functional domain. The new method enables proteins having a common
 CC function to be identified. Identification of novel SH3 proteins will be
 CC useful for a better understanding of cell growth, malignancy, signal
 CC transduction processes, etc. New candidate drugs can be identified, and
 CC their specificities (e.g. pharmacological activities) can be assessed
 CC using the method of the invention
 XX Sequence 434 AA;
 Query Match 100.0%; Score 61; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGA 13
 DB 24 RAQEKVLQKLGA 36
 RESULT 6
 AAW06602
 ID AAW06602 standard; protein; 451 AA.
 AC AAW06602;
 XX 07-FEB-1997 (first entry)
 DT Human box-dependent myc-interacting protein (BIN1).
 DE Box-dependent myc-interacting protein; BIN1; MIP-99; oncogene;
 KW oncoprotein; breast cancer; liver cancer; apoptosis;
 KW tumour suppressor protein; hyperplasia; diagnosis; therapy.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Domain 1. .222
 FT

XX MPI; 1998-207038/18.
 DR N-PSDB; AAC68498.
 XX
 PT New isolated BIN1-associated UL-specific protein - which acts as a tumour
 PT suppressor, used to develop products for treating e.g. cancers, hyper-
 PT plastic disease states or degenerative diseases.
 XX
 PS Disclosure; Fig 3; 22pp; English.
 XX
 CC The present invention relates to mammalian BIN1-associated UL-specific
 CC (Bau) protein. The Bau protein is useful in the detection, diagnosis and
 CC treatment of cancers or other disorders associated with inappropriate
 CC BIN1 levels and/or deregulation, deficiency or amplification of the c-Myc
 CC oncogenes. The proteins are also useful as antigens for the development
 CC of anti-Bau antisera and antibodies to Bau, or to a desired fragment of
 CC the Bau protein, as diagnostic reagents, in gene therapy, and in
 CC screening and developing chemical compounds or proteins which may be used
 CC for the treatment of cancers characterized by Bau or BIN1, which regulate
 CC inappropriate MYC levels
 XX
 SQ Sequence 451 AA;
 Query Match 100.0%; Score 61; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAOEKVLQKLGKA 13
 DB 21 RAOEKVLQKLGKA 33
 RESULT 9
 AAW94504
 ID AAW94504 standard; protein; 451 AA.
 AC AAW94504;
 DT 22-APR-1999 (first entry)
 DE Human Bin1 protein.
 XX
 KW Bin1; brain-specific; box-dependent myc-interacting protein; cancer;
 KW diagnosis; hyperplastic disease; tumour suppressor; gene therapy;
 KW benign prostatic hypertrophy; neurodegeneration.
 XX
 OS Homo sapiens.
 XX
 FN WO9855151-A1.
 XX
 PD 10-DEC-1998.
 XX
 PF 04-JUN-1998; 98WO-US011647.
 XX
 PR 06-JUN-1997; 97US-00870126.
 XX
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX
 PI Prendergast GC, Sakamuro D;
 XX
 DR WPI; 1999-059881/05.
 DR N-PSDB; AAX16322.
 XX
 PT New splice variant exons of Box-dependent myc-interacting polypeptide -
 PT associated with loss of tumour suppressor activity, used for diagnosis of
 PT cancer and in gene therapy.
 XX
 PS Example 1; Page 81-82; 133pp; English.
 XX
 CC The present invention describes Bin1 (Box-dependent myc-interacting
 CC protein 1) brain-specific alternative splice variants exon 12A, B, C and
 CC D. Bin1 specific antibodies (when labelled) are used to detect cancers or
 CC other hyperplastic conditions (e.g. benign prostatic hypertrophy)

CC associated with a deficit of normal Bin1 and/or aberrant forms of Bin1.
 CC The same diseases can also be diagnosed at the nucleic acid level using
 CC fragments of Bin1 nucleotide sequences in standard amplification and/or
 CC hybridisation assays. Cancers that can be detected are carcinomas and
 CC epithelial cell tumours, specifically of prostate, liver and colon/
 CC rectum, also melanoma. Bin1 nucleotide sequences, when included in a
 CC vector, and Bin1 proteins may also be used to treat these diseases, and
 CC also degenerative conditions such as neurodegeneration. Bin1 proteins may
 CC be used to raise antibodies, and the nucleotide sequences can be
 CC used to express the corresponding proteins. Also anti-idiotypic
 CC antibodies can be used therapeutically, and more generally similar
 CC materials can be used to treat or diagnose any condition involving
 CC deregulation, defect or amplification of the c-myc oncogene. Bin1
 CC nucleotide sequence, proteins and antibodies are also useful to screen
 CC for agents that may be used to treat Bin1-related cancers. The present
 CC sequence represents human Bin1 protein
 XX
 SQ Sequence 451 AA;
 Query Match 100.0%; Score 61; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAOEKVLQKLGKA 13
 DB 21 RAOEKVLQKLGKA 33
 RESULT 10
 ABR69631
 ID ABR69631 standard; protein; 453 AA.
 AC ABR69631;
 DT 12-AUG-2003 (first entry)
 DE Human CGDD-31 protein.
 XX
 KW Human; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;
 KW neuroprotective; cerebroprotective; anti-HIV; anti-allergic;
 KW antiinflammatory; gynaecological; cancer; atherosclerosis; epilepsy;
 KW Huntington's disease; stroke; AIDS; allergy; placenta; reproductive;
 KW CGDD; cell growth; cell differentiation; cell death.
 XX
 OS Homo sapiens.
 XX
 FN WO2003027263-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 26-SEP-2002; 2002WO-US031095.
 XX
 PR 28-SEP-2001; 2001US-0326389P.
 PR 05-OCT-2001; 2001US-0327380P.
 PR 05-OCT-2001; 2001US-0328186P.
 PR 12-OCT-2001; 2001US-0329690P.
 PR 26-OCT-2001; 2001US-0345384P.
 PR 26-OCT-2001; 2001US-0348165P.
 PR 02-NOV-2001; 2001US-0350213P.
 PR 09-NOV-2001; 2001US-0344518P.
 PR 09-NOV-2001; 2001US-0345143P.
 PR 16-NOV-2001; 2001US-0332375P.
 PR 03-DEC-2001; 2001US-0336908P.
 PR 07-DEC-2001; 2001US-0340747P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Azimzai Y, Baughn MR, Becha SD, Borowsky ML, Chawla NK;
 PI Elliott VS, Emerling BN, Gandhi AR, Gietzen KJ, Gorvad AE;
 PI Griffin JA, Hafalia AJA, Ison CH, Kable AE, Kalafus DP;
 PI Lehr-Mason PM, Lu DAM, Marquis JP, Nguyen DB, Rammumar J;
 PI Richardson TW, Sapperstein SK, Swarnakar A, Tang YT, Tran UK;
 PI Warren BA, Xu Y, Yao MG, Yue H, Yue H;

XX WPI; 2003-421159/39.
 DR N-PSDB; ACC90608.
 XX
 PT New human proteins associated with cell growth, differentiation, and
 PT death (CGDD), useful for diagnosing, treating and preventing diseases or
 PT conditions associated with the aberrant CGDD expression e.g. cancer,
 PT AIDS, or epilepsy.
 XX
 PS Claim 1; Page 281-282; 350pp; English.
 XX
 CC The invention relates to an isolated polypeptide associated with cell
 CC growth, differentiation and death (CGDD). Also disclosed are the
 CC polynucleotides encoding the polypeptides. The polypeptides and
 CC polynucleotides are useful in diagnosing, treating and preventing
 CC diseases or conditions associated with the decreased expression or over
 CC expression of CGDD. Such diseases include cell proliferative (e.g.
 CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's
 CC disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and
 CC reproductive disorders, or disorders of the placenta. They are also
 CC useful in assessing the effects of exogenous compounds on the expression
 CC of nucleic acid and amino acid sequences of CGDD. The CGDD or its
 CC fragments are useful in screening compounds for effectiveness as an
 CC agonist or antagonist of the polypeptides, or in altering the expression
 CC of the target polynucleotide and compounds that specifically bind to or
 CC modulate the activity of the polypeptide. Microarrays consisting
 CC polynucleotides of the invention are useful in monitoring or measuring
 CC protein-protein interactions, drug-target interactions, and gene
 CC expression profiles. Sequences given in records AAR69601-AAR69657
 CC represent CGDD polypeptides of the invention
 XX
 SQ Sequence 453 AA;
 Query Match 100.0%; Score 61; DB 6; Length 453;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGKA 13
 Db |||||
 24 RAQEKVLQKLGKA 36
 RESULT 11
 ABUS9771
 ID ABUS9771 standard; protein; 482 AA.
 XX
 AC ABUS9771;
 XX
 DT 10-JUL-2003 (first entry)
 XX
 DE Protein differentially expressed in cardiovascular disease #65.
 XX
 KW Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
 KW myocardial infarction; cardiast; antiarteriosclerotic; antianginal;
 KW gene therapy; differential gene expression.
 XX
 XX Homo sapiens.
 OS
 XX WO2003031650-A2.
 PN
 XX 17-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-EP011034.
 XX
 PR 08-OCT-2001; 2001GB-00024145.
 XX
 XX (FARB) BAYER AG.
 PA
 XX Munnes M, Gehrman M, Wick M, Schmitz G;
 PI
 XX WPI; 2003-403108/38.
 DR
 DR N-PSDB; ACA89944.
 XX

PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
 PT angina, ischemia, myocardial infarction or arteriosclerosis by detection
 PT of a polynucleotide in a biological sample comprises detecting a
 PT hybridization complex.
 XX
 PS Claim 3; Page 433-435; 454pp; English.
 XX
 CC The invention describes a method of predicting, diagnosing or prognosing
 CC a cardiovascular disease by detection of a polynucleotide in a biological
 CC sample comprises hybridising at least one of the polynucleotide to a
 CC nucleic acid material of a biological sample, thus forming a
 CC hybridisation complex, and detecting the hybridisation complex. The
 CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
 CC are useful for preparing compositions for preventing, predicting or
 CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.
 CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
 CC This sequence represents a protein identified in the invention a being
 CC differentially expressed in individuals with cardiovascular disease
 XX
 SQ Sequence 482 AA;
 Query Match 100.0%; Score 61; DB 6; Length 482;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGKA 13
 Db |||||
 24 RAQEKVLQKLGKA 36
 RESULT 12
 AAB62100
 ID AAB62100 standard; protein; 564 AA.
 XX
 AC AAB62100;
 XX
 DT 29-MAY-2001 (first entry)
 XX
 DE Human bridging integrator-2 (Bin2) protein.
 XX
 KW Bridging integrator-2 protein; Bin2; cancer; leukemia; blood disorder;
 KW hyperplastic disease; cytostatic; cell growth regulator;
 KW chromosome 4q22.1.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 23..35
 FT Peptide /note= "specifically claimed fragment"
 FT Peptide 138..155
 FT /note= "specifically claimed fragment"
 XX
 PN WO200116158-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 30-AUG-2000; 2000WO-US023723.
 XX
 PR 31-AUG-1999; 99US-0151554P.
 XX
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX
 PI Prendergast GC, Ge K;
 XX
 DR WPI; 2001-235087/24.
 DR N-PSDB; AAF57268.
 XX
 XX New bridging integrator-2 (Bin2) protein and nucleic acid molecules,
 PT useful for regulating cell growth, and for diagnosing or treating
 PT conditions associated with inappropriate expression of Bin2, e.g. cancers
 PT or hepatocarcinoma.
 XX
 PS Claim 1; Fig 1A-C; 62pp; English.

XX This represents a human bridging integrator-2 (Bin2) protein. The Bin2
 CC protein can be expressed by standard recombinant methodology. The Bin2
 CC proteins or peptides are useful in regulating cell growth, cell survival,
 CC differentiation, endocytosis and actin organization. These peptides or
 CC proteins are also useful for diagnosing or treating conditions associated
 CC with inappropriate expression of Bin2, e.g. liver cancer, breast cancer,
 CC hepatocarcinoma, myeloid and lymphoid leukemias or blood disorders. The
 CC peptides, nucleic acid sequences or anti-Bin2 antibodies are useful for
 CC diagnosing inappropriate expression of Bin2. Bin2 is also useful for
 CC treating disorders associated with excessive Bin1 levels, e.g. liver,
 CC colorectal, prostate or breast cancers, epithelia cell cancers, melanoma,
 CC or hyperplastic disease states

XX
 CC Sequence 564 AA;
 Query Match 100.0%; Score 61; DB 4; Length 564;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 |||||
 DB 23 RAQEKVLQKLGKA 35

RESULT 13
 ABG21411
 ID ABG21411 standard; protein; 572 AA.
 XX
 AC ABG21411;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21402.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US0008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Dermanac RT, Liu C, Tang YT;
 XX
 PI WPI; 2001-639362/73.
 DR N-PSDB; AAS85598.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 51770; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (I) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pot_sequences
 XX
 XX Sequence 572 AA;
 SQ Query Match 100.0%; Score 61; DB 4; Length 572;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 |||||
 DB 30 RAQEKVLQKLGKA 42

RESULT 14
 ADD45951
 ID ADD45951 standard; protein; 588 AA.
 XX
 AC ADD45951;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein O08839, SEQ ID NO 11623.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 PI WPI; 2003-268312/26.
 DR GENBANK; O08839.
 DR
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PT
 XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 588 AA;

Query Match 100.0%; Score 61; DB 7; Length 588;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 DB 24 RAQEKVLQKLGKA 36
 |||||

RESULT 15
 ADE60848
 ID ADE60848 standard; protein; 588 AA.
 XX
 AC ADE60848;

DT 29-JAN-2004 (first entry)

DE Rat Protein O08839, SEQ ID NO 6761.

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

FN WO2003016475-A2.

XX 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; O08839.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 588 AA;

Query Match 100.0%; Score 61; DB 7; Length 588;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 DB 24 RAQEKVLQKLGKA 36
 |||||

RESULT 16
 ADE60840
 ID ADE60840 standard; protein; 588 AA.
 XX
 AC ADE60840;

DT 29-JAN-2004 (first entry)

DE Rat Protein O08839, SEQ ID NO 6753.

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

FN WO2003016475-A2.

XX 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; O08839.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 588 AA;

Query Match 100.0%; Score 61; DB 7; Length 588;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 |||||
 Db 24 RAQEKVLQKLGKA 36

RESULT 17
 ADE60844
 ID ADE60844 standard; protein; 588 AA.

AC ADE60844;
 DT 29-JAN-2004 (first entry)
 XX Rat Protein O08839, SEQ ID NO 6757.
 DE
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.

PN WO2003016475-A2.
 XX
 XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.
 XX
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; O08839.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 588 AA;

Query Match 100.0%; Score 61; DB 7; Length 588;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 |||||
 Db 24 RAQEKVLQKLGKA 36

RESULT 18
 ADE60852
 ID ADE60852 standard; protein; 588 AA.

AC ADE60852;
 DT 29-JAN-2004 (first entry)
 XX Rat Protein O08839, SEQ ID NO 6765.

DE
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

PN WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.

DR GENBANK; O08839.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 588 AA;

SQ Query Match 100.0%; Score 61; DB 7; Length 588;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RAQEKVLQKLGA 13
 DB 24 RAQEKVLQKLGA 36

RESULT 19

AD560842
 ID ADE60842 standard; protein; 593 AA.

XX AC ADE60842;

XX 29-JAN-2004 (first entry)

XX Human Protein Q99688, SEQ ID NO 6755.

XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-269312/26.

PS GENBANK; Q99688.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 593 AA;

SQ Query Match 100.0%; Score 61; DB 7; Length 593;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RAQEKVLQKLGA 13

DB 24 RAQEKVLQKLGA 36

RESULT 20

ADD45953
 ID ADD45953 standard; protein; 593 AA.

XX AC ADD45953;

XX 29-JAN-2004 (first entry)

XX Human Protein Q99688, SEQ ID NO 11625.

XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

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XX (GHEO ) GEN HOSPITAL CORP.
XX (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; Q99698.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal, subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 593 AA;
XX
XX Query Match 100.0%; Score 61; DB 7; Length 593;
XX Best Local Similarity 100.0%; Pred. No. 0.035;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 RAQEKVLQKLGKA 13
XX |||||
XX 24 RAQEKVLQKLGKA 36
XX
XX RESULT 21
XX ADE60850
XX ID ADE60850 standard; protein; 593 AA.
XX
XX ADE60850;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human Protein Q99698, SEQ ID NO 6763.
XX
XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX W02003016475-A2.
XX
XX 27-FEB-2003.
XX

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14-AUG-2002; 2002WO-US025765.
14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
Wolff C, D'urso D, Befort K, Costigan M;
WPI; 2003-268312/26.
GENBANK; Q99688.
New composition comprising two or more isolated polypeptides, useful for
preparing a medicament for treating pain in an animal.
Claim 1; Page; 1017pp; English.
The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a human protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
Sequence 593 AA;
Query Match 100.0%; Score 61; DB 7; Length 593;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGA 13
DB 24 RAQEKVLQKLGA 36
RESULT 22
ADE60846
ID ADE60846 standard; protein; 593 AA.
XX AC ADE60846;
XX
XX
29-JAN-2004 (first entry)
Human Protein Q99688, SEQ ID NO 6759.
Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
OS Homo sapiens.

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XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; Q99688.
 XX New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 XX or human polynucleotides or a polynucleotide which represents a fragment,
 XX derivative or allelic variation of the nucleic acid sequence. Also
 XX claimed are a vector comprising the novel polynucleotide, a host cell
 XX comprising the vector, a method for identifying a nucleotide sequence
 XX which is differentially regulated in an animal subjected to pain and a
 XX kit to perform the method, an array, a method for identifying an agent
 XX that increases or decreases the expression of the polynucleotide sequence
 XX that is differentially regulated in neuronal tissue of a first animal
 XX subjected to pain, a method for identifying a compound which regulates
 XX the expression of a polynucleotide sequence which is differentially
 XX expressed in an animal subjected to pain, a method for identifying a
 XX compound that regulates the activity of one or more of the
 XX polynucleotides, a method for producing a pharmaceutical composition, a
 XX method for identifying a compound or small molecule that regulates the
 XX activity in an animal of one or more of the polypeptides given in the
 XX specification, a method for identifying a compound useful in treating
 XX pain and a pharmaceutical composition comprising the one or more
 XX polypeptides or their antibodies. The polynucleotide or the compound that
 XX modulates its activity is useful for preparing a medicament for treating
 XX pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 XX therapy). The sequence presented is a human protein (shown in Table 2 of
 XX the specification) which is differentially expressed during pain. Note:
 XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic form directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 593 AA;
 XX Query Match 100.0%; Score 61; DB 7; Length 593;
 XX Best Local Similarity 100.0%; Pred. No. 0.035;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 RAQEKVLQKLGKA 13
 XX |||||
 XX Db 24 RAQEKVLQKLGKA 36
 XX |||||
 XX
 XX RESULT 23
 XX ADE60854
 XX ID ADE60854 standard; protein; 593 AA.
 XX XX
 XX AC ADE60854;
 XX XX
 XX DT 29-JAN-2004 (first entry)
 XX XX
 XX DE Human Protein Q99688, SEQ ID NO 6767.
 XX XX

KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; Q99688.
 XX New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 XX or human polynucleotides or a polynucleotide which represents a fragment,
 XX derivative or allelic variation of the nucleic acid sequence. Also
 XX claimed are a vector comprising the novel polynucleotide, a host cell
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 XX which is differentially regulated in an animal subjected to pain and a
 XX kit to perform the method, an array, a method for identifying an agent
 XX that increases or decreases the expression of the polynucleotide sequence
 XX that is differentially expressed in neuronal tissue of a first animal
 XX subjected to pain, a method for identifying a compound which regulates
 XX the expression of a polynucleotide sequence which is differentially
 XX expressed in an animal subjected to pain, a method for identifying a
 XX compound that regulates the activity of one or more of the
 XX polynucleotides, a method for producing a pharmaceutical composition, a
 XX method for identifying a compound or small molecule that regulates the
 XX activity in an animal of one or more of the polypeptides given in the
 XX specification, a method for identifying a compound useful in treating
 XX pain and a pharmaceutical composition comprising the one or more
 XX polypeptides or their antibodies. The polynucleotide or the compound that
 XX modulates its activity is useful for preparing a medicament for treating
 XX pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 XX therapy). The sequence presented is a human protein (shown in Table 2 of
 XX the specification) which is differentially expressed during pain. Note:
 XX The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic form directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 593 AA;
 XX Query Match 100.0%; Score 61; DB 7; Length 593;
 XX Best Local Similarity 100.0%; Pred. No. 0.035;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 RAQEKVLQKLGKA 13
 XX |||||
 XX Db 24 RAQEKVLQKLGKA 36
 XX |||||
 XX
 XX RESULT 24
 XX ABG20887
 XX ID ABG20887 standard; protein; 594 AA.
 XX XX
 XX AC ABG20887;

XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #20878.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS85074.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 51246; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
XX CC patent did not appear in the invention. Note: The sequence data for this
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 594 AA;
XX
XX Query Match 100.0%; Score 61; DB 4; Length 594;
XX Best Local Similarity 100.0%; Pred. NO. 0.035;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RAQEKVLQKLGKA 13
XX Db |||||
XX 52 RAQEKVLQKLGKA 64
XX
XX RESULT 25
XX ABG20324
XX ID ABG20324 standard; protein; 594 AA.
XX AC ABG20324;
XX DT 13-FEB-2002 (first entry)
XX DE

XX DE Novel human diagnostic protein #20315.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS84511.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 50683; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
XX CC patent did not appear in the invention. Note: The sequence data for this
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 594 AA;
XX
XX Query Match 100.0%; Score 61; DB 4; Length 594;
XX Best Local Similarity 100.0%; Pred. NO. 0.035;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RAQEKVLQKLGKA 13
XX Db |||||
XX 52 RAQEKVLQKLGKA 64
XX
XX RESULT 26
XX ADD44887
XX ID ADD44887 standard; protein; 683 AA.
XX AC ADD44887;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein O08838, SEQ ID NO 10318.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 OS WO2003016475-A2.
 PN 27-FEB-2003.
 PD 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-03412147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR GENBANK; 008938.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 683 AA;
 SQ Query Match 100.0%; Score 61; DB 7; Length 683;
 Best Local Similarity 100.0%; Pred. No. 0.04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RAQEKVLQKLGA 13
 Db 19 RAQEKVLQKLGA 31
 RESULT 27
 AA22091
 ID AA22091 standard; protein; 695 AA.
 XX
 AC AA22091;

XX 25-JUL-2002 (first entry)
 DT Human amphiphysin-1 protein.
 XX
 DE Cellular senescence; amphiphysin-1 protein; caveolin-1 protein; human;
 KW gene therapy.
 KW
 OS Homo sapiens.
 OS WO200221140-A1.
 PN 14-MAR-2002.
 PD 06-JUL-2001; 2001WO-KR001159.
 XX 08-SEP-2000; 2000KR-00053341.
 PR 08-SEP-2000; 2000KR-00053342.
 XX (META-) METABOLIC ENG LAB CO LTD.
 PA Park S, Park W, Park J, Cho K, Kim D;
 PI WPI; 2002-362263/39.
 DR N-PSDB; RAD35148.
 XX Modulating cellular senescence in patient involves administering protein
 PT involved in cellular senescence e.g., amphiphysin protein or caveolin
 PT protein or polynucleotide encoding the proteins.
 PS Claim 23; Page 92-95; 103pp; English.
 XX The invention relates to a method of modulating cellular senescence in a
 CC patient. The method involves administering protein involved in cellular
 CC senescence e.g. amphiphysin-1 protein or caveolin-1 protein or
 CC polynucleotides encoding such proteins. The method is useful for
 CC detecting and modulating cellular senescence in a mammalian cell. It is
 CC also used in gene therapy. The present sequence is human amphiphysin-1
 CC protein
 XX Sequence 695 AA;
 SQ Query Match 100.0%; Score 61; DB 5; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RAQEKVLQKLGA 13
 Db 19 RAQEKVLQKLGA 31
 RESULT 28
 AAU75110
 ID AAU75110 standard; protein; 695 AA.
 XX
 AC AAU75110;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Synaptic vesicle and endocytosis associated protein, amphiphysin.
 KW MAPKAP-K3; AP-3 delta; APP-695; amyloid A4; Hsp8; heat shock protein 8;
 KW Li30; NY-REN-58; P38 Alpha; P38 Beta; ERK3; KIAA0934; CDK9;
 KW cell cycle dependent kinase 9; CLK; C-NAP-1; clathrin heavy chain;
 KW amphiphysin; PN9109; KIAA1106; neurodegenerative disorder;
 KW non-insulin dependent diabetes mellitus; NIDDM; Alzheimer's disease;
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disorder;
 KW atherosclerosis; cardiac hypertrophy; hypoxic brain injury;
 KW yeast two-hybrid; signal transduction pathway; human; endocytosis;
 KW synaptic vesicle; mitogen activated protein kinase.
 OS Homo sapiens.
 OS

PH Key Location/Qualifiers
 FT 93..273
 FT /notes="This region binds the centrosomal Nek-2
 FT associated protein 1 (C-NAP1) (see ABK1313), the bait
 FT protein in a yeast two-hybrid assay, producing a complex
 FT claimed in claim 1"
 XX
 XX W0200198524-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 21-JUN-2001; 2001WO-US019762.
 XX
 XX 22-JUN-2000; 2000US-0213245P.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 XX
 XX Heichman K, Bartel PL;
 XX WPI; 2002-122287/16.
 XX
 XX New protein complexes comprising protein-protein interactions (e.g.
 PT MAPKAP-K3/AP-3 delta or C-NAP-1/Claithrin HC), useful for diagnosing
 PT physiological generative disorders or screening drugs for these diseases.
 XX
 XX Example 11; Page: 60pp; English.
 XX
 CC The invention describes an isolated protein complex, comprising two
 CC proteins. The protein complex comprises: protein kinase MAPKAP-K3 and AP-
 CC 3 adaptor complex delta sub-unit; MAPKAP-K3 and amyloid A4 precursor
 CC protein, APP-695; MAPKAP-K3 and heat shock protein (Hsp) 8; leucine rich
 CC Li30 and NY-REN-59; P38 Alpha and P38 Beta; protein kinase ERK3 and
 CC KIAA0934 (unknown function); ERK3 and cell cycle dependent kinase (CDK) 9
 CC; ERK3 and protein kinase CLK; C-NAP-1 and Claithrin heavy chain; C-NAP-1
 CC and Amphiphysin; C-NAP-1 and novel protein. P93109 or C-NAP-1 and KIAA1106
 CC (unknown function) interactions. The protein complexes are useful for
 CC diagnosing physiological generative disorders, drug screening for agents
 CC that modulate the interaction of the proteins (thus identify drug
 CC targets), and identifying additional proteins in the pathway common to
 CC the proteins. These physiological disorders include non-insulin dependent
 CC diabetes mellitus (NIDDM), neurodegenerative disorders (e.g. Alzheimer's
 CC disease), inflammatory diseases (e.g. rheumatoid arthritis and
 CC inflammatory bowel disorder) and other human disease such as
 CC atherosclerosis, cardiac hypertrophy and hypoxic brain injury. This
 CC sequence represents the synaptic vesicle and endocytosis associated
 CC protein amphiphysin, residues 93-273 of which binds to the bait protein
 CC centrosomal Nek-2 associated protein 1 (C-NAP1) (see ABK1313) in a yeast
 CC two-hybrid assay for determining components of signal transduction
 CC pathways and forms an interaction claimed in claim 1 of the invention.
 CC Note: This sequence does not appear in the specification but has been
 CC obtained from a reference given in the invention
 XX
 XX Sequence 695 AA;
 XX
 Query Match 100.0%; Score 61; DB 5; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RAQEKVLQKLKGA 13
 DB 19 RAQEKVLQKLKGA 31
 RESULT 29
 ADD44889
 ID ADD44889 standard; protein; 695 AA.
 XX
 AC ADD44889;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 DE Human Protein P49418, SEQ ID NO 10320.
 XX
 XX

KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX W02003016475-A2.
 XX
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US025765.
 XX
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 XX (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 XX GENBANK; P49418.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page: 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 695 AA;
 XX
 Query Match 100.0%; Score 61; DB 7; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RAQEKVLQKLKGA 13
 DB 19 RAQEKVLQKLKGA 31
 RESULT 30
 ABG22457
 ID ABG22457 standard; protein; 594 AA.
 XX
 XX AC ABG22457;

XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #22448.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 XX DR N-PSDB; AAS86644.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX PS Claim 20; SEQ ID NO 52816; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 594 AA;
 Query Match 83.6%; Score 51; DB 4; Length 594;
 Best Local Similarity 84.6%; Pred. No. 2;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGKA 13
 |||||
 Db 52 RAQEKALXKLGKA 64
 |||||
 RESULT 31
 ABB63948
 ID ABB63948 standard; protein; 602 AA.
 XX AC ABB63948;
 XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 18636.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL08051.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX PS Disclosure; SEQ ID NO 18636; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
 CC sequences (ABU01840-ABU16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 602 AA;
 Query Match 77.0%; Score 47; DB 4; Length 602;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGK 12
 |||||
 Db 19 RAKSKILQNLQK 30
 |||||
 RESULT 32
 AAU03699
 ID AAU03699 standard; protein; 373 AA.
 XX AC AAU03699;
 XX DT 12-SEP-2001 (first entry)
 XX DE Group B Streptococcus antigenic protein, ID-176.
 XX KW Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;
 KW meningitis; neonate; anti-genic; vaccine; infection; genital tract;
 KW capsid polysaccharide vaccination.
 XX OS Streptococcus agalactiae.
 XX PN WO200132882-A2.
 XX PD 10-MAY-2001.
 XX PF 07-SEP-2000; 2000WO-GB003437.

XX PR 07-SEP-1999; 99GB-00021125.
 XX PA (MICR-) MICROBIAL TECHNIQS LTD.
 XX FI Le Page RWP, Wells JM, Hanniffy SB;
 XX PI WPI; 2001-316444/33.
 DR N-PSDB; AAS07116.
 XX
 XX New polypeptides derived from Streptococcus agalactiae are useful to
 PT provide detection of, and vaccination against, Group B Streptococcus
 PT infections, particularly to prevent infection in neonates.
 XX
 PS Claim 1; Fig 1; 178pp; English.
 XX
 CC AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus
 CC agalactiae) amino acid sequences of the invention. S. agalactiae is an
 CC encapsulated bacterium which is a major pathogen of humans causing sepsis
 CC and meningitis in neonates as well as adults. The S. agalactiae antigenic
 CC polypeptides are used to vaccinate against Group B Streptococcus
 CC infections, particularly to prevent infection in new born children
 CC arising from the maternal genital tract. An immunogenic composition is
 CC useful in the preparation of a medicament for the treatment or
 CC prophylaxis of Group B Streptococcus infection. The invention does not
 CC have the disadvantages of varied response rate associated with prior art
 CC capsid polysaccharide vaccination against Group B Streptococcus
 XX
 SQ Sequence 373 AA;
 Query Match 67.2%; Score 41; DB 4; Length 373;
 Best Local Similarity 63.6%; Pred. No. 69;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QEKVLQKLGKA 13
 DB 337 EEKILKKLGKS 347
 RESULT 33
 ABP30317
 ID ABP30317 standard; protein; 651 AA.
 XX
 AC ABP30317;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Streptococcus polypeptide SEQ ID NO 9810.
 XX
 KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus agalactiae.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB004789.
 XX
 PR 27-OCT-2000; 2000GB-00026333.
 PR 24-NOV-2000; 2000GB-00028727.
 PR 07-MAR-2001; 2001GB-00005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI; 2002-352536/38.
 DR N-PSDB; ABN70948.
 XX

XX
 PT New Streptococcus protein for the treatment or prevention of infection or
 PT disease caused by Streptococcus bacteria, such as meningitis, and for
 PT detecting a compound that binds to the protein.
 XX
 PS Claim 1; Page 4109; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABM66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins
 XX
 SQ Sequence 651 AA;
 Query Match 67.2%; Score 41; DB 5; Length 651;
 Best Local Similarity 63.6%; Pred. No. 1.2e+02;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QEKVLQKLGKA 13
 DB 334 EEKILKKLGKS 344
 RESULT 34
 ABP29732
 ID ABP29732 standard; protein; 654 AA.
 XX
 AC ABP29732;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Streptococcus polypeptide SEQ ID NO 8640.
 XX
 KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus agalactiae.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB004789.
 XX
 PR 27-OCT-2000; 2000GB-00026333.
 PR 24-NOV-2000; 2000GB-00028727.
 PR 07-MAR-2001; 2001GB-00005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI; 2002-352536/38.
 DR N-PSDB; ABN70363.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection or
 PT disease caused by Streptococcus bacteria, such as meningitis, and for

PT detecting a compound that binds to the protein.

XX Claim 1; Page 3977; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GBS (Streptococcus agalactiae) or group A Streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins

XX Sequence 654 AA;

Query Match 67.2%; Score 41; DB 5; Length 654;
 Best Local Similarity 63.6%; Pred. No. 1.2e+02;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 QEKVLQKLGKA 13

DB 337 EEKILKLGKS 347

RESULT 35

ABP26469

ID ABP26469 standard; protein; 654 AA.

XX AC ABP26469;

XX 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 2114.

XX Streptococcus; GAS; GBS; group B Streptococcus; Streptococcus agalactiae;
 XX group A Streptococcus; Streptococcus pyogenes; antibacterial;
 XX antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus agalactiae.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB004789.

XX 27-OCT-2000; 2000GB-00026333.

XX 24-NOV-2000; 2000GB-00028727.

XX 07-MAR-2001; 2001GB-00005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Maignani V, Margarit Y RosI, Grandi G, Fraser C;

XX Tettelin H;

XX WPI; 2002-352536/38.

XX DR N-PSDB; ABN67100.

XX New Streptococcus protein for the treatment or prevention of infection or

XX disease caused by Streptococcus bacteria, such as meningitis, and for
 XX detecting a compound that binds to the protein.

XX Claim 1; Page 3364; 4525pp; English.

XX

CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC Streptococcus/GBS (Streptococcus agalactiae) or group A Streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins

XX Sequence 654 AA;

Query Match 67.2%; Score 41; DB 5; Length 654;
 Best Local Similarity 63.6%; Pred. No. 1.2e+02;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 QEKVLQKLGKA 13

DB 337 EEKILKLGKS 347

RESULT 36

ABBS7920

ID ABBS7920 standard; protein; 1381 AA.

XX AC ABBS7920;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 552.

XX Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEXE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-556860/75.

XX N-PSDB; ABL02023.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 552; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins (AB857737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1381 AA;
 Query Match 67.2%; Score 41; DB 4; Length 1381;
 Best Local Similarity 81.8%; Pred. NO. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 QEKVLQKLGA 13
 | | | | |
 Db 663 QSKELQKLGA 673

RESULT 37
 ADB07514
 ID ADB07514 standard; protein; 264 AA.
 AC ADB07514;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Alloicoccus otitis antigenic protein SEQ ID NO:1454.
 XX
 KW Alloicoccus otitis; antigenic protein; immunogenic; immunisation;
 XX gene therapy; Gram-positive bacterium; infection.
 XX
 OS Alloicoccus otitis.
 XX
 FN WO2003048304-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 25-NOV-2002; 2002WO-US036123.
 XX
 PR 29-NOV-2001; 2001US-0333777P.
 PR 18-NOV-2002; 2002US-0426742P.
 XX
 PA (AMHP) WYETH HOLDINGS CORP.
 XX
 PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;
 PI
 DR WPI; 2003-505284/47.
 DR N-PSDB; ADB07513.
 XX
 PT New Alloicoccus otitis polynucleotides and polypeptides, useful for
 PT treating and diagnosing diseases, drug screening assays and monitoring of
 PT effects during drug clinical trials.
 XX
 PS Claim 33; SEQ ID NO 1454; 1019pp; English.
 XX

The present invention describes an isolated polynucleotide (1) of
 CC Alloicoccus otitis genomic DNA, which encodes an antigenic protein.
 CC Alloicoccus otitis is a Gram-positive bacterium. Also described: (1)
 CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
 CC expression vector comprising the novel isolated polynucleotide (1), its
 CC complement, degenerate variant or fragment; (3) a genetically engineered
 CC host cell, transfected, transformed or infected with the vector of (2);
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
 CC composition comprising the polypeptide, its complement, biological
 CC equivalent or fragment, or the polynucleotide that is comprised in the
 CC expression vector; (6) a pharmaceutical composition comprising the
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)
 CC immunising against Alloicoccus otitis by administering to a host the
 CC immunogenic composition; (9) detecting and/or identifying Alloicoccus
 CC otitis in the biological sample; (10) a kit comprising a container
 CC containing the novel polynucleotide, its degenerate variant or fragment,
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the
 CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (1) can be used in gene therapy. The

CC polynucleotides, polypeptides, antibodies and compositions of the present
 CC invention can be used for treating and diagnosing diseases, drug
 CC screening assays and monitoring of effects during drug clinical trials.
 CC The polynucleotides are useful for expressing and detecting Alloicoccus
 CC otitis. The present sequence represents an Alloicoccus otitis
 CC antigen protein from the present invention.
 XX
 SQ Sequence 264 AA;
 Query Match 65.6%; Score 40; DB 6; Length 264;
 Best Local Similarity 72.7%; Pred. NO. 72;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 QEKVLQKLGA 13
 | | | | |
 Db 117 QEKVAQLGKS 127

RESULT 38
 ADB07516
 ID ADB07516 standard; protein; 297 AA.
 AC ADB07516;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Alloicoccus otitis antigenic protein SEQ ID NO:1456.
 XX
 KW Alloicoccus otitis; antigenic protein; immunogenic; immunisation;
 XX gene therapy; Gram-positive bacterium; infection.
 XX
 OS Alloicoccus otitis.
 XX
 FN WO2003048304-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 25-NOV-2002; 2002WO-US036123.
 XX
 PR 29-NOV-2001; 2001US-0333777P.
 PR 18-NOV-2002; 2002US-0426742P.
 XX
 PA (AMHP) WYETH HOLDINGS CORP.
 XX
 PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;
 PI
 DR WPI; 2003-505284/47.
 DR N-PSDB; ADB07515.
 XX
 PT New Alloicoccus otitis polynucleotides and polypeptides, useful for
 PT treating and diagnosing diseases, drug screening assays and monitoring of
 PT effects during drug clinical trials.
 XX
 PS Claim 33; SEQ ID NO 1456; 1019pp; English.
 XX

The present invention describes an isolated polynucleotide (1) of
 CC Alloicoccus otitis genomic DNA, which encodes an antigenic protein.
 CC Alloicoccus otitis is a Gram-positive bacterium. Also described: (1)
 CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
 CC expression vector comprising the novel isolated polynucleotide (1), its
 CC complement, degenerate variant or fragment; (3) a genetically engineered
 CC host cell, transfected, transformed or infected with the vector of (2);
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
 CC composition comprising the polypeptide, its complement, biological
 CC equivalent or fragment, or the polynucleotide that is comprised in the
 CC expression vector; (6) a pharmaceutical composition comprising the
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)
 CC immunising against Alloicoccus otitis by administering to a host the
 CC immunogenic composition; (9) detecting and/or identifying Alloicoccus
 CC otitis in the biological sample; (10) a kit comprising a container
 CC containing the novel polynucleotide, its degenerate variant or fragment,
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the
 CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (1) can be used in gene therapy. The

CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (I) can be used in gene therapy. The
 CC polynucleotides, polypeptides, antibodies and compositions of the present
 CC invention can be used for treating and diagnosing diseases, drug
 CC screening assays and monitoring of effects during drug clinical trials.
 CC The polynucleotides are useful for expressing and detecting *Alloicoccus*
 CC otitidis. The present sequence represents an *Alloicoccus* otitidis
 CC antigen protein from the present invention.
 XX
 SQ Sequence 297 AA;

Query Match 65.6%; Score 40; DB 6; Length 297;
 Best Local Similarity 72.7%; Pred. No. 82;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 QEKVLQKLGA 13
 |||||:|:
 Db 150 QEKVAQELGKS 160

RESULT 39
 AAE15583
 ID AAE15583 standard; protein; 154 AA.

XX AC AAE15583;

XX DT 12-MAR-2002 (first entry)

XX DE Mutated Glycine max ankyrin-related protein 2 (GMAdelta4).

XX KW Glycine max ankyrin-related protein; GMA2; GmsUT1; sugar transport;
 XX KW sucrose/proton symporter; soybean ankyrin-related protein; SAR; ANK;
 XX KW sugar allocation; nutritional value; mutant; mutein; GMAdelta4.

XX OS Glycine max.
 XX OS Synthetic.

XX PN WO200188139-A2.

XX PD 22-NOV-2001.

XX PF 11-MAY-2001; 2001WO-US015315.

XX PR 12-MAY-2000; 2000US-0203974P.

XX PA (UNIW) UNIV WASHINGTON STATE RES FOUND.

XX PI Grimes HD, Elmer AM, Murphy KA;

XX DR WPI; 2002-062385/08.

XX PT New purified protein having Glycine max ankyrin-related (GMA) protein
 XX PT biological activity, useful to alter GMA levels in plants to confer
 XX PT altered sugar transport and/or altered sugar allocation properties.

XX PS Example 2; Pg -; 60pp; English.

XX CC The invention relates to (soybean) Glycine max (Gm) ankyrin (ANK) -
 XX CC related proteins 1 and 2 referred to as GMA1 and GMA2 and nucleic acid
 XX CC molecules encoding them. GMA proteins also known as soybean ankyrin-
 XX CC related (SAR) proteins interact with Gm sucrose/H+ (proton) symporter
 XX CC designated as (SUT1). Manipulating the expression of GmsUT1 and GMA in
 XX CC plants is useful to confer altered sugar transport and/or altered sugar
 XX CC allocation properties. Alteration of GMA protein levels in plants could
 XX CC be used to increase the nutritional value of plant tissues, for instance
 XX CC plant seeds or grain. The present sequence is GMA2 mutant protein. This
 XX CC sequence is obtained from the wild type GMA2 protein by deleting all the
 XX CC four carboxy terminal ANK repeats. Note: This sequence is not found in
 XX CC the specification but is derived from the wild type GMA2 protein shown as
 XX CC SEQ ID NO:6 (AAE15309) in Fig 2 of the specification

XX SQ Sequence 154 AA;

Query Match 63.9%; Score 39; DB 5; Length 154;
 Best Local Similarity 80.0%; Pred. No. 62;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 EKVLQKLGA 13
 |||||:|:
 Db 106 EVLQKLGA 115

RESULT 40

AAE15580

ID AAE15580 standard; protein; 179 AA.

XX AC AAE15580;

XX DT 12-MAR-2002 (first entry)

XX DE Mutated Glycine max ankyrin-related protein 1 (GMAdelta4).

XX KW Glycine max ankyrin-related protein; GMA1; GmsUT1; sugar transport;
 XX KW sucrose/proton symporter; soybean ankyrin-related protein; SAR; ANK;
 XX KW sugar allocation; nutritional value; mutant; mutein; GMAdelta4.

XX OS Glycine max.

XX OS Synthetic.

XX PN WO200188139-A2.

XX PD 22-NOV-2001.

XX PF 11-MAY-2001; 2001WO-US015315.

XX PR 12-MAY-2000; 2000US-0203974P.

XX PA (UNIW) UNIV WASHINGTON STATE RES FOUND.

XX PI Grimes HD, Elmer AM, Murphy KA;

XX DR WPI; 2002-062385/08.

XX PT New purified protein having Glycine max ankyrin-related (GMA) protein
 XX PT biological activity, useful to alter GMA levels in plants to confer
 XX PT altered sugar transport and/or altered sugar allocation properties.

XX PS Example 2; Pg -; 60pp; English.

XX CC The invention relates to (soybean) Glycine max (Gm) ankyrin (ANK) -
 XX CC related proteins 1 and 2 referred to as GMA1 and GMA2 and nucleic acid
 XX CC molecules encoding them. GMA proteins also known as soybean ankyrin-
 XX CC related (SAR) proteins interact with Gm sucrose/H+ (proton) symporter
 XX CC designated as (SUT1). Manipulating the expression of GmsUT1 and GMA in
 XX CC plants is useful to confer altered sugar transport and/or altered sugar
 XX CC allocation properties. Alteration of GMA protein levels in plants could
 XX CC be used to increase the nutritional value of plant tissues, for instance
 XX CC plant seeds or grain. The present sequence is GMA1 mutant protein. This
 XX CC sequence is obtained from the wild type GMA1 protein by deleting all the
 XX CC four carboxy terminal ANK repeats. Note: This sequence is not found in
 XX CC the specification but is derived from the wild type GMA1 protein shown as
 XX CC SEQ ID NO:4 (AAE15308) in Fig 2 of the specification

XX SQ Sequence 179 AA;

Query Match 63.9%; Score 39; DB 5; Length 179;
 Best Local Similarity 80.0%; Pred. No. 73;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 EKVLQKLGA 13
 |||||:|:
 Db 131 EVLQKLGA 140

RESULT 41

AAE15579

ID AAE15579 standard; protein; 206 AA.

AC AAE15579;

XX 12-MAR-2002 (first entry)

DE Mutated Glycine max ankyrin-related protein 1 (GMAldelta).

XX Glycine max ankyrin-related protein; GMA1; GmsUT1; sugar transport;
KW sucrose/proton symporter; soybean ankyrin-related protein; SAR; ANK;
KW sugar allocation; nutritional value; mutant; mitein; GMAldelta.

XX Glycine max.

OS Synthetic.

XX WO200188139-A2.

FN 22-NOV-2001.

XX 11-MAY-2001; 2001WO-US015315.

PF 12-MAY-2000; 2000US-0203974P.

PR (UNIW) UNIV WASHINGTON STATE RES FOUND.

XX Grimes HD, Elmer AM, Murphy KA;

XX WPI; 2002-062385/08.

XX New purified protein having Glycine max ankyrin-related (GMA) protein
PT biological activity, useful to alter GMA levels in plants to confer
PT altered sugar transport and/or altered sugar allocation properties.

XX Example 2; Pg -; 60pp; English.

XX The invention relates to (soybean) Glycine max (Gm) ankyrin (ANK)-
CC related proteins 1 and 2 referred to as GMA1 and GMA2 and nucleic acid
CC molecules encoding them. GMA proteins also known as soybean ankyrin-
CC related (SAR) proteins interact with Gm sucrose/H+ (proton) symporter
CC designated as (SUT1). Manipulating the expression of GmsUT1 and GMA in
CC plants is useful to confer altered sugar transport and/or altered sugar
CC allocation properties. Alteration of GMA protein levels in plants could
CC be used to increase the nutritional value of plant tissues, for instance
CC plant seeds or grain. The present sequence is GMA1 mutant protein. This
CC sequence is obtained from the wild type GMA1 protein by truncation of
CC three of the four carboxy terminal ANK repeats. Note: This sequence is
CC not found in the specification but is derived from the wild type GMA1
CC protein shown as SEQ ID NO:4 (AAE15308) in Fig 2 of the specification

XX Sequence 206 AA;

Query Match 63.9%; Score 39; DB 5; Length 206;

Best Local Similarity 80.0%; Pred. No. 84;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 EKVQLKGLKA 13

Db 131 EEVLQKLGQA 140

RESULT 42

AAE15309

ID AAE15309 standard; protein; 268 AA.

XX AAE15309;

XX 12-MAR-2002 (first entry)

DE Glycine max ankyrin-related protein 2 (GMA2).

XX Glycine max ankyrin-related protein; GMA2; GmsUT1; sugar transport;
KW sucrose/proton symporter; soybean ankyrin-related protein; SAR; ANK;
KW sugar allocation; nutritional value.

XX Glycine max.

XX Key

FT Domain Location/Qualifiers

FT 145..171 /note= "Ankyrin (ANK) repeat motif #4"

FT 176..205 /note= "Ankyrin (ANK) repeat motif"

FT 209..238 /note= "Ankyrin (ANK) repeat motif"

FT 242..268 /note= "Ankyrin (ANK) repeat motif"

FT Misc-difference 267..268 /note= "Ankyrin (ANK) repeat motif"

FT Misc-difference 268 /note= "Encoded by CTG"

FT /note= "This residue is absent in the sequence shown as

SEQ ID NO:6 in page 58-59 of the specification"

XX WO200188139-A2.

XX 22-NOV-2001.

XX 11-MAY-2001; 2001WO-US015315.

XX 12-MAY-2000; 2000US-0203974P.

XX (UNIW) UNIV WASHINGTON STATE RES FOUND.

XX Grimes HD, Elmer AM, Murphy KA;

XX WPI; 2002-062385/08.

XX N-PSDB; AAD24775.

XX New purified protein having Glycine max ankyrin-related (GMA) protein

PT biological activity, useful to alter GMA levels in plants to confer

PT altered sugar transport and/or altered sugar allocation properties.

XX Claim 1; Fig 2; 60pp; English.

XX The invention relates to (soybean) Glycine max (Gm) ankyrin (ANK)-
CC related proteins 1 and 2 referred to as GMA1 and GMA2 and nucleic acid
CC molecules encoding them. GMA proteins also known as soybean ankyrin-
CC related (SAR) proteins interact with Gm sucrose/H+ (proton) symporter
CC designated as (SUT1). Manipulating the expression of GmsUT1 and GMA in
CC plants is useful to confer altered sugar transport and/or altered sugar
CC allocation properties. Alteration of GMA protein levels in plants could
CC be used to increase the nutritional value of plant tissues, for instance
CC plant seeds or grain. The present sequence is GMA2 protein. Note: This
CC sequence is stated to be the same as that shown as SEQ ID NO:6 (AAE15582)
CC in sequence listing (page 56-57) of the specification. However the
CC sequences differ at several positions

XX Sequence 268 AA;

Query Match 63.9%; Score 39; DB 5; Length 268;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 EKVQLKGLKA 13

Db 106 EEVLQKLGQA 115

RESULT 43

AAE15308

ID AAE15308 standard; protein; 293 AA.

XX AAE15308;

XX 12-MAR-2002 (first entry)

DE Glycine max ankyrin-related protein 1 (GMA1).

KW Glycine max ankyrin-related protein; GMA1; GmsUT1; sugar transport;
 KW sucrose/proton symporter; soybean ankyrin-related protein; SAR; ANK;
 XX sugar allocation; nutritional value.
 OS Glycine max.
 FH Key Location/Qualifiers
 FT Misc-difference 3
 FT /note= "Encoded by GGT; this residue is given as Gly in
 FT the sequence shown as SEQ ID NO:4 in page 55-56 of the
 FT specification"
 FT 170..196
 FT Domain
 FT /note= "Ankyrin (ANK) repeat motif #4"
 FT 201..230
 FT Domain
 FT /note= "Ankyrin (ANK) repeat motif"
 FT 234..263
 FT Domain
 FT /note= "Ankyrin (ANK) repeat motif"
 FT 267..293
 FT Domain
 FT /note= "Ankyrin (ANK) repeat motif"
 FT Misc-difference 292..293
 FT /note= "Encoded by CTG"
 FT Misc-difference 293
 FT /note= "This residue is absent in the sequence shown as
 FT SEQ ID NO:4 in page 55-56 of the specification"
 FT FT
 PN W0200188139-A2.
 XX 22-NOV-2001.
 PD
 XX 11-MAY-2001; 2001WO-US015315.
 PF
 XX 12-MAY-2000; 2000US-0203974P.
 PR
 XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX Grimes HD, Elmer AM, Murphy KA;
 XX WPI; 2002-062385/08.
 XX N-PSDB; AAD24774.
 XX
 XX New purified protein having Glycine max ankyrin-related (GMA) protein
 XX biological activity, useful to alter GMA levels in plants to confer
 XX altered sugar transport and/or altered sugar allocation properties.
 XX
 PS Claim 1; Fig 2; 60pp; English.
 XX
 CC The invention relates to (soybean) Glycine max (Gm) ankyrin (ANK)-
 CC related proteins 1 and 2 referred to as GMA1 and GMA2 and nucleic acid
 CC molecules encoding them. GMA proteins also known as soybean ankyrin-
 CC related (SAR) proteins interact with Gm sucrose/H+ (proton) symporter
 CC designated as (SUT1). Manipulating the expression of GmsUT1 and GMA in
 CC plants is useful to confer altered sugar transport and/or altered sugar
 CC allocation properties. Alteration of GMA protein levels in plants could
 CC be used to increase the nutritional value of plant tissues, for instance
 CC plant seeds or grain. The present sequence is GMA1 protein
 XX
 SQ Sequence 293 AA;
 Query Match 63.9%; Score 39; DB 5; Length 293;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EKVQLKLGKA 13
 |:|||||:
 Db 131 EEVLKLGQA 140
 RESULT 44
 AAE15582
 ID AAE15582 standard; protein; 295 AA.
 XX
 AC AAE15582;
 XX

DT 12-MAR-2002 (first entry)
 XX
 DE Alternative version of Glycine max ankyrin-related protein 2 (GMA2).
 XX
 KW Glycine max ankyrin-related protein; GMA2; GmsUT1; sugar transport;
 KW sucrose/proton symporter; soybean ankyrin-related protein; SAR; ANK;
 XX sugar allocation; nutritional value.
 OS Glycine max.
 FH Key Location/Qualifiers
 FT Domain
 FT 145..171
 FT /note= "Ankyrin (ANK) repeat motif #4"
 FT 176..205
 FT Domain
 FT /note= "Ankyrin (ANK) repeat motif"
 FT 209..238
 FT Domain
 FT /note= "Ankyrin (ANK) repeat motif"
 FT 242..268
 FT Domain
 FT /note= "Ankyrin (ANK) repeat motif"
 FT Misc-difference 267
 FT /note= "Encoded by CTG TAG"
 FT Misc-difference 268..295
 FT /note= "These residues are absent in the sequence shown
 FT as SEQ ID NO:6 in Fig 2 of the specification"
 FT Misc-difference 268
 FT /note= "Encoded by TTG TAA"
 FT Misc-difference 288
 FT /note= "Encoded by TGG TGA"
 FT FT
 XX W0200188139-A2.
 PN
 XX 22-NOV-2001.
 PD
 XX 11-MAY-2001; 2001WO-US015315.
 PF
 XX 12-MAY-2000; 2000US-0203974P.
 PR
 XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX Grimes HD, Elmer AM, Murphy KA;
 XX WPI; 2002-062385/08.
 XX N-PSDB; AAD24775.
 XX
 XX New purified protein having Glycine max ankyrin-related (GMA) protein
 XX biological activity, useful to alter GMA levels in plants to confer
 XX altered sugar transport and/or altered sugar allocation properties.
 XX
 PS Claim 1; Page 56-57; 60pp; English.
 XX
 CC The invention relates to (soybean) Glycine max (Gm) ankyrin (ANK)-
 CC related proteins 1 and 2 referred to as GMA1 and GMA2 and nucleic acid
 CC molecules encoding them. GMA proteins also known as soybean ankyrin-
 CC related (SAR) proteins interact with Gm sucrose/H+ (proton) symporter
 CC designated as (SUT1). Manipulating the expression of GmsUT1 and GMA in
 CC plants is useful to confer altered sugar transport and/or altered sugar
 CC allocation properties. Alteration of GMA protein levels in plants could
 CC be used to increase the nutritional value of plant tissues, for instance
 CC plant seeds or grain. The present sequence is GMA2 protein. Note: This
 CC sequence is stated to be the same as that shown as SEQ ID NO:6 (AAE15309)
 CC in Fig 2 of the specification. However the sequences differ at several
 CC positions
 XX
 SQ Sequence 295 AA;
 Query Match 63.9%; Score 39; DB 5; Length 295;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EKVQLKLGKA 13
 |:|||||:
 Db 106 EEVLKLGQA 115

RESULT 45
AAU38014
ID AAU38014 standard; protein; 506 AA.
XX
AC AAU38014;
XX
DT 24-MAY-2000 (first entry)
XX
DE Streptococcus pneumoniae type 4 protein sequence #120.
XX
KW Streptococcus pneumoniae; vaccine; screening; protein antigen;
KW antibacterial; antiinflammatory; meningitis; infection; diagnosis;
KW pneumococcal disease.
XX
OS Streptococcus pneumoniae.
XX
PN WO200006737-A2.
XX
PD 10-FEB-2000.
XX
PF 27-JUL-1999; 99WO-GB002451.
XX
PR 27-JUL-1998; 98GB-00016337.
PR 19-MAR-1999; 99US-0125164P.
XX
PA (MICR-) MICROBIAL TECHNIQS LTD.
XX
PI Gilbert CFG, Hansbro PM;
XX
DR WPI; 2000-195300/17.
XX
PT New Streptococcal protein, useful as a vaccine, for diagnosis of
PT pneumococcal diseases and for screening agents capable of antagonizing or
PT inhibiting expression of the protein.
XX
PS Claim 1; Page 84; 108pp; English.
XX
CC AAU38014 to AAU38014 represent specifically claimed protein sequences
CC isolated from Streptococcus pneumoniae. AAU38014 to AAU38014 represent
CC specifically claimed nucleotide sequences isolated from S. pneumoniae.
CC The sequences have antibacterial and antiinflammatory properties. The
CC protein sequences, and fragments of them, are useful as immunogens and/or
CC antigens. The nucleotide sequences can be used in vaccines and in
CC diagnostic assays. The proteins and nucleotides can be useful for the
CC detection and diagnosis of S. pneumoniae. The protein sequences are also
CC useful for screening an agent capable of antagonising, inhibiting or
CC interfering with the function or expression of the proteins in which the
CC agent is useful for treatment or prophylaxis of S. pneumoniae infection
CC and meningitis. AAU38014 to AAU38014 represent primers used in the
CC exemplification of the present invention
XX
SQ Sequence 506 AA;
Query Match 63.9%; Score 39; DB 3; Length 506;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 KVLQKLGKA 13
DB 3 KVLQKVGKA 11
RESULT 46
AAU38014
ID AAU38014 standard; protein; 510 AA.
XX
AC AAU38014;
XX
DT 14-FEB-2002 (first entry)
XX
DE Streptococcus pneumoniae cellular proliferation protein #443.
XX

KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
OS Streptococcus pneumoniae.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS55873.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 13607; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 510 AA;
Query Match 63.9%; Score 39; DB 4; Length 510;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 KVLQKLGKA 13
DB 8 KVLQKVGKA 16
RESULT 47
AAU37881
ID AAU37881 standard; protein; 510 AA.
XX
AC AAU37881;
XX
DT 14-FEB-2002 (first entry)
XX
DE Streptococcus pneumoniae cellular proliferation protein #310.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;

KW antibacterial; drug design.
 XX Streptococcus pneumoniae.
 OS WO200170955-A2.
 PN 27-SEP-2001.
 XX
 PD
 XX
 FF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI; 2001-611495/70.
 DR N-PSDB; AAS55740.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 13474; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are *Escherichia*
 CC *coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 510 AA;
 Query Match 63.9%; Score 39; DB 4; Length 510;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 KVLQKLGKA 13
 |||||:
 Db 8 KVLQKVGKA 16
 RESULT 48
 ABU02157
 ID ABU02157 standard; protein; 510 AA.
 XX
 AC ABU02157;
 XX
 DT 23-OCT-2003 (revised)
 DT 11-FEB-2003 (first entry)
 XX
 DE S. pneumoniae type 4 strain protein from coding region #1734.
 XX Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;
 KW

KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
 XX gene therapy; vaccine.
 OS Streptococcus pneumoniae; type 4 strain.
 PN WO200277021-A2.
 XX
 PD 03-OCT-2002.
 XX
 FF 27-MAR-2002; 2002WO-IB002163.
 XX
 PR 27-MAR-2001; 2001GB-00007658.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Masignani V, Tettelin H, Fraser C;
 XX
 DR WPI; 2003-040579/03.
 DR N-PSDB; ABX07446.
 XX
 PT New proteins and nucleic acid molecules from *Streptococcus pneumoniae*,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to *Streptococcus bacteria*, such as pneumonia, sepsis, otitis media or
 PT ear infection.
 XX
 PS Claim 1; SEQ ID NO 3468; 56pp; English.
 XX
 CC The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identified DNA coding regions from the
 CC *Streptococcus pneumoniae* type 4 strain genomic sequence appearing as
 CC AB356454. Also included are an antibody which binds one of the proteins,
 CC treating a patient by administering the protein, DNA or antibody (in a
 CC composition), a kit comprising first and second primers, which are the
 CC nucleic acid cited above or fragments between nucleotides 8-100 of a
 CC sequence not defined within a *Streptococcus* nucleic acid sequence, where
 CC the first primer is substantially complementary to the target sequence
 CC and the second primer is substantially complementary to the target sequence
 CC of the target sequence, and where the parts of the primers having
 CC substantial complementarity define the termini of the target sequence to
 CC be amplified, assay comprising contacting a test compound with the
 CC protein, and determining whether the test compound binds to the protein
 CC and a *Streptococcus pneumoniae* bacterium, where one or more genes
 CC encoding the proteins has been rendered inactive. The proteins, nucleic
 CC acid molecules, antibody and compositions are useful as medicaments for
 CC treating or preventing a disease or infection due to *Streptococcus*
 CC bacteria, particularly *S. pneumoniae*, such as pneumonia, sepsis, otitis
 CC media or ear infection. They are also useful in developing vaccines,
 CC diagnostics and antibiotics. The methods are useful for identifying
 CC immunodominant proteins. The present sequence is one of the 2469 proteins
 CC expressed by the identified coding regions from the genomic sequence.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 510 AA;
 Query Match 63.9%; Score 39; DB 6; Length 510;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 KVLQKLGKA 13
 |||||:
 Db 8 KVLQKVGKA 16
 RESULT 49
 ABU46197
 ID ABU46197 standard; protein; 510 AA.

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGKA 13
 |||||:||||
 Db 8 KVLQKVGKA 16

RESULT 50
 AAU58951
 ID AAU58951 standard; protein; 80 AA.
 XX
 XX AAU58951;
 AC
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #19847.
 XX
 DE SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 XX Propionibacterium acnes.
 OS
 XX WO200181581-A2.
 XX
 XX PN
 XX
 PD 01-NOV-2001.
 XX
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PF 21-APR-2000; 2000US-0199047P.
 XX
 PR 02-JUN-2000; 2000US-0208841P.
 PR
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX
 PF Skieyi YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 XX WPI; 2001-616774/71.
 DR N-PSDB; AAS59596.
 XX
 DR
 DR
 DR
 PPT Propionibacterium acnes polypeptides and nucleic acids useful for
 PPT vaccinating against and diagnosing infections, especially useful for
 PPT treating acne vulgaris.
 XX
 XX Example 1; SEQ ID NO 20146; 1069pp; English.
 XX
 XX Sequences AAU38105-AAU68017 represent Propionibacterium acnes immunogenic
 CCC polypeptides. The proteins and their associated DNA sequences are used in
 CCC the treatment, prevention and diagnosis of medical conditions caused by
 CCC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CCC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CCC P. acnes is also involved in infections of bone, joints and the central
 CCC nervous system, however it is particularly involved in the inflammatory
 CCC lesions associated with acne vulgaris. A method for detecting the
 CCC presence or absence of P. acnes in a patient comprises contacting a
 CCC sample with a binding agent that binds to the proteins of the invention
 CCC and determining the amount of bound protein in the sample. The
 CCC polypeptides may be used as antigens in the production of antibodies
 CCC specific for P. acnes proteins. These antibodies can be used to
 CCC downregulate expression and activity of P. acnes polypeptides and
 CCC therefore treat P. acnes infections. The antibodies may also be used as
 CCC diagnostic agents for determining P. acnes presence, for example, by
 CCC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CCC this patent did not form part of the printed specification, but was
 CCC obtained in electronic format directly from WIPO at
 CCC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 80 AA;

Query Match 62.3%; Score 38; DB 4; Length 80;
 Best Local Similarity 63.6%; Pred. No. 47;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLG 11
 Db 66 RQEEVMQRLG 76

Search completed: March 4, 2004, 17:44:17
 Job time : 47.3548 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:41:21 ; Search time 13.4194 Seconds
(without alignments)
50.013 Million cell updates/sec

Title: US-10-069-540A-2_COPY_23_35
Perfect score: 61
Sequence: 1 RAEKVKLQKGA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	434	4	US-08-630-915A-22
2	61	100.0	451	1	US-08-435-454-4
3	61	100.0	451	1	US-08-652-972A-4
4	61	100.0	451	2	US-08-919-145-6
5	61	100.0	451	3	US-08-870-126-4
6	61	100.0	451	3	US-08-344-889-6
7	61	100.0	451	4	US-08-445-247-4
8	61	100.0	451	5	PCT-US96-06231A-4
9	40	85.6	502	4	US-09-252-991A-22157
10	38	62.3	128	4	US-09-134-000C-3570
11	38	62.3	427	4	US-08-065-844A-2
12	38	62.3	487	4	US-09-543-681A-5185
13	38	62.3	490	4	US-09-328-352-4282
14	38	62.3	501	4	US-09-540-236-2078
15	38	62.3	562	4	US-09-489-039A-12840
16	37	60.7	209	4	US-09-370-838-182
17	37	60.7	447	4	US-09-205-258-408
18	36	59.0	279	4	US-09-134-000C-4472
19	36	59.0	285	1	US-08-410-540-2
20	36	59.0	285	3	US-08-659-254-18
21	36	59.0	323	4	US-08-552-991A-21134
22	36	59.0	410	4	US-09-880-137-3
23	36	59.0	418	4	US-09-880-137-1
24	36	59.0	418	4	US-09-880-137-2
25	35	57.4	153	4	US-09-107-532A-6174
26	35	57.4	228	4	US-09-702-953B-10
27	35	57.4	382	4	US-09-880-137-8

28	35	57.4	399	4	US-09-107-532A-6398	Sequence 6398, Ap
29	35	57.4	409	4	US-09-880-137-4	Sequence 4, Appli
30	35	57.4	409	4	US-09-880-137-7	Sequence 7, Appli
31	35	57.4	468	4	US-09-328-352-6321	Sequence 6321, Ap
32	35	57.4	574	4	US-09-702-953B-4	Sequence 4, Appli
33	35	57.4	627	4	US-09-702-953B-3	Sequence 3, Appli
34	35	57.4	647	4	US-09-702-953B-2	Sequence 2, Appli
35	34.5	56.6	227	4	US-09-914-259-61	Sequence 61, Appl
36	34	55.7	215	4	US-09-107-532A-3730	Sequence 3730, Ap
37	34	55.7	589	4	US-09-107-532A-6086	Sequence 6086, Ap
38	33	54.1	80	2	US-08-808-277A-3	Sequence 3, Appli
39	33	54.1	80	3	US-08-746-160-3	Sequence 3, Appli
40	33	54.1	276	3	US-08-659-254-2	Sequence 2, Appli
41	33	54.1	284	2	US-08-538-360-2	Sequence 2, Appli
42	33	54.1	296	4	US-08-134-001C-4230	Sequence 4230, Ap
43	33	54.1	423	3	US-08-855-910-13	Sequence 13, Appl
44	33	54.1	427	4	US-09-134-000C-5142	Sequence 5142, Ap
45	33	54.1	464	2	US-08-477-451-18	Sequence 18, Appl
46	33	54.1	496	1	US-08-313-075A-50	Sequence 50, Appl
47	33	54.1	586	4	US-09-519-232-8	Sequence 8, Appli
48	33	54.1	822	4	US-09-107-532A-6359	Sequence 6359, Ap
49	33	54.1	826	4	US-09-543-681A-5053	Sequence 5053, Ap
50	33	54.1	1105	4	US-09-540-236-3299	Sequence 3299, Ap
51	32.5	53.3	749	4	US-09-562-737-100	Sequence 100, App
52	32	52.5	90	4	US-09-621-976-5404	Sequence 5404, Ap
53	32	52.5	96	4	US-09-636-215-827	Sequence 827, App
54	32	52.5	96	4	US-09-685-166A-827	Sequence 827, App
55	32	52.5	100	4	US-09-198-452A-1076	Sequence 1076, Ap
56	32	52.5	165	4	US-09-896-866B-13	Sequence 13, Appl
57	32	52.5	165	4	US-09-855-341-4	Sequence 4, Appli
58	32	52.5	166	4	US-09-134-000C-4121	Sequence 4121, Ap
59	32	52.5	170	4	US-09-855-341-16	Sequence 16, Appl
60	32	52.5	171	4	US-09-328-352-8227	Sequence 8227, Ap
61	32	52.5	224	4	US-09-636-215-825	Sequence 825, App
62	32	52.5	224	4	US-09-685-166A-825	Sequence 825, App
63	32	52.5	227	4	US-09-896-866B-17	Sequence 17, Appl
64	32	52.5	227	4	US-09-855-341-8	Sequence 8, Appli
65	32	52.5	310	1	US-08-363-255-6	Sequence 6, Appli
66	32	52.5	310	2	US-09-047-026A-25	Sequence 25, Appl
67	32	52.5	319	4	US-09-107-532A-4723	Sequence 4723, Ap
68	32	52.5	332	4	US-09-252-991A-30897	Sequence 30897, A
69	32	52.5	344	4	US-09-415-277C-5	Sequence 5, Appli
70	32	52.5	353	4	US-09-543-681A-5613	Sequence 5613, Ap
71	32	52.5	355	4	US-09-134-001C-3622	Sequence 3622, Ap
72	32	52.5	388	4	US-09-880-137-5	Sequence 5, Appli
73	32	52.5	388	4	US-09-880-137-6	Sequence 6, Appli
74	32	52.5	399	4	US-09-800-170-18	Sequence 18, Appl
75	32	52.5	423	4	US-09-252-991A-27261	Sequence 27261, A
76	32	52.5	427	4	US-09-107-532A-5530	Sequence 5530, Ap
77	32	52.5	442	1	US-08-363-255-4	Sequence 4, Appli
78	32	52.5	442	1	US-08-363-255-11	Sequence 11, Appl
79	32	52.5	445	1	US-08-363-255-5	Sequence 5, Appli
80	32	52.5	445	1	US-08-363-255-12	Sequence 12, Appl
81	32	52.5	453	4	US-09-134-000C-4191	Sequence 4191, Ap
82	32	52.5	486	4	US-09-733-524A-2	Sequence 2, Appli
83	32	52.5	486	4	US-09-543-681A-6439	Sequence 6439, Ap
84	32	52.5	508	4	US-09-457-040B-16	Sequence 16, Appl
85	32	52.5	517	1	US-09-134-000C-5318	Sequence 5318, Ap
86	32	52.5	577	1	US-07-820-154A-30	Sequence 30, Appl
87	32	52.5	577	2	US-08-663-566A-11	Sequence 11, Appl
88	32	52.5	577	2	US-08-097-554A-30	Sequence 30, Appl
89	32	52.5	577	2	US-08-023-610-11	Sequence 11, Appl
90	32	52.5	577	2	US-08-288-065A-11	Sequence 11, Appl
91	32	52.5	577	2	US-08-362-240A-11	Sequence 11, Appl
92	32	52.5	577	3	US-08-480-640A-30	Sequence 30, Appl
93	32	52.5	577	3	US-08-295-802-30	Sequence 30, Appl
94	32	52.5	577	3	US-08-804-372A-9	Sequence 9, Appli
95	32	52.5	577	3	US-08-488-237A-30	Sequence 30, Appl
96	32	52.5	577	4	US-08-375-992A-30	Sequence 30, Appl
97	32	52.5	577	4	US-08-472-679H-30	Sequence 30, Appl
98	32	52.5	577	5	PCT-US93-00324-30	Sequence 30, Appl
99	32	52.5	577	5	PCT-US95-10245-11	Sequence 11, Appl
100	32	52.5	577	5	PCT-US95-10245-11	Sequence 11, Appl

SEQUENCE CHARACTERISTICS:

CITY: New York

LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-454-4

Query Match 100.0%; Score 61; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQKVLQKLGKA 13
Db 21 RAQKVLQKLGKA 33

RESULT 3

US-08-652-972A-4
Sequence 4, Application US/08652972A
Patent No. 5723581

GENERAL INFORMATION:

APPLICANT: Prendergast, George C.

APPLICANT: Sakamuro, Daitoku

TITLE OF INVENTION: Murine and Human Box-Dependent

TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P O Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,972A

FILING DATE: 24-MAY-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,454

FILING DATE: 05-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST60BUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-972A-4

Query Match 100.0%; Score 61; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQKVLQKLGKA 13
Db 21 RAQKVLQKLGKA 33

RESULT 4

US-08-919-145-6

Sequence 6, Application US/08919145

Patent No. 5958753

GENERAL INFORMATION:

APPLICANT: Prendergast, George C.
TITLE OF INVENTION: Bau, A Bin1 Interacting Protein, and
TITLE OF INVENTION: Uses Therefor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,145

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/025,482

FILING DATE: 29-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kodroff, Cathy A.

REGISTRATION NUMBER: 33,980

REFERENCE/DOCKET NUMBER: WST73AUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-919-145-6

Query Match 100.0%; Score 61; DB 2; Length 451;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQKVLQKLGKA 13

Db 21 RAQKVLQKLGKA 33

RESULT 5

US-08-870-126-4

Sequence 4, Application US/08870126

Patent No. 6048702

GENERAL INFORMATION:

APPLICANT: Prendergast, George C.

APPLICANT: Sakamuro, Daitoku

TITLE OF INVENTION: Murine and Human Box-Dependent

TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P O Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/870,126

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,972
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST60CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-870-126-4

Query Match 100.0%; Score 61; DB 3; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
|||||
Db 21 RAQEKVLQKLGKA 33

RESULT 6
US-09-344-889-6
Sequence 6; Application US/09344889
Patent No. 6140465
GENERAL INFORMATION:
APPLICANT: Prendergast, George C.
TITLE OF INVENTION: Bau, A Binl Interacting Protein, and
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/919,145
FILING DATE:
APPLICATION NUMBER: US 60/025,482
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST73AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-344-889-6

Query Match 100.0%; Score 61; DB 3; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
|||||
Db 21 RAQEKVLQKLGKA 33

RESULT 7
US-09-445-247-4
Sequence 4; Application US/09445247
Patent No. 6410238
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
Sakamuro, Daitoku
TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
(Bin1) Compositions and Uses Therefor
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/445,247
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/870,126
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60DPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-445-247-4

Query Match 100.0%; Score 61; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
|||||
Db 21 RAQEKVLQKLGKA 33

RESULT 8
PCT-US96-06231A-4
Sequence 4; Application PC/TUS9606231A
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
TITLE OF INVENTION: Murine and Human Box-Dependent
Myc-Interacting Protein (Bin1) and Uses Therefor

1 NUMBER OF SEQUENCES: 7
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Howson and Howson
4 STREET: Spring House Corporate Cntr, P O Box 457
5 CITY: Spring House
6 STATE: Pennsylvania
7 COUNTRY: USA
8 ZIP: 19477
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent in Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: PCT/US96/06231A
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/435,454
21 FILING DATE: 05-MAY-1995
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Bak, Maty E.
24 REGISTRATION NUMBER: 31,215
25 REFERENCE/DOCKET NUMBER: WST60APCT
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 215-540-9200
28 TELEFAX: 215-540-5818
29 INFORMATION FOR SEQ ID NO: 4:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 451 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34 MOLECULE TYPE: protein
35 PCT-JS96-06231A-4

Query Match 100.0%; Score 61; DB 5; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 13
DB 21 RAQEKVLQKLGK 33

RESULT 9
US-09-252-991A-22157
1 Sequence 22157, Application US/09252991A
2 Patent No. 6551795
3 GENERAL INFORMATION:
4 APPLICANT: Marc J. Rubenfield et al.
5 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
6 FILE REFERENCE: 107196.136
7 CURRENT APPLICATION NUMBER: US/09/252,991A
8 PRIOR FILING DATE: 1999-02-18
9 PRIOR APPLICATION NUMBER: US 60/074,788
10 PRIOR FILING DATE: 1998-02-18
11 PRIOR APPLICATION NUMBER: US 60/094,190
12 PRIOR FILING DATE: 1998-07-27
13 NUMBER OF SEQ ID NOS: 33142
14 SEQ ID NO 22157
15 LENGTH: 502
16 TYPE: PRT
17 ORGANISM: Pseudomonas aeruginosa
18 US-09-252-991A-22157

Query Match 65.6%; Score 40; DB 4; Length 502;
Best Local Similarity 72.7%; Pred. No. 49;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLG 11
DB 110 RAQEKVFSKLG 120

RESULT 10
US-09-134-000C-3570
1 Sequence 3570, Application US/09134000C
2 Patent No. 6617156
3 GENERAL INFORMATION:
4 APPLICANT: Lynn Doucette-Stamm et al
5 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
6 FILE REFERENCE: 032798-032
7 CURRENT APPLICATION NUMBER: US/09/134,000C
8 CURRENT FILING DATE: 1998-08-13
9 PRIOR APPLICATION NUMBER: US 60/055,778
10 PRIOR FILING DATE: 1997-08-15
11 NUMBER OF SEQ ID NOS: 6812
12 SOFTWARE: Patent in version 3.1
13 SEQ ID NO 3570
14 LENGTH: 128
15 TYPE: PRT
16 ORGANISM: Enterococcus faecalis
17 US-09-134-000C-3570

Query Match 62.3%; Score 38; DB 4; Length 128;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 QEKVLQKLGK 12
DB 2 EERILQKVGK 11

RESULT 11
US-08-065-844A-2
1 Sequence 2, Application US/08065844A
2 Patent No. 6333168
3 GENERAL INFORMATION:
4 APPLICANT: Jesell, Thomas M.
5 APPLICANT: Basler, Konrad
6 APPLICANT: Yomada, Toshiya
7 TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF
8 TITLE OF INVENTION: DORSALIN-1
9 NUMBER OF SEQUENCES: 18
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Cooper & Dunham
12 STREET: 30 Rockefeller Plaza
13 CITY: New York
14 STATE: New York
15 COUNTRY: United States of America
16 ZIP: 10112
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patent in Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/065,844A
24 FILING DATE: 19930520
25 CLASSIFICATION: 424
26 ATTORNEY/AGENT INFORMATION:
27 NAME: White, John P.
28 REGISTRATION NUMBER: 28,678
29 REFERENCE/DOCKET NUMBER: 0576/40314
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (212) 977-9550
32 TELEFAX: (212) 664-0525
33 TELEX: 422523 COOP U
34 INFORMATION FOR SEQ ID NO: 2:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 427 amino acids
37 TYPE: amino acid
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein

US-08-065-844A-2

Query Match 62.3%; Score 38; DB 4; Length 427;
Best Local Similarity 80.0%; Pred. No. 91;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 QAEKVLQKLGK 12
Db 282 QESVNLKLGK 291

RESULT 12

US-09-543-681A-5185
; Sequence 5185, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5185
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5185

Query Match 62.3%; Score 38; DB 4; Length 487;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
Db 67 KAQEKVFHQLGR 78

RESULT 13

US-09-328-352-4282
; Sequence 4282, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4282
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4282

Query Match 62.3%; Score 38; DB 4; Length 490;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
Db 89 KAQEKVFSELGR 100

RESULT 14

US-09-540-236-2078
; Sequence 2078, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2078
; LENGTH: 501
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2078

Query Match 62.3%; Score 38; DB 4; Length 501;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
Db 99 KAQEKVFSELGR 110

RESULT 15

US-09-489-039A-12840
; Sequence 12840, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12840
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12840

Query Match 62.3%; Score 38; DB 4; Length 562;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
Db 142 KAQEKVFHQLGR 153

RESULT 16

US-09-370-838-182
; Sequence 182, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Monamath, Roadoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-182

Query Match 60.7%; Score 37; DB 4; Length 209;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQEKVLQKLG 11
|:|||||
Db 141 AREKVLQTLG 150

RESULT 17
US-09-205-258-408
; Sequence 408, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 408
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (447)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-408

Query Match 60.7%; Score 37; DB 4; Length 447;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQEKVLQKLG 11
|:|||||
Db 378 AREKVLQTLG 387

RESULT 18
US-09-134-000C-4472
; Sequence 4472, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4472
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4472

Query Match 59.0%; Score 36; DB 4; Length 279;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;


```

QY 3 QEKVLQKLG 11
Db 9 QEKIIQELG 17

RESULT 19
US-08-410-540-2
; Sequence 2, Application US/08410540
; Patent No. 5807678
; GENERAL INFORMATION:
; APPLICANT: Miller, Walter L.
; APPLICANT: Lin, Dong
; APPLICANT: Straus, III, Jerome F.
; TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
; TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,540
; FILING DATE: 23-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-238/000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 853 5070
; TELEFAX: 415 857 0663
; TELEX: 380816CCOLEYPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-410-540-2

Query Match 59.0%; Score 36; DB 1; Length 285;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGK 12
Db 155 KVLQKIGK 162

RESULT 20
US-08-659-254-18
; Sequence 18, Application US/08659254
; Patent No. 6194555
; GENERAL INFORMATION:
; APPLICANT: Stocco, Douglas M.
; APPLICANT: Clark, Dr. Barbara J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
; TITLE OF INVENTION: OF STEROIDOGENESIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue
; CITY: Austin
; STATE: TX
; COUNTRY: U.S.A.

Query Match 59.0%; Score 36; DB 1; Length 285;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGK 12
Db 155 KVLQKIGK 162

RESULT 20
US-08-659-254-18
; Sequence 18, Application US/08659254
; Patent No. 6194555
; GENERAL INFORMATION:
; APPLICANT: Stocco, Douglas M.
; APPLICANT: Clark, Dr. Barbara J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION
; TITLE OF INVENTION: OF STEROIDOGENESIS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.
; STREET: 1900 Frost Bank Plaza, 816 Congress Avenue
; CITY: Austin
; STATE: TX
; COUNTRY: U.S.A.

Query Match 59.0%; Score 36; DB 1; Length 285;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGK 12
Db 155 KVLQKIGK 162

RESULT 21
US-09-252-991A-21134
; Sequence 21134, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21134
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21134

Query Match 59.0%; Score 36; DB 4; Length 323;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
Db 15 RSQDEVAERLGQA 27

RESULT 22
US-09-880-137-3
; Sequence 3, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel

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; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,254
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/538,960
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: 43375.0006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/499-6200
; TELEFAX: 512/499-6290
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-659-254-18

Query Match 59.0%; Score 36; DB 3; Length 285;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGK 12
Db 155 KVLQKIGK 162

RESULT 21
US-09-252-991A-21134
; Sequence 21134, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21134
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21134

Query Match 59.0%; Score 36; DB 4; Length 323;
Best Local Similarity 46.2%; Pred. No. 1.5e+02;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
Db 15 RSQDEVAERLGQA 27

RESULT 22
US-09-880-137-3
; Sequence 3, Application US/09880137
; Patent No. 6640025
; GENERAL INFORMATION:
; APPLICANT: Berstein, Gabriel

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RESULT 6
Q9UKN4 PRELIMINARY; PRT; 564 AA.
AC Q9UKN4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Bridging integrator-2.
GN BIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20366138; PubMed=10903846;
RA Ge X., Fendergast G.C.;
RT "Bin2, a Functionally Nonredundant Member of the BAR Adaptor Gene
RT Family.";
RL Genomics 67:210-220(2000).
DR EMBL; AF146531; AAS4227.1; -.
DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 564 AA; 61747 MW; 3CB3791A56CE53BC CRC64;

Query Match 100.0%; Score 61; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 23 RAQEKVLQKLGKA 35

RESULT 7
Q9UBW5 PRELIMINARY; PRT; 565 AA.
AC Q9UBW5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Breast cancer associated protein BRAP1.
GN BRAP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Miki Y., Saito H.;
RT "Genomic structure and chromosome location of the BRAP1 gene.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032710; BAA88125.1; -.
DR EMBL; AB032699; BAA88125.1; JOINED.
DR EMBL; AB032700; BAA88125.1; JOINED.
DR EMBL; AB032701; BAA88125.1; JOINED.
DR EMBL; AB032702; BAA88125.1; JOINED.
DR EMBL; AB032703; BAA88125.1; JOINED.
DR EMBL; AB032704; BAA88125.1; JOINED.
DR EMBL; AB032705; BAA88125.1; JOINED.
DR EMBL; AB032706; BAA88125.1; JOINED.
DR EMBL; AB032707; BAA88125.1; JOINED.
DR EMBL; AB032708; BAA88125.1; JOINED.
DR EMBL; AB032709; BAA88125.1; JOINED.
DR EMBL; AB032698; BAA88108.1; -.

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DR Genew; HGNC:1053; BIN2.
DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 565 AA; 61902 MW; 28D1FB89A7779860 CRC64;

Query Match 100.0%; Score 61; DB 4; Length 565;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 23 RAQEKVLQKLGKA 35

RESULT 8
Q86VVO PRELIMINARY; PRT; 565 AA.
AC Q86VVO;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Breast cancer associated protein BRAP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Ovary;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047686; AAH47686.1; -.
DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 565 AA; 61875 MW; B1D1FB89A7707EA3 CRC64;

Query Match 100.0%; Score 61; DB 4; Length 565;

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Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 23 RAQEKVLQKLGKA 35

RESULT 9
Q7QF7 PRELIMINARY; PRT; 686 AA.
AC Q7QF7;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054718; AAH54718.1; -
KW Hypothetical protein.
SQ SEQUENCE 686 AA; 75013 MW; D292E24653A442A5 CRC64;

Query Match 100.0%; Score 61; DB 11; Length 686;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 19 RAQEKVLQKLGKA 31

RESULT 10
Q8N4G0 PRELIMINARY; PRT; 695 AA.
AC Q8N4G0;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Amphiphysin (Stiff-Man syndrome with breast cancer 128KD
DE autoantigen).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; BC034376; AAH34376.1; -
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR003017; Amphiphysin_1.
DR InterPro; IPR006532; BAR.
DR InterPro; IPR004148; BAR_dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD003208; Amphiphysin_1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 695 AA; 76229 MW; 4FC92E8B028BBFE CRC64;

Query Match 100.0%; Score 61; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 19 RAQEKVLQKLGKA 31

RESULT 11
Q803I3 PRELIMINARY; PRT; 524 AA.
AC Q803I3;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Similar to bridging integrator 2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044473; AAH44473.1; -
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006532; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 524 AA; 59280 MW; F4A2988732D153FF CRC64;

Query Match 93.4%; Score 57; DB 13; Length 524;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
DB 31 RAQEKVLQKLGK 42
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RESULT 12
Q8WQ54 ID Q8WQ54 PRELIMINARY; PRT; 414 AA.
AC Q8WQ54; 2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Putative aggregation factor.
GN GPCVAF.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA Schutze J., Kraso A., Diehl-Seifert B., Mueller W.E.G.;
RT "Cloning and Expression of the Putative Aggregation Factor from the
RT Marine Sponge Geodia cydonium."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ311598; CAC89970.1; -
DR GO; GO:0006897; P:cytoskeleton; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; PS50002; SH3; 1.
SQ SEQUENCE 414 AA; 46558 MW; 90CABDAB20152310 CRC64;

Query Match 80.3%; Score 49; DB 5; Length 414;
Best Local Similarity 69.2%; Pred. No. 2.8;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
Db 30 RVQEKMMQKLGKS 42

RESULT 13
Q9Y092 ID Q9Y092 PRELIMINARY; PRT; 602 AA.
AC Q9Y092;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Amphiphysin protein (LD19810P).
GN AMPH OR CG8604.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Berkely;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchman M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

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Query Match 77.0%; Score 47; DB 5; Length 602;

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Best Local Similarity 75.0%; Pred. No. 8.9;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
DB 19 RAKEKILQNLGK 30

RESULT 14
Q9FE28 PRELIMINARY; PRT; 461 AA.
ID C9FE28;
AC C9FE28;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P005A05.3 protein (P0436E04.22 protein).
GN P005A05.3 OR P0436E04.22.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone:P005A05.3";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone:P0436E04.22";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002863; BAB16899.1; -
DR EMBL; AP002818; BAB16339.1; -
DR Gramene; Q9FE28; -
SQ SEQUENCE 461 AA; 51281 MW; B5BCP4085F4EC37C CRC64;

Query Match 67.2%; Score 41; DB 10; Length 461;
Best Local Similarity 61.5%; Pred. No. 77;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 145 RLKKAQLQKLGKA 157

RESULT 15
P94544 PRELIMINARY; PRT; 570 AA.
ID P94544;
AC P94544;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein yshc.
GN YSHC.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97217425; PubMed=9063446;
RA Goethel S.F., Schmid R., Wipat A., Carter N.M., Emerson P.T.,
RA Harwood C.R., Marahel M.A.;
RT "An internal PK506-binding domain is the catalytic core of the prolyl
RT isomerase activity associated with the Bacillus subtilis trigger
RT factor.";
RL Eur. J. Biochem. 244:59-65(1997).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz S., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.W., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Toato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; 275208; CAA99568.1; -
DR EMBL; 299118; CABI4819.1; -
DR PIR; C69985; C69985.
DR HSSP; P06766; 13PB.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR002054; DNA_polX.
DR InterPro; IPR004013; PHP_C.
DR InterPro; IPR003141; PHP_N.
DR Pfam; PF02811; PHP_C; 1.
DR Pfam; PF02231; PHP_N; 1.
DR SMART; SM00481; POLI1AC; 1.
DR SMART; SM00483; POLXc; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 570 AA; 64119 MW; 06AEA028BFA3D3F5 CRC64;

Query Match 67.2%; Score 41; DB 16; Length 570;
Best Local Similarity 53.8%; Pred. No. 95;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 134 KSEKILQALGEA 146

RESULT 16
Q8ESM0 PRELIMINARY; PRT; 651 AA.
ID Q8ESM0;
AC Q8ESM0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN GBS0962.

```

OS Streptococcus agalactiae (serotype III).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216495;
 RN [1];

RP SEQUENCE FROM N.A.
 RC STRAIN=NEM316 / Serotype III;
 RX MEDLINE=22242508; PubMed=12354221;
 RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
 RA Meadek T., Zouine M., Couve E., Laliou L., Poyart C., Trieu-Cuot P.,
 RA Kunst F.,
 RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
 RT invasive neonatal disease."
 RL Mol. Microbiol. 45:1459-1513 (2002).
 DR EMBL; AL766848; CAD46621.1; -.
 DR Sagalish; gbs0962; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003838; DUF214.
 DR Pfam; PF02687; FtsX; 1.
 KW Hypothetical protein, Complete proteome.
 SQ SEQUENCE 651 AA; 74102 MW; 1383BB8A214335C5 CRC64;

Query Match 67.2%; Score 41; DB 16; Length 651;
 Best Local Similarity 63.6%; Pred. No. 1.1e+02;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 QEKVLQKLGKA 13

Db 334 EKKLKLKLGKS 344

RESULT 17

Q8DX0 PRELIMINARY; PRT; 651 AA.

ID Q8DX0;
 AC Q8DX0;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE ABC transporter, permease protein, putative.
 GN SAG0975.

OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1];

RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=2222988; PubMed=12200547;
 RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarcelli M., Mora M.,
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
 RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;

"Complete genome sequence and comparative genomic analysis of an
 emerging human pathogen, serotype V Streptococcus agalactiae."
 Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL; AE014236; AAM99858.1; -.

DR TIGR; SAG0975; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003838; DUF214.
 DR Pfam; PF02687; FtsX; 1.
 KW Complete proteome.

SQ SEQUENCE 651 AA; 74016 MW; A782A8A2143FDA8 CRC64;

Query Match 67.2%; Score 41; DB 16; Length 651;
 Best Local Similarity 63.6%; Pred. No. 1.1e+02;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 QEKVLQKLGKA 13

Db 334 EKKLKLKLGKS 344

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RESULT 18

Q84PY5 PRELIMINARY; PRT; 874 AA.

ID Q84PY5;
 AC Q84PY5;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE P0443G08.4 protein.
 GN P0443G08.4.

OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;

RN [1];

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC
 RT clone:P0443G08.4";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004461; BAC64982.1; -.
 SQ SEQUENCE 874 AA; 97030 MW; C1AD2927BB2554D6 CRC64;

Query Match 67.2%; Score 41; DB 10; Length 874;
 Best Local Similarity 61.5%; Pred. No. 1.4e+02;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RAQKVLQKLGKA 13

Db 145 RLKRLKQKMGKA 157

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RESULT 19

Q943V8 PRELIMINARY; PRT; 876 AA.

ID Q943V8;
 AC Q943V8;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE B1146B04.1 protein (B115IH08.15 protein).
 GN B1146B04.1 OR B115IH08.15.

OS Oryza sativa (Rice), and

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzae; Oryza.
 OX NCBI_TaxID=4530, 39947;

RN [1];

RP SEQUENCE FROM N.A.

RC SPECIES=O. sativa; STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
 RT clone:B1146B04.1";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2];

RP SEQUENCE FROM N.A.

RC SPECIES=O. sativa (japonica cultivar-group); STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
 RT clone:B115IH08.15";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003205; BAB64572.1; -.

DR Gramene; Q943V8; -.

SQ SEQUENCE 876 AA; 97403 MW; 4BFA6DF145ACC814 CRC64;

Query Match 67.2%; Score 41; DB 10; Length 876;
 Best Local Similarity 61.5%; Pred. No. 1.4e+02;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGKA 13
 Db 145 RLKRALQKMGKA 157

RESULT 20

Q7XXG7 PRELIMINARY; PRT; 876 AA.
 AC Q7XXG7;
 DT 01-OCT-2003 (TREMELrel. 25, Created)
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE OSJNB0089K24.1 protein.
 GN OSJNB0089K24.1
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
 RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
 RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
 RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
 RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
 RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
 RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
 RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
 RA Zhang R.Q., Guan J.P., Hong G.P.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL606509; CAD39392.1; --
 SQ SEQUENCE 876 AA; 97416 MW; 94D8EDF9DF37475 CRC64;

Query Match 67.2%; Score 41; DB 10; Length 876;
 Best Local Similarity 61.5%; Pred. No. 1.4e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13

Db 145 RLKRALQKMGKA 157

RESULT 21

Q8SX64 PRELIMINARY; PRT; 1235 AA.
 AC Q8SX64;
 DT 01-JUN-2002 (TREMELrel. 21, Created)
 DT 01-OCT-2003 (TREMELrel. 21, Last sequence update)
 DE LD40094p.
 GN CG12734.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan X., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY094827; AAU1180.1; --
 DR FlyBase; FBgn0035411; CG12734.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002017; Spectrin.
 DR PROSITE; PS00190; CYTOCHROME C; 1.
 SQ SEQUENCE 1235 AA; 142401 MW; C7C813ECBD86C58A CRC64;

Query Match 67.2%; Score 41; DB 5; Length 1235;
 Best Local Similarity 81.8%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QEKVLQKLGKA 13

Db 663 QSKELQKLGKA 673

RESULT 22

O9VZT7 PRELIMINARY; PRT; 1381 AA.
 AC O9VZT7;
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE CG12734 protein.
 GN CG12734.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gall R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Galbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mozhayeva A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Nusskern D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Palazzi M., Pan S., Pohlman J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AS003477; AAF47730.1; --
 DR HSSP; P03069; IYSA.
 DR FlyBase; FBgn0035411; CG12734.


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DR InterPro: IPR002017; Spectrin.
SQ SEQUENCE 1381 AA; 157512 MW; 2A75A71D74DD44E5 CRC64;

Query Match 67.2%; Score 41; DB 5; Length 1381;
Best Local Similarity 81.8%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QEKVLQKLGKA 13
Db 663 QSEKVLQKLGKA 673

RESULT 23
QSRWL3 ID QSRWL3 PRELIMINARY; PRT; 176 AA.
AC QSRWL3
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein DR0653.
GN DR0653.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=R1 / ATCC 13939 / DSM 20539 / NCBI 9279;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.; Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.;
RL Science 286:1571-1577 (1999).
RL EMBL; AE001922; RAF10228.1; -.
DR PIR; B75494; B75494.
DR TIGR; DR0653; -.
DR GO; GO:0008080; F.N-acetyltransferase activity; IEA.
DR InterPro: IPR000182; GCN5acetyl_trans.
DR InterPro: IPR001092; HLH basic.
DR Pfam; PF00563; Acetyltransf; 1.
DR PROSITE; PS00038; HLH 1; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 176 AA; 19099 MW; 1B4A7EC9E1D5EC3B CRC64;

Query Match 65.6%; Score 40; DB 16; Length 176;
Best Local Similarity 61.5%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
Db 144 RASERVLEKIGFA 156

RESULT 24
QSR132 ID QSR132 PRELIMINARY; PRT; 502 AA.
AC QSR132
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Putative aminopeptidase.
GN TW261.
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=218496;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=22495039; PubMed=12606174;
RA Bentley S.D., Mairwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrell B.G., Parkhill J., Relman D.A.;
RT "Sequencing and analysis of the genome of the Whipple's disease
RT bacterium Tropheryma whipplei.";
RL Lancet 361:637-644 (2003).
DR EMBL; BX251410; CAD6937.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR008330; Ctsl_aminptdase_B.
DR InterPro: IPR000819; Peptidase_M17_C.
DR InterPro: IPR008283; Peptidase_M17_N.
DR Pfam; PF00883; Peptidase_M17; 1.
DR 2fam; PF02789; Peptidase_M17_N; 1.
DR PRINTS; PR00481; LAVNOPPTDASE.
DR PROSITE; PS00631; CYTOSOL_AP; 1.
DR PIRSF; PIRSF036388; Ctsl_aminptdase_B; 1.
KW Aminopeptidase; Complete proteome.
SQ SEQUENCE 502 AA; 53336 MW; 5249BEC6BD06C73 CRC64;

Query Match 63.9%; Score 39; DB 16; Length 502;
Best Local Similarity 72.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLG 11
Db 42 RAYEDILQKLG 52

RESULT 25
Q97PE5 ID Q97PE5 PRELIMINARY; PRT; 505 AA.
AC Q97PE5
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE PTS system, IIBC components.
GN SPI684.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radure D.,
RA Holtzapf E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Anguoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506 (2001).
RL EMBL; AE007461; AAK75763.1; -.
DR PIR; B95196; B95196.
DR TIGR; SPI684; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005351; P:sugar porter activity; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro: IPR001936; Ptrans_EIIB.
DR InterPro: IPR003352; Ptrans_EIIC.
DR Pfam; PF00367; PTS_EIIB; 1.
DR 2fam; PF02378; PTS_EIIC; 1.
DR TIGRfams; TIGR00826; EIIB_glc; 1.

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KW Complete proteome.
 SQ SEQUENCE 505 AA; 54470 MW; 5E6A20E3C6DAD89E CRC64;
 Query Match 63.9%; Score 39; DB 16; Length 505;
 Best Local Similarity 88.9%; Pred. No. 1.9e+02;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGKA 13
 |||||:
 3 KVLQKVGKA 11

Db
 |||||:
 3 KVLQKVGKA 11

RESULT 26
 Q8DN7 PRELIMINARY; PRT; 510 AA.
 AC Q8DN7; 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Phosphotransferase system sugar-specific EII component [EC
 2.7.1.69]
 DE 2.7.1.69)
 GN PTS-EII OR SPR1528.
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1711101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21429245; PubMed=11544234;
 RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
 RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
 RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
 RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 RA McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
 RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
 RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
 RA Glass J.I.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717(2001).
 RL EMBL; AB008521; AAL0032.1; -;
 DR PIR; G98062; G98062.
 DR DR; GO:0016020; C:membrane; IEA.
 DR GO; GO:0003551; F:sugar porter activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001996; P:trans_EIIB.
 DR InterPro; IPR003352; P:trans_EIIC.
 DR Pfam; PF00367; P:trans_EIIB; 1.
 DR Pfam; PF02378; P:trans_EIIC; 1.
 DR TIGRFAMs; TIGR00826; E:IB_glc; 1.
 SW Transferase; Complete proteome.
 SQ SEQUENCE 510 AA; 55033 MW; 5A34BA199F15DF33 CRC64;
 Query Match 63.9%; Score 39; DB 16; Length 510;
 Best Local Similarity 88.9%; Pred. No. 1.9e+02;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGKA 13
 |||||:
 8 KVLQKVGKA 16

Db
 |||||:
 8 KVLQKVGKA 16

RESULT 27
 Q8RN7 PRELIMINARY; PRT; 513 AA.
 AC Q8RN7; 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein TTS0779.
 GN TTS0779.

OS Thermoanaerobacter tengcongensis.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.
 NCBI_TaxID=119072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MB4 / JCM 11007;
 RX MEDLINE=2192816; PubMed=11997336;
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.,
 RA "A complete sequence of T. tengcongensis genome.";
 RL Genome Res. 12:689-700(2002).
 DR EMBL; AF013045; AAM24036.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 513 AA; 56120 MW; 3B91AE6C63402894 CRC64;
 Query Match 63.9%; Score 39; DB 16; Length 513;
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQKVLQKLGK 12
 |||||:
 388 RIREKILEKTKG 399

Db
 |||||:
 388 RIREKILEKTKG 399

RESULT 28
 Q42701 PRELIMINARY; PRT; 516 AA.
 AC Q42701; 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome P450 (Fragment).
 GN CYP72C.
 OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vinaceae;
 OC Catharanthus
 NCBI_TaxID=4058;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cp3;
 RA Mangold U., Bichel J., Batschauer A., Lanz T., Kaiser T.,
 RA Spangenberg G., Werck-Reichhart D., Schroeder J.;
 RT "Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from
 Catharanthus roseus, and transgenic expression in tobacco and
 Arabidopsis thaliana.";
 RL Plant Sci. 96:129-136(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cp3;
 RA Joachim Schroeder;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; L19075; AAA17746.1; -;
 DR PIR; T10000; T10000.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PS00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 DR Heme; Monooxygenase; Oxidoreductase.
 KW NON TER
 FT NON TER
 SQ SEQUENCE 516 AA; 59720 MW; 02A7D9B0936D931P CRC64;
 Query Match 63.9%; Score 39; DB 10; Length 516;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQKVLQKLGK 12

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Db          346 RAREEVLQAFGK 357
|||||
RESULT 29
ID Q83G32 PRELIMINARY; PRT; 522 AA.
AC Q83G32;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Aminopectidase A/I (EC 3.4.11.1).
DE PPBP OR TWT501.
GS Tropheryma whipplei (strain Twist) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinomycetales;
OC Micrococineae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267;
RN [1]
RP SEQUENCE FROM N.A.
RA Raoult D., Audic S., Robert C., Ogata H., Suhre K., Drancourt M.,
RA Claverie J.-M.;
RA "Tropheryma whipplei illustrates the diversity of gene loss patterns
RT in small genome bacterial pathogens.";
RT Submitted (JUL-2002) to the EMBL/GenBank/DDBB databases.
RL EMBSI; AE016851; AAO44598.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004178; F:leucyl aminopeptidase activity; IEA.
DR CO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008330; Ctsl_ammptdse_B.
DR InterPro; IPR000819; Peptidase_M17_C.
DR InterPro; IPR008283; Peptidase_M17_N.
DR Pfam; PF00883; Peptidase_M17; I._N.
DR Pfam; PF02789; Peptidase_M17_N; 1.
DR PRINTS; PR00481; LAMNOPTDASE.
DR PROSITE; PS00631; CYTOSOL_AP; 1.
DR PIRSF; PIRSF036388; Ctsl_ammptdse_B; 1.
KW Hydrolase; Aminopeptidase; Complete proteome.
SQ SEQUENCE 522 AA; 55712 MW; CACBF8161657D726 CRC64;

Query Match 63.98; Score 39; DB 16; Length 522;
Best Local Similarity 72.7%; Pred.No. 2e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps

QY 1 RAQEKVQLKLQ 11
|||:|||
DB 62 RAYEDIQLKG 72

RESULT 30
ID Q42700 PRELIMINARY; PRT; 524 AA.
AC Q42700;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome P450.
GS CYP72B.
OC Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
OC Catharanthus..
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Cp3;
RA Mangold U., Bichel J., Batschauer A., Lanz T., Kaiser T.,
RA Spangenberg G., Werck-Reichhart D., Schroeder J.;
RA "Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from
RT Catharanthus roseus, and transgenic expression in tobacco and
RT Arabidopsis thaliana.";
RT Plant Sci. 96:129-136(1994).

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RESULT 32

Q9BS66 ID Q9BS66 PRELIMINARY; PRT; 88 AA.
 AC Q9BS66
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Similar to epilepsy, progressive myoclonus type 2, Lafora disease (Laforin).
 DE Laforin.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005286; AA05286.1; -.
 DR GO; GO:0004721; F:protein phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000387; TYR phosphatase.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 SQ SEQUENCE 88 AA; 9933 MW; D28FAB18CC285D07 CRC64;

Query Match 62.3%; Score 38; DB 4; Length 88;
 Best Local Similarity 66.7%; Pred. No. 53;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12

Db 69 RAQEDFFQKFGK 80

RESULT 33

Q8IU96 ID Q8IU96 PRELIMINARY; PRT; 193 AA.
 AC Q8IU96
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Laforin.
 GN EPM2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Ganesh S., Yamakawa K.;
 RL "Cloning of differentially spliced transcripts of the EPM2A gene."
 DR EMBL; AF454492; AA015524.1; -.
 DR EMBL; AF454493; AA015525.1; -.
 DR GO; GO:0008138; F:protein tyrosine/serine/threonine phosphatase...; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS phosphatase.
 DR InterPro; IPR000387; TYR phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 SQ SEQUENCE 193 AA; 22160 MW; 3DC9436A9885B915 CRC64;

Query Match 62.3%; Score 38; DB 4; Length 193;
 Best Local Similarity 66.7%; Pred. No. 11e+02;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12

Db 174 RAQEDFFQKFGK 185

RESULT 34

Q9UEN2 ID Q9UEN2 PRELIMINARY; PRT; 250 AA.
 AC Q9UEN2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE LAPTase (Fragment).
 DE LAPTase (Fragment).
 GN EMP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Serracosa J.M., Gomez-Garre P., Gallardo E., Anta B.,
 RA Beltran-Valero de Bernabe D., Lindhout D., Augustin P.B.,
 RA Tassinari C., Michelucci R., Malafosse A., Topcu M., Grid D.,
 RA Dravet C., Berkevic S., Rodriguez de Cordoba S.;
 RT "A novel protein tyrosine phosphatase gene is mutated in progressive myoclonus epilepsy of the Lafora type (EPM2).";
 RL Hum. Mol. Genet. 8:0-0(1999).
 DR EMBL; AJ130763; CAA10199.1; -.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0008138; F:protein tyrosine/serine/threonine phosphatase...; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR000340; DS_Phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR Pfam; PF00782; DSPC; 1.
 DR PRODOM; PD001568; CBD_4; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
 FT NON TER
 SQ SEQUENCE 250 AA; 28750 MW; 6AA1913D31F2A8E3 CRC64;

Query Match 62.3%; Score 38; DB 4; Length 250;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12

Db 231 RAQEDFFQKFGK 242

RESULT 35

Q8IX25 ID Q8IX25 PRELIMINARY; PRT; 257 AA.
 AC Q8IX25
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Laforin (Fragment).
 GN EPM2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Ganesh S., Yamakawa K.;
 RL "Cloning of differentially spliced transcripts of the EPM2A gene."
 DR EMBL; AF454491; AA015523.1; -.
 DR GO; GO:0008138; F:protein tyrosine/serine/threonine phosphatase...; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000340; DS phosphatase.
 DR InterPro; IPR000387; TYR phosphatase.
 DR SMART; SM00195; DSPC; 1.
 DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

DR PROSITE; PSS0054; TYR_PHOSPHATASE_DUAL; 1.
 FT NON_TER 1
 SQ SEQUENCE 257 AA; 29473 MW; BB3BEEB5C9E1E4CE CRC64;
 Query Match 62.3%; Score 38; DB 4; Length 257;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGK 12
 DB 238 RAQEDFFQKFGK 249
 RESULT 36
 Q8TT25 PRELIMINARY; PRT; 300 AA.
 AC Q8TT25;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE 3-hydroxyisobutyrate dehydrogenase.
 GN MA0614.
 OS Methanobacteria acetivorans.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanobacteriales; Methanobacteriaceae; Methanobacterina.
 CX NCBI_TaxID=2214;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nuebaum C., Roy A., Endrizzi M.G., Macdonald P.,
 RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
 RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
 RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Fitchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanobacterina acetivorans reveals extensive metabolic
 RT and physiological diversity.";
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AE010722; BAM04058.1;
 DR GO; GO:0004616; P:phosphogluconate dehydrogenase (decarboxyla. . .; IEA.
 DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
 DR InterPro; IPR006193; 6PGD.
 DR Pfam; PF03446; NAD binding 2; 1.
 DR PRINTS; PR00076; 6PGDHRGNASE.
 KW Complete proteome.
 SQ SEQUENCE 300 AA; 32287 MW; FB1B7A8A98A8E8A7E CRC64;
 Query Match 62.3%; Score 38; DB 17; Length 300;
 Best Local Similarity 61.5%; Pred. No. 1.7e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGKA 13
 DB 153 RKHKPLNKLKGS 165
 RESULT 37
 O95278 PRELIMINARY; PRT; 331 AA.
 AC O95278;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE LAFORIN (PROGRESSIVE MYOCLONUS epilepsy type 2).
 GN EPM2A.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=98442653; PubMed=9771710;
 RA Minassian B.A., Lee J.R., Herbrick J.A., HuiZenga J., Soder S.,
 RA Mubgall A.J., Dunham I., Gardner R., Fong C.Y., Carpenter S.,
 RA Jardim L., Satishchandra P., Andermann E., Shead O.C. III,
 RA Lopes-Cendes I., Tsui L.C., Delgado-Escueta A.V., Rouleau G.A.,
 RA Scherer S.W.;
 RT "Mutations in a gene encoding a novel protein tyrosine phosphatase
 RT cause progressive myoclonus epilepsy.";
 RL Nat. Genet. 20:171-174(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lee J.R., Scherer S.W.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Minassian B.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX PubMed=11001928;
 RA Ganesh S., Agarwala K.I., Ueda K., Akagi T., Shoda K., Usui T.,
 RA Hashikawa T., Osada H., Delgado-Escueta A.V., Yamakawa K.;
 RT "Laforin, defective in the progressive myoclonus epilepsy of Lafora
 RT type, is a dual-specificity phosphatase associated with
 RT polyribosomes.";
 RL Hum. Mol. Genet. 9:2251-2261(2000).
 DR EMBL; AF084535; AAC83347.2; -.
 DR EMBL; AF284580; AAG18377.1; -.
 DR Genbank; HGNC:3413; EPM2A.
 DR GO; GO:0003824; P:catalytic activity; IEA.
 DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphatase. . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR002044; CBD 4.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000340; DS_phosphatase.
 DR Pfam; PF00782; DSPc; 1.
 DR ProDom; PD001568; CBD 4; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
 DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
 SQ SEQUENCE 331 AA; 37157 MW; DD79F917262AB458 CRC64;
 Query Match 62.3%; Score 38; DB 4; Length 331;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGK 12
 DB 312 RAQEDFFQKFGK 323
 RESULT 38
 Q7T2D2 PRELIMINARY; PRT; 408 AA.
 AC Q7T2D2;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 CX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22386257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A.C., Young J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

SEQUENCE FROM N.A.

RC TISSUE-Kidney;

RA Strausberg R.;

DL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC054595; AAH54595.1; -

KW Hypothetical protein.

SQ SEQUENCE 408 AA; 46057 MW; DCC7PE40A8E67A00 CRC64;

Query Match 62.3%; Score 38; DB 13; Length 408;
 Best Local Similarity 58.3%; Pred. No. 2.3e+02;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12

DB 100 RLQERLLKLGK 111

RESULT 39

Q89AC2 PRELIMINARY; PRT; 445 AA.

AC Q89AC2;

DT 01-JUN-2003 (TRENBLrel. 24, Created)

DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN YLEA OR BHP392.

OS Buchnera aphidicola (subsp. Baizongia pistaciae).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Buchnera.

OX NCBI_TaxID=135842;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2425901; PubMed=1252265;

RA Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

RA Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

RA Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.,

RT "Reductive genome evolution in Buchnera aphidicola.",

RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).

DR EMBL; AE014017; RA027104.1; -

DR InterPro; IPR007197; Radical SAM.

DR InterPro; IPR002792; TRAM.

DR InterPro; IPR005839; UPF0004.

DR Pfam; PF04055; Radical SAM; 1.

DR Pfam; PF01938; TRAM; 1.

DR Pfam; PF00919; UPF0004; 1.

DR PROSITE; PS01278; UPF0004; 1.

DR Hypothetical protein; Complete proteome.

KW SEQUENCE 445 AA; 51265 MW; 55B5F5BF3BCEIDE CRC64;

SQ SEQUENCE 445 AA; 51265 MW; 55B5F5BF3BCEIDE CRC64;

Query Match 62.3%; Score 38; DB 16; Length 445;

Best Local Similarity 59.3%; Pred. No. 2.5e+02;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12

DB 100 RLQERLLKLGK 111

QY 1 RAQEKVLQKLGK 12

DB 55 KAQEKVFLQGR 66

RESULT 40

Q89J99 PRELIMINARY; PRT; 452 AA.

AC Q89J99;

DT 01-OCT-2002 (TRENBLrel. 22, Created)

DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Hypothetical protein XAC2461.

GN XAC2461.

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=305 / ATCC 13902 / XV 101;

RX MEDLINE=2202145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formigueri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities.",

RL Nature 417:459-463(2002).

DR EMBL; AE011883; AA037312.1; -

DR InterPro; IPR006463; M1AB_methylase.

DR InterPro; IPR007197; Radical SAM.

DR InterPro; IPR002792; TRAM.

DR InterPro; IPR005839; UPF0004.

DR Pfam; PF04055; Radical SAM; 1.

DR Pfam; PF01938; TRAM; 1.

DR Pfam; PF00919; UPF0004; 1.

DR TIGRFAMs; TIGR01574; m1AB-methylase; 1.

DR TIGRFAMs; TIGR00089; TIGR00089; 1.

DR PROSITE; PS01278; UPF0004; 1.

DR Hypothetical protein; Complete proteome.

KW SEQUENCE 452 AA; 49662 MW; ODSBEAB175C4PB3E CRC64;

SQ SEQUENCE 452 AA; 49662 MW; ODSBEAB175C4PB3E CRC64;

Query Match 62.3%; Score 38; DB 16; Length 452;

Best Local Similarity 58.3%; Pred. No. 2.5e+02;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12

DB 55 KAQEKVFLQGR 66

RESULT 41

Q21004 PRELIMINARY; PRT; 461 AA.

ID Q21004

AC Q21004;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE F58G6.1 protein.

GN F58G6.1.

OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lloyd C.R.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 CC 1- SIMILARITY; CONTAINS 1 SH3 DOMAIN.
 DR EMBL; Z68217; CAA92465.1; -.
 DR PIR; T22946; T22946.
 DR WormPep; F58G6.1; CE03428.
 DR GO; GO:0006897; P:Endocytosis; IEA.
 DR GO; GO:0007268; P:Synaptic transmission; IEA.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR_dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PRO1251; AMPHIPHYSIN.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW SH3 domain.
 SQ SEQUENCE 461 AA; 51910 MW; 771C989E21EF7BEC8 CRC64;
 Query Match 62.3%; Score 38; DB 5; Length 461;
 Best Local Similarity 53.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGK 13
 DB 15 RTKXKLEGIGKA 27
 RESULT 42
 QSKTEO PRELIMINARY; PRT; 474 AA.
 ID Q9KTE0
 AC Q9KTE0
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein VC0962.
 GN VC0962.
 OS Vibrio cholerae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 CC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.P., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Emmlaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004177; AAF94124.1; -.
 DR PIR; E82261; E82261.

TIGR; VC0962;
 DR InterPro; IPR006638; E1p3.
 DR InterPro; IPR006463; M1AB_methiolase.
 DR InterPro; IPR007197; Radical_SAM.
 DR InterPro; IPR002792; TRAM.
 DR InterPro; IPR005839; UPF0004.
 DR Pfam; PF04055; Radical_SAM; 1.
 DR Pfam; PF01938; TRAM; 1.
 DR Pfam; PF00919; UPF0004; 1.
 DR SMART; SM00729; E1p3; 1.
 DR TIGRFAMs; TIGR01574; m1AB-methiolase; 1.
 DR TIGRFAMs; TIGR00089; TIGR00089; 1.
 DR PROSITE; PS01278; UPF0004; 1.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 474 AA; 53613 MW; C1C5DF73CC96C467 CRC64;
 Query Match 62.3%; Score 38; DB 16; Length 474;
 Best Local Similarity 58.3%; Pred. No. 2.7e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGK 12
 DB 54 KAQEKVFHQLGR 65
 RESULT 43
 Q9RCI2 PRELIMINARY; PRT; 474 AA.
 ID Q9RCI2
 AC Q9RCI2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE M1AB protein (Methylthiolation of isopentenylated A37 derivatives in
 DE rRNA).
 GN M1AB OR STM0670.
 OS Salmonella typhimurium.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20042346; PubMed=10572129;
 RA Esberg B., Leung H.C.E., Tsui H.C.T., Bjoerk G.R., Winkler M.E.;
 RT "Identification of the m1AB gene involved in the methylthiolation of
 RT isopentenylated A37 derivatives in the tRNA of Salmonella typhimurium
 RT and Escherichia coli.";
 RL J. Bacteriol. 181:7256-7265(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L72 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL; AJ249116; CAB62263.1; -.
 DR EMBL; AE008727; AAL19621.1; -.
 DR InterPro; IPR006638; E1p3.
 DR InterPro; IPR006463; M1AB_methiolase.
 DR InterPro; IPR007197; Radical_SAM.
 DR InterPro; IPR002792; TRAM.
 DR InterPro; IPR005839; UPF0004.
 DR Pfam; PF04055; Radical_SAM; 1.
 DR Pfam; PF01938; TRAM; 1.
 DR Pfam; PF00919; UPF0004; 1.
 DR SMART; SM00729; E1p3; 1.
 DR TIGRFAMs; TIGR01574; m1AB-methiolase; 1.
 DR TIGRFAMs; TIGR00089; TIGR00089; 1.
 DR PROSITE; PS01278; UPF0004; 1.

KW Complete proteome.
SQ SEQUENCE 474 AA; 53716 MW; 25E5CED9F28D38C CRC64;

Query Match 62.3%; Score 38; DB 16; Length 474;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
:|||||:|:
DB 54 KAQEKVFLQGR 65

RESULT 44
QSDFF8 PRELIMINARY; PRT; 474 AA.
AC Q8DFE8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2-methylthioadenine synthetase.
GN VV10266.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H.; Kim S.Y.; Chung S.S.; Kim J.J.; Moon Y.H.; Jeong H.;
RA Choy H.E.;
RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016797; AAC08800.1; -;
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR006463; MiaB_methiolase.
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR SMART; SMO0729; Elp3; 1.
DR TIGSFAMS; TIGR01574; miaB-methiolase; 1.
DR TIGSFAMS; TIGR00089; TIGR00089; 1.
DR PROSITE; PS01278; UPF0004; 1.
DR Complete proteome.
SQ SEQUENCE 474 AA; 53592 MW; 4B2BC7B749B688A2 CRC64;

Query Match 62.3%; Score 38; DB 16; Length 474;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
:|||||:|:
DB 54 KAQEKVFLQGR 65

RESULT 45
Q8CX45 PRELIMINARY; PRT; 474 AA.
AC Q8CX45;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TRNA-i(6)A37 modification enzyme MiaB.
GN MIAB OR S01181.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;

RX MEDLINE=22297686; PubMed=12369813;
RA Heidelberg J.P.; Paulsen I.T.; Nelson K.E.; Gaidos E.J.; Nelson W.C.;
RA Read T.D.; Eisen J.A.; Seshadri R.; Ward N.; Methe B.; Clayton R.A.;
RA Meyer T.; Tsapin A.; Scott J.; Beanan M.; Brinkac L.; Daugherty S.;
RA DeBoy R.T.; Dodson R.J.; Durkin A.S.; Haft D.H.; Kolonay J.F.;
RA Madupu R.; Peterson J.B.; Umayam L.A.; White O.; Wolf A.M.;
RA Vamathevan J.; Weidman J.; Imbraim M.; Lee K.; Berry K.; Lee C.;
RA Mueller J.; Khouri H.; Gill J.; Utterback T.R.; McDonald L.A.;
RA Felblyum T.V.; Smith H.O.; Venter J.C.; Neallson K.H.; Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT *Shewanella oneidensis*.";
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL; AE015582; AAN54251.1; -;
DR TIGR; S01181; -;
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR006463; MiaB_methiolase.
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR SMART; SMO0729; Elp3; 1.
DR TIGSFAMS; TIGR01574; miaB-methiolase; 1.
DR TIGSFAMS; TIGR00089; TIGR00089; 1.
DR PROSITE; PS01278; UPF0004; 1.
DR Complete proteome.
KW SEQUENCE 474 AA; 53760 MW; 976DCE04F6091BD2 CRC64;
SQ

Query Match 62.3%; Score 38; DB 16; Length 474;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
:|||||:|:
DB 54 KAQEKVFLQGR 65

RESULT 46
Q87RP4 PRELIMINARY; PRT; 474 AA.
ID Q87RP4;
AC Q87RP4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conserved hypothetical protein.
GN VP0733.
OS *Vibrio parahaemolyticus*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD 2210633 / Serotype O3:K6;
RA MEDLINE=22508454; PubMed=12820739;
RA Makino K.; Oshima K.; Kurokawa K.; Yokoyama K.; Uda T.; Tagomori K.;
RA Iijima Y.; Najima M.; Nakano M.; Yamashita A.; Kubota Y.; Kimura S.;
RA Yasunaga T.; Honda T.; Shinagawa H.; Hattori M.; Iida T.;
RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
RT distinct from that of *V. cholerae*.";
RL Lancet 361:743-749 (2003).
DR EMBL; AP005075; BAC58996.1; -;
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR PROSITE; PS01278; UPF0004; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 474 AA; 53713 MW; 0CA152B9F875A657 CRC64;

Query Match 62.3%; Score 38; DB 16; Length 474;

```

Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
Db 54 KAQEKVFLHGR 65

RESULT 47
Q83LY3
ID Q83LY3 PRELIMINARY; PRT; 474 AA.
AC
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Orf, conserved hypothetical protein (Hypothetical protein ylea).
GN YLEA OR SF0621 OR S0643.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigellia.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE015093; AAN42258.1; -
DR EMBL; AE015980; AAP16129.1; -
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR006463; MlaB_methiolase.
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR SMART; SM00729; Elp3; 1.
DR TIGRFAMs; TIGR01574; MlaB_methiolase; 1.
DR TIGRFAMs; TIGR00089; TIGR00089; 1.
DR PROSITE; PS01278; UPF0004; 1.
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SQ SEQUENCE 474 AA; 53695 MW; 537A6093888F79D9D CRC64;

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RESULT 48
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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RA Van Cluyt M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., da Silva F.R.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Perio M.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuranae E.E.,
RA Martino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.B. Jr., Sassaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa."
RL J.Bacteriol. 185:1018-1026(2003).
DR EMBL; AE012539; AAO29613.1; -
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR PROSITE; PS01278; UPF0004; 1.
KW Hypothetical protein; Complete proteome.
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Query Match 62.3%; Score 38; DB 16; Length 475;
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QY 1 RAQEKVLQKLGK 12
Db 77 KAQEKVFLHGR 88

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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN HD0226.
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.,
RT "The complete genome sequence of Haemophilus ducreyi."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017151; AAP95213.1; -
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SQ SEQUENCE 475 AA; 53638 MW; CB0F3B354C5F2DFA CRC64;

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 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein XCC2328.
 GN XCC2328.
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."
 RL Nature 417:459-463(2002).
 DR EMEL; AB012340; AM41606.1; -;
 DR InterPro; IPR006463; MiaB_methylase.
 DR InterPro; IPR007197; Radical_SAM.
 DR InterPro; IPR002792; TRAM.
 DR InterPro; IPR005839; UPF0004.
 DR Pfam; PF04055; Radical_SAM; 1.
 DR Pfam; PF01938; TRAM; 1.
 DR Pfam; PF00919; UPF0004; 1.
 DR TIGRFAMs; TIGR01574; miaB-methylase; 1.
 DR TIGRFAMs; TIGR00089; TIGR00089; 1.
 DR PROSITE; PS01278; UPF0004; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 485 AA; 52737 MW; 08C9EA7E10528FEE CRC64;

Query Match 62.3%; Score 38; DB 16; Length 485;
 Best Local Similarity 58.3%; Pred. No. 2.7e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
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 Job time : 37.6129 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:46:32 ; Search time 23.0645 Seconds
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Gapop 10.0 , Gapext 0.5

Searched: 809742 segs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	41	67.2	373	14	US-10-091-007-198	Sequence 198, Appl
5	39	63.9	505	10	US-09-769-787-120	Sequence 120, Appl
6	39	63.9	510	9	US-09-815-242-13474	Sequence 13474, A
7	39	63.9	510	9	US-09-815-242-13607	Sequence 13607, A
8	38	62.3	320	15	US-10-369-493-13329	Sequence 13329, A
9	38	62.3	357	14	US-10-161-051-57	Sequence 57, Appl
10	38	62.3	427	13	US-10-002-278-2	Sequence 2, Appl
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14	37	60.7	209	14	US-10-144-649A-182	Sequence 182, Appl
15	37	60.7	375	15	US-10-369-493-1040	Sequence 1040, Ap

16	37	60.7	403	15	US-10-369-493-1103	Sequence 1103, Ap
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 OPERATING SYSTEM: PC-DOS/MS-DOS
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 FILING DATE: 16-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/445,247
 FILING DATE: 03-Dec-1999
 APPLICATION NUMBER: US 08/870,126
 FILING DATE: 06-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: WST60DPCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9200
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 451 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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RESULT 3

US-10-116-275-238
 ; Sequence 238, Application US/10116275
 ; Publication No. US20030211476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Pharmaceutical Technology
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Brayden, David
 ; APPLICANT: Byrne, Daragh
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa
 ; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
 ; FILE REFERENCE: E1067/20087
 ; CURRENT APPLICATION NUMBER: US/10/116,275
 ; CURRENT FILING DATE: 2002-10-04
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 238
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-116-275-238

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 Best Local Similarity 100.0%; Pred. No. 0.023;
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 DB 24 RAQEKVLQKLGKA 36

RESULT 4

US-10-091-007-198

; Sequence 198, Application US/10091007
 ; Publication No. US20030170782A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Microbial Technics Limited
 ; APPLICANT: Le Page, Richard W F
 ; APPLICANT: Hanniffy, Sean B
 ; TITLE OF INVENTION: Proteins
 ; FILE REFERENCE: PWC/P21978WO
 ; CURRENT APPLICATION NUMBER: US/10/091,007
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: GB 9921125.2
 ; PRIOR FILING DATE: 1999-09-07
 ; NUMBER OF SEQ ID NOS: 276
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 198
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: Streptococcus agalactiae
 US-10-091-007-198

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 Best Local Similarity 63.6%; Pred. No. 0.47;
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 DB 337 EEKILKLGKS 347

RESULT 5

US-09-769-787-120
 ; Sequence 120, Application US/09769787
 ; Publication No. US20030091577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Microbial Technics Limited
 ; APPLICANT: Gilbert, Christophe FG
 ; APPLICANT: Hansbro, Philip M
 ; TITLE OF INVENTION: Proteins
 ; FILE REFERENCE: PWC/P21129WO
 ; CURRENT APPLICATION NUMBER: US/09/769,787
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: GB 9816337.1
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: US 60/125164
 ; PRIOR FILING DATE: 1999-03-19
 ; NUMBER OF SEQ ID NOS: 388
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 120
 ; LENGTH: 505
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-769-787-120

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RESULT 6

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 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zvekind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13474
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13474

Query Match 63.9%; Score 39; DB 9; Length 510;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGKA 13
|||:|
DB 8 KVLQKVGKA 16

RESULT 7
US-09-815-242-13607
; Sequence 13607, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13607

; LENGTH: 510
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13607
Query Match 63.9%; Score 39; DB 9; Length 510;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 KVLQKLGKA 13
|||:|
DB 8 KVLQKVGKA 16
RESULT 8
US-10-369-493-13329
; Sequence 13329, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13329
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(320)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-13329
Query Match 62.3%; Score 38; DB 15; Length 320;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
|||:|
DB 2 RQYRVLQQLGK 13

RESULT 9
US-10-161-051-57
; Sequence 57, Application US/10161051
; Publication No. US20030152945A1
; GENERAL INFORMATION:
; APPLICANT: Peter Deak
; APPLICANT: David M Glover
; APPLICANT: Carol Midgley
; TITLE OF INVENTION: Cell cycle progression proteins
; FILE REFERENCE: CCI-021CP
; CURRENT APPLICATION NUMBER: US/10/161,051
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: GB 0007268.6
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-161-051-57

Query Match 62.3%; Score 38; DB 14; Length 357;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 QEKVLQKLGKA 13
|:|:|:|:|:
Db 29 QKQWLEKLGKA 39

RESULT 10

US-10-002-278-2
; Sequence 2, Application US/10002278
; Publication No. US20020132334A1
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M.
; APPLICANT: Basler, Konard
; APPLICANT: Yamada, Toshiva
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF DORSALIN-1
; FILE REFERENCE: 0575/40314-A
; CURRENT APPLICATION NUMBER: US/10/002,278
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Chick
US-10-002-278-2

Query Match 62.3%; Score 38; DB 13; Length 427;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QEKVLQKLGK 12
||| ||| |||
Db 282 QBSVLNKLK 291

RESULT 11

US-09-864-761-47746
; Sequence 47746, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Ranzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-09-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47746
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009640.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EST_HUMAN HIT: BF692371.1, EVALUE 2.00e-08
US-09-864-761-47746

Query Match 60.7%; Score 37; DB 9; Length 33;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
|:|:|:|:|:
Db 3 QAERKILKLGKA 15

RESULT 12

US-09-738-973-182
; Sequence 182, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-738-973-182

Query Match 60.7%; Score 37; DB 9; Length 209;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQEKVLQKLG 11
|:|:|:|:|:
Db 141 AREKVLQTLG 150

```

; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1040
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-10-369-493-1040

Query Match          60.7%; Score 37; DB 15; Length 375;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 EKVQLKLGK 13
Db      248 EKELKLGK 257

RESULT 16
US-10-369-493-1103
; Sequence 1103, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1103
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Methanobacterium thermoautotrophicum
US-10-369-493-1103

Query Match          60.7%; Score 37; DB 15; Length 403;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 QEKVLQKLGK 12
Db      362 QGKTLQKLGK 371

RESULT 17
US-09-933-767-408
; Sequence 408, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24

US-09-933-767-408

Query Match          60.7%; Score 37; DB 14; Length 209;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 AQEKVLQKLG 11
Db      141 AREKVLQTLG 150

RESULT 15
US-10-369-493-1040
; Sequence 1040, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1040
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-10-369-493-1040

Query Match          60.7%; Score 37; DB 9; Length 209;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 AQEKVLQKLG 11
Db      141 AREKVLQTLG 150

RESULT 14
US-10-144-649A-182
; Sequence 182, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-144-649A-182

Query Match          60.7%; Score 37; DB 9; Length 209;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 AQEKVLQKLG 11
Db      141 AREKVLQTLG 150

RESULT 13
US-09-854-133-182
; Sequence 182, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 182
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-854-133-182

Query Match          60.7%; Score 37; DB 9; Length 209;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 AQEKVLQKLG 11
Db      141 AREKVLQTLG 150
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; PRIOR APPLICATION NUMBER: 60/193,170
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/205,258
 ; PRIOR FILING DATE: 1998-12-04
 ; PRIOR APPLICATION NUMBER: PCT/US98/11422
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/048,885
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,375
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,881
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,880
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,896
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,020
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,876
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,895
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,884
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,894
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,971
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,964
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,882
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,899
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,893
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,900
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,901
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,892
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,915
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,019
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,972
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,916
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,373
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,875
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/049,374
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,917
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,949
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,874
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,883
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,897
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,898
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,962
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,963

; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,877
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/048,878
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,054
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/068,064
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/068,053
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/070,923
 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/073,160
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/073,159
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/073,165
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/073,164
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: 60/085,925
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/085,921
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/085,923
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/085,922
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/092,921
 ; PRIOR FILING DATE: 1998-07-15
 ; PRIOR APPLICATION NUMBER: 60/094,657
 ; PRIOR FILING DATE: 1998-07-30
 ; NUMBER OF SEQ ID NOS: 1245
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 408
 ; LENGTH: 447
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (447)
 ; OTHER INFORMATION: Xaa equals stop translation
 US-09-933-767-408

 Query Match 60.7%; Score 37; DB 10; Length 447;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 Qy 2 AQEKVLQKLG 11
 Db 378 AREKVLQTLG 387

 RESULT 18
 US-10-023-282-408
 ; Sequence 408, Application US/10023282
 ; Publication No. US20030092893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young et al.
 ; TITLE OF INVENTION: 207 Human Secreted Proteins
 ; FILE REFERENCE: P2007P1
 ; CURRENT APPLICATION NUMBER: US/10/023,282
 ; CURRENT FILING DATE: 2001-12-20
 ; EARLIER APPLICATION NUMBER: 09/205,258
 ; EARLIER FILING DATE: 1998-12-04
 ; EARLIER APPLICATION NUMBER: PCT/US98/11422
 ; EARLIER FILING DATE: 1998-06-04
 ; EARLIER APPLICATION NUMBER: 60/048,885
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/049,375
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/048,881

EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
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EARLIER APPLICATION NUMBER: 60/049,374
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EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30

NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 408
LENGTH: 447
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (447)
OTHER INFORMATION: Xaa equals stop translation
US-10-023-282-408

Query Match 60.7%; Score 37; DB 14; Length 447;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 AOEKVLQKLG 11
|:|||||
Db 378 AREKVLQTLG 387

RESULT 19

US-09-935-390A-26
Sequence 26, Application US/09935390A
Patent No. US20020076761A1
GENERAL INFORMATION:
APPLICANT: Escobedo, Jaime
Quianjin, Hu
Garcia, Pablo
Williams, Lewis T.
Kothakota, Srinivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,390A
FILING DATE: 22-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/988,671
FILING DATE: 1997-12-11
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2718
TELEFAX: (510) 655-3542
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20020076761A1e
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-935-390A-26

Query Match 60.7%; Score 37; DB 9; Length 451;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AOEKVLQKLG 11
DB 383 AREKVLQTLG 392

RESULT 20
US-09-989-722-301
Sequence 301, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashtkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 9; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AOEKVLQKLG 11

Db 393 AREKVLQTLG 402

RESULT 21

US-09-989-723-301
Sequence 301, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-24
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 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 9; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY 2 AOEKVLQKIG 11
 Db 393 AREKVLQTLG 402

RESULT 22

US-09-989-279-301
 ; Sequence 301, Application US/09989279
 ; Patent No. US20020072496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 9; Length 461;

Best Local Similarity 80.0%; Pred. No. 2.8e+02;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AQEKLQKLG 11

Db 393 AREKVLQTLG 402

RESULT 23

US-09-989-727-301

; Sequence 301, Application US/09989727

; Patent No. US20020072497A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; PRIOR APPLICATION NUMBER: 60/088734
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 9; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AOEKVLQKLG 11
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 Db 393 AREKVLQTLG 402

RESULT 24
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 ; Sequence 301, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.

APPLICANT: ROY, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 9; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e-02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AREKVLQKLG 11
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 Db 393 AREKVLQTLG 402

RESULT 25
 US-09-989-732-301
 Sequence 301, Application US/09989732
 Patent No. US20020123463A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Garber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730PLC57
 CURRENT APPLICATION NUMBER: US/09/989,732
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
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 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
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 ; PRIOR FILING DATE: 1997-06-16

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Query Match 60.7%; Score 37; DB 9; Length 461;
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 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Botstein, David
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 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
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 / APPLICANT: Godowski, Paul J.
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 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watanabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
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Query Match 60.7%; Score 37; DB 9; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
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 ; APPLICANT: Godowski, Paul J.
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 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 60.7%; Score 37; DB 9; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 393 AREKVLQTLG 402

RESULT 31

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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Query Match      60.7%; Score 37; DB 9; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 393 AREKVLQTLG 402

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RESULT 32

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US-09-992-598-301
; Sequence 301, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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TITLE OF INVENTION: Acids Encoding the Same
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Query Match 60.7%; Score 37; DB 9; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AOEKVLQKLG 11
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; Sequence 301, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
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;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C61
;; CURRENT APPLICATION NUMBER: US/09/989, 735
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 9; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQEKVLQKLG 11
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 DB 393 AREKVLQTLG 402

RESULT 35
 US-09-990-444-301
 ; Sequence 301, Application US/09990444
 ; Publication No. US20020193300A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
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Query Match 60.7%; Score 37; DB 9; Length 461;

Best Local Similarity 80.0%; Pred. No. 2.8e+02;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 AQEKVLQKLG 11
Db 393 AREKVLQTLG 402

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RESULT 36

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; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181

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 ; PRIOR FILING DATE: 1998-07-07
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 9; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AOEKVLQKLG 11
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 Db 393 AREKVLQTLG 402

RESULT 37

US-09-989-730-301
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 ; Publication No. US20020197674A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC69
 ; CURRENT APPLICATION NUMBER: US/09/989,730
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          60.7%; Score 37; DB 9; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 AQEKLQKLG 11
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Db      393 AREVLQTLG 402

RESULT 38
US-09-990-436-301
; Sequence 301, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC14
; CURRENT APPLICATION NUMBER: US/09/990,436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 60.7% Score 37; DB 9; Length 461;
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 Matches 8; Conservative 1; Mismatches 0; Gaps 0;
 QY 2 AQEYVQLKLG 11
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RESULT 39

US-09-993-687-301
 ; Sequence 301, Application US/09993687
 ; Publication No. US20020198149A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
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 ; APPLICANT: Gurney, Austin L.
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730PIC11
 ; CURRENT APPLICATION NUMBER: US/09/993,687
 ; CURRENT FILING DATE: 2002-11-14
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      60.7%; Score 37; DB 9; Length 461;
Best Local Similarity 80.0%; Pred. NO. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db      393 AREKVLQIG 402

RESULT 40
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Wickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC64
; CURRENT APPLICATION NUMBER: US/09/989,734
; CURRENT FILING DATE: 2001-11-19
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 10; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AOEKVLQKLG 11
 Db 393 AREKVLQKLG 402
 RESULT 41
 US-09-997-653-301
 ; Sequence 301, Application US/09997653
 ; Publication No. US20030008297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: KJavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C38
 ; CURRENT APPLICATION NUMBER: US/09/997,653
 ; CURRENT FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 10; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Caps 0;

QY 2 AOEKVLQKLG 11
 Db 393 AFEKVLQTLG 402

RESULT 42
 US-09-993-667-301

; Sequence 301, Application US/05993667
; Publication No. US2003022187A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC4
; CURRENT APPLICATION NUMBER: US/09/993,667
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APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C44
CURRENT APPLICATION NUMBER: US/09/997,428
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05

Query Match 60.7%; Score 37; DB 10; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AOEKVLQKLG 11

Db 393 AREKVLQTLG 402

RESULT 43

US-09-997-428-301
Sequence 301, Application US/09997428
Publication No. US20030027162A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnocytes, Luc

; PRIOR APPLICATION NUMBER: 60/088212
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 ; PRIOR FILING DATE: 1998-06-24
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 10; Length 461;

Best Local Similarity 80.0%; Pred. No. 2.8e+02; Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AOEKVLQKLG 11
 Db 393 AREKVLQTLG 402

RESULT 44

US-09-997-666-301
 ; Sequence 301, Application US/09997666
 ; Publication No. US20030027163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC42
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US/09/997,666
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24

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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

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Query Match      60.7%; Score 37; DB 10; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

Oy 2 AOEKVLQKLG 11
Db 393 AREKVLQTLG 402

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RESULT 45
US-03-990-438-301
; Sequence 301, Application US/09990438
; Publication No. US2003002754A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann

```

```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC3
; CURRENT APPLICATION NUMBER: US/09/990,438
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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;; PRIOR APPLICATION NUMBER: 60/091478
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;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 10; Length 461;

Best Local Similarity 80.0%; Pred. No. 2.8e+02;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AOEKVLQKLG 11

Db 393 AREKVLQTLG 402

RESULT 46

US-08-990-562-301
; Sequence 301, Application US/09990562
; Publication No. US20030027985A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

1 TITLE OF INVENTION: Acids Encoding the Same
2 FILE REFERENCE: P2730PLC18
3 CURRENT APPLICATION NUMBER: US/09/590,562
4 CURRENT FILING DATE: 2001-11-14
5 PRIOR APPLICATION NUMBER: 60/049787
6 PRIOR FILING DATE: 1997-06-16
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93 PRIOR APPLICATION NUMBER: 60/089600
94 PRIOR FILING DATE: 1998-06-17
95 PRIOR APPLICATION NUMBER: 60/089653
96 PRIOR FILING DATE: 1998-06-17
97 PRIOR APPLICATION NUMBER: 60/089801
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100 PRIOR FILING DATE: 1998-06-18
101 PRIOR APPLICATION NUMBER: 60/089908
102 PRIOR FILING DATE: 1998-06-18
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107 PRIOR APPLICATION NUMBER: 60/089952
108 PRIOR FILING DATE: 1998-06-19
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120 PRIOR FILING DATE: 1998-06-24
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122 PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      60.7%; Score 37; DB 10; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AOEKVLQKLG 11
Db      393 AREKVLQTLG 402

RESULT 47
US-09-990-711-301
; Sequence 301; Application US/09990711
; Publication No. US20030302023A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC2
; CURRENT APPLICATION NUMBER: US/09/990,711
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/065186
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 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.7%; Score 37; DB 10; Length 461;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AOEKVLQKLG 11
 DB 393 AREKVLQTLG 402

RESULT 48

US-09-989-726-301
 ; Sequence 301, Application US/09989726
 ; Publication No. US20030040473A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavir, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730F1C60
 ; CURRENT APPLICATION NUMBER: US/09/989,726
 ; CURRENT FILING DATE: 2001-11-19
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 ; PRIOR FILING DATE: 1997-11-24

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63	PRIOR APPLICATION NUMBER: 60/089105
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; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          60.7%; Score 37; DB 10; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  2 AQEVLQKLG 11
Db  393 AREVLQTLG 402

RESULT 49
US-09-998-156-301
; Sequence 301, Application US/09998156
; Publication No. US20030044806A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P27301C28
; CURRENT APPLICATION NUMBER: US/09/998,156
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/043787
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; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978

; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 60.7% Score 37; DB 10; Length 461;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQEKVLQKLG 11
|:|||||
Db 393 AREKVLQTLG 402

RESULT 50

US-09-990-437-301
; Sequence 301, Application US/09990437
; Publication No. US20030045463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hauspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C49
; CURRENT APPLICATION NUMBER: US/09/990,437
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02

Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AOEKVLQKLG 11
|:|||||
Db 393 AREKVLQTLG 402

Search completed: March 4, 2004, 17:55:15
Job time : 27.0845 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:24:55 ; Search time 9.29045 Seconds
(without alignments)
1228.072 Million cell updates/sec

Title: US-10-069-540A-2_COPY_1_221
Perfect score: 1125
Sequence: 1 MAEGKAGGAGLFAKQVQK.....IGCVTIFQNISLRDVFYR 221

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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4: /cgm2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgm2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	689	61.2	434	US-08-630-915A-22	Sequence 22, Appl
2	671.5	59.7	451	US-08-435-454-4	Sequence 4, Appli
3	671.5	59.7	451	US-08-652-972A-4	Sequence 4, Appli
4	671.5	59.7	451	US-08-919-145-6	Sequence 6, Appli
5	671.5	59.7	451	US-08-870-126-4	Sequence 4, Appli
6	671.5	59.7	451	US-09-344-889-6	Sequence 6, Appli
7	671.5	59.7	451	US-09-445-247-4	Sequence 4, Appli
8	671.5	59.7	451	PCT-US96-06231A-4	Sequence 4, Appli
9	559.5	49.7	404	US-08-630-915A-24	Sequence 24, Appli
10	113	10.0	1972	US-08-875-435B-3	Sequence 3, Appli
11	111.5	9.9	2954	US-09-150-867-1	Sequence 1, Appli
12	110	9.8	816	US-08-533-306A-6	Sequence 6, Appli
13	110	9.8	816	US-08-742-923A-6	Sequence 6, Appli
14	110	9.8	885	US-08-533-306A-4	Sequence 6, Appli
15	110	9.8	885	US-08-742-923A-4	Sequence 4, Appli
16	108	9.6	1972	US-08-875-435B-4	Sequence 4, Appli
17	107	9.5	975	US-09-914-259-19	Sequence 19, Appli
18	107	9.5	8991	US-08-714-741-32	Sequence 22, Appli
19	106.5	9.5	2285	US-09-308-375-2	Sequence 2, Appli
20	104	9.2	1581	US-09-866-108A-15754	Sequence 15754, A
21	103.5	9.2	2551	US-09-328-352-8156	Sequence 8156, Ap
22	103.5	9.2	818	US-09-134-000C-6355	Sequence 6355, Ap
23	103.5	9.2	906	US-09-107-532A-6450	Sequence 6450, Ap
24	103.5	9.2	1010	US-09-134-001C-5178	Sequence 5178, Ap
25	103	9.2	967	US-09-914-259-21	Sequence 21, Appli
26	103	9.2	2662	US-09-595-684B-31	Sequence 31, Appli
27	103	9.2	3878	US-09-914-259-11	Sequence 11, Appli

Sequence 558, App
Sequence 4820, Ap
Sequence 5466, Ap
Sequence 5, Appli
Sequence 15753, A
Sequence 5352, Ap
Sequence 220, App
Sequence 5067, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 11, Appli
Sequence 5178, Ap
Sequence 53, Appli
Sequence 2, Appli
Sequence 5756, Ap

28 102.5 9.1 325 4 US-09-138-452A-558
29 102 9.1 1211 4 US-09-134-001C-4820
30 101.5 9.0 979 4 US-09-543-681A-5466
31 101 9.0 1507 3 US-08-929-329-5
32 101 9.0 1695 4 US-09-866-108A-15753
33 100.5 8.9 431 4 US-09-134-000C-5352
34 100.5 8.9 433 4 US-09-079-030-220
35 99.5 8.8 710 4 US-09-107-532A-5067
36 99 8.8 477 1 US-08-402-217A-3
37 99 8.8 477 1 US-08-700-178-3
38 99 8.8 477 3 US-08-995-654-3
39 99 8.8 606 4 US-08-477-831C-2
40 99 8.8 631 4 US-08-477-831C-11
41 98.5 8.8 1799 4 US-09-134-000C-5178
42 98 8.7 284 4 US-09-914-259-53
43 98 8.7 576 2 US-08-533-306A-2
44 98 8.7 576 2 US-08-742-923A-2
45 98 8.7 1208 4 US-09-134-000C-5756

ALIGNMENTS

RESULT 1
US-08-630-915A-22
; Sequence 22, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-915A-22

Query Match 61.2%, Score 689, DB 4, Length 434;
Best Local Similarity 61.9%, Pred. No. 1.3e-54;
Matches 138; Conservative 30; Mismatches 53; Indels 2; Gaps 2;

QY 1 MAE-GKACGAGLFAKQVOKKFSRAQEKVLQKLGAVETKDERPEQASNFYQQAEGHK 59
Db 1 MAEMSGKGTAGKIASNVQKLTTRAQEKVLQKLGKADTKDEQEQCVQNFKNKLTGTR 60
QY 60 LYKDLNFLSAVKVWHSESKRVSETLQEIYSSEWMDGHEELKAIWVNDLLWEDYEELAD 119
Db 61 LQKDLATYLSAVKAMHEASKLSECLQEVYEPWFGRDEANKIAENNDLLWMDYHQLVD 120
QY 120 QAVRTWEIYVAQSEIKERIAKRGKLVYDSARHHLAVQNA-KDEAKTAKAEFEFNK 178
Db 121 QALLTMDTTLGQFPDIKRSIAKRGKLVYDSARHHLAVQNA-KDEAKTAKAEFEFNK 180
QY 179 AQTVEFDLNOELLELPILYNSRICGYVTIFONISNLRDVFYR 221
Db 181 AQVFEWMDLQBELPSLWNSRVGFYVNTFQSIAGLEENFK 223

RESULT 2

US-08-435-454-4
; Sequence 4, Application US/08435454
; Patent No. 5605830
; GENERAL INFORMATION:
; APPLICANT: Prndergast, George C.
; APPLICANT: Sakamuro, Daitoku
; TITLE OF INVENTION: Murine and Human C-Myc Interacting
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,454
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-435-454-4

Query Match 59.7%; Score 671.5; DB 1; Length 451;
Best Local Similarity 61.5%; Pred. No. 5.4e-53;
Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;
QY 10 AGLEAKVQKFSRAQEKVLQKLGAVETKDERPEQASNFYQQAEGHKLYKDLNPLS 69
Db 8 AKIASNVQKLTTRAQEKVLQKLGKADTKDEQEQCVQNFKNKLTGTRLQKDLTYLA 67
QY 70 AVKVMHSESKRVSETLQEIYSSEWMDGHEELKAIWVNDLLWEDYEELADQAVRTWEIYV 129
Db 68 SVKAMHEASKLNECLQEVYEPWFGRDEANKIAENNDLLWMDYHQLVDQALLTMDTTL 127
QY 130 AQVFEWMDLQBELPSLWNSRVGFYVNTFQSIAGLEENFK 223
Db 181 AQVFEWMDLQBELPSLWNSRVGFYVNTFQSIAGLEENFK 223

Db 128 GQFPDIKRSIAKRGKLVYDSARHHLAVQNA-KDEAKTAKAEFEFNK 187
QY 189 ELLELPILYNSRICGYVTIFONISNLRDVFYR 221
Db 188 DLQBELPSLWNSRVGFYVNTFQSIAGLEENFK 220

RESULT 3

US-08-652-972A-4
; Sequence 4, Application US/08652972A
; Patent No. 5723581
; GENERAL INFORMATION:
; APPLICANT: Prndergast, George C.
; APPLICANT: Sakamuro, Daitoku
; TITLE OF INVENTION: Murine and Human Box-Dependent
; TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,972A
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,454
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-652-972A-4

Query Match 59.7%; Score 671.5; DB 1; Length 451;
Best Local Similarity 61.5%; Pred. No. 5.4e-53;
Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;
QY 10 AGLEAKVQKFSRAQEKVLQKLGAVETKDERPEQASNFYQQAEGHKLYKDLNPLS 69
Db 8 AKIASNVQKLTTRAQEKVLQKLGKADTKDEQEQCVQNFKNKLTGTRLQKDLTYLA 67
QY 70 AVKVMHSESKRVSETLQEIYSSEWMDGHEELKAIWVNDLLWEDYEELADQAVRTWEIYV 129
Db 68 SVKAMHEASKLNECLQEVYEPWFGRDEANKIAENNDLLWMDYHQLVDQALLTMDTTL 127
QY 130 AQVFEWMDLQBELPSLWNSRVGFYVNTFQSIAGLEENFK 221
Db 188 DLQBELPSLWNSRVGFYVNTFQSIAGLEENFK 220

RESULT 4

US-08-919-145-6
 ; Sequence 6, Application US/08919145
 ; Patent No. 5958753
 ; GENERAL INFORMATION:
 ; APPLICANT: Prendergast, George C.
 ; TITLE OF INVENTION: Bau, A Binl Interacting Protein, and
 ; TITLE OF INVENTION: Uses Therefor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, P.O. Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19477
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/919,145
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/025,482
 ; FILING DATE: 29-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kodroff, Cathy A.
 ; REGISTRATION NUMBER: 33,980
 ; REFERENCE/DOCKET NUMBER: WST73AUSA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-540-9200
 ; TELEFAX: 215-540-5818
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 451 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-919-145-6

Query Match 59.7%; Score 671.5; DB 2; Length 451;
 Best Local Similarity 61.5%; Pred. No. 5.4e-53;
 Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;
 QY 10 AGLFAKOVKKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQOAEHGKLYKDLKNFLS 69
 Db 8 AGKIASNVQKLTTRAQEKVLQKLGKADETKDEQEQVQNFNQLTETGTRLQKDLRTYLA 67
 QY 70 AVKVMHSSKRVSETLQETIYSSEWDGHEELKAIWNNLLWEDYBEKLAQAVRTWEIYV 129
 Db 68 SVKAMHEASKKNECLQEVYEPDMPGDEANKIAENNDLLWMDYHOKLVDQALLTMDTYL 127
 QY 130 AQPSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKAQTVFEDLNQ 188
 Db 128 GQFPDIKSRIAKGRKLVYDSARHYESLQAKKDEAKIAKAEELIKAKQVFENN 187
 QY 189 ELLEELPLIYNISRGCVVTIFQNISNLRDVFYR 221
 Db 188 DLQELPGLMNSRVGFYNTFQSIAGLEENFHK 220

RESULT 5
 US-08-919-145-6
 ; Sequence 4, Application US/08870126
 ; Patent No. 6048702
 ; GENERAL INFORMATION:
 ; APPLICANT: Prendergast, George C.
 ; APPLICANT: Sakamuro, Daitoku
 ; TITLE OF INVENTION: Murine and Human Box-Dependent
 ; TITLE OF INVENTION: MYC-Interacting Protein (Binl) and Uses Therefor
 ; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, P O Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19477
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/870,126
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/435,454
 ; FILING DATE: 05-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/652,972
 ; FILING DATE: 24-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kodroff, Cathy A.
 ; REGISTRATION NUMBER: 33,980
 ; REFERENCE/DOCKET NUMBER: WST60CUSA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-540-9200
 ; TELEFAX: 215-540-5818
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 451 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-870-126-4

Query Match 59.7%; Score 671.5; DB 3; Length 451;
 Best Local Similarity 61.5%; Pred. No. 5.4e-53;
 Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;
 QY 10 AGLFAKOVKKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQOAEHGKLYKDLKNFLS 69
 Db 8 AGKIASNVQKLTTRAQEKVLQKLGKADETKDEQEQVQNFNQLTETGTRLQKDLRTYLA 67
 QY 70 AVKVMHSSKRVSETLQETIYSSEWDGHEELKAIWNNLLWEDYBEKLAQAVRTWEIYV 129
 Db 68 SVKAMHEASKKNECLQEVYEPDMPGDEANKIAENNDLLWMDYHOKLVDQALLTMDTYL 127
 QY 130 AQPSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKAQTVFEDLNQ 188
 Db 128 GQFPDIKSRIAKGRKLVYDSARHYESLQAKKDEAKIAKAEELIKAKQVFENN 187
 QY 189 ELLEELPLIYNISRGCVVTIFQNISNLRDVFYR 221
 Db 188 DLQELPGLMNSRVGFYNTFQSIAGLEENFHK 220

RESULT 6
 US-09-344-889-6
 ; Sequence 6, Application US/09344889
 ; Patent No. 6140465
 ; GENERAL INFORMATION:
 ; APPLICANT: Prendergast, George C.
 ; TITLE OF INVENTION: Bau, A Binl Interacting Protein, and
 ; TITLE OF INVENTION: Uses Therefor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, P.O. Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA

ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/919,145
FILING DATE:
APPLICATION NUMBER: US 60/025,482
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST73AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-344-889-6

Query Match 59.7%; Score 671.5; DB 3; Length 451;
Best Local Similarity 61.5%; Pred. No. 5.4e-53;
Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;
QY 10 AGLFAQVQKFSRAQEKVLQKLGKAVETKDERPEQSASNFYQQAEGHKLKLNFLS 69
DB 8 AGKIASNVQKLTQAEKVLQKLGKADETKDEQFQCVQNFKNQLTGTRLQKDLRYLA 67
QY 70 AVKWHSESKRVSETLOEILYSSEWGHHEELKAVIWNNDLLWEDYEEKLAQAVRTMEIYV 129
DB 68 SVKAMEASKGLNECLQEVYEPDWPGRDEANKIAENNDLLWMDYHQKLVQALLTMDTYL 127
QY 130 AQPSEIKERIAKGRKLVVDYSARHLEAVONA-KKDEAKTAKAEFEFNKAQTVFEDLNQ 188
DB 128 GQFPDIKSRIAKGRKLVVDYSARHLYESLQTKAKKDEAKIAKAEELIKAKQVFEEMNV 187
QY 189 ELLEELPILYNSRIGCVYTFIFONISNLRDVFYR 221
DB 188 DLQELPSLWNSRVGFYNTFQSIAGLEENFHK 220

RESULT 7
US-09-445-247-4
Sequence 4, Application US/09445247
Patent No. 6410238
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
Prendergast, George C.
Sakamuro, Daitoku
TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/445,247
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/870,126
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60DPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-445-247-4

Query Match 59.7%; Score 671.5; DB 4; Length 451;
Best Local Similarity 61.5%; Pred. No. 5.4e-53;
Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;
QY 10 AGLFAQVQKFSRAQEKVLQKLGKAVETKDERPEQSASNFYQQAEGHKLKLNFLS 69
DB 8 AGKIASNVQKLTQAEKVLQKLGKADETKDEQFQCVQNFKNQLTGTRLQKDLRYLA 67
QY 70 AVKWHSESKRVSETLOEILYSSEWGHHEELKAVIWNNDLLWEDYEEKLAQAVRTMEIYV 129
DB 68 SVKAMEASKGLNECLQEVYEPDWPGRDEANKIAENNDLLWMDYHQKLVQALLTMDTYL 127
QY 130 AQPSEIKERIAKGRKLVVDYSARHLEAVONA-KKDEAKTAKAEFEFNKAQTVFEDLNQ 188
DB 128 GQFPDIKSRIAKGRKLVVDYSARHLYESLQTKAKKDEAKIAKAEELIKAKQVFEEMNV 187
QY 189 ELLEELPILYNSRIGCVYTFIFONISNLRDVFYR 221
DB 188 DLQELPSLWNSRVGFYNTFQSIAGLEENFHK 220

RESULT 8
PCT-US96-06231A-4
Sequence 4, Application PC/JUS9606231A
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
TITLE OF INVENTION: Murine and Human Box-Dependent
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06231A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60APCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-06231A-4

Query Match 59.7%; Score 671.5; DB 5; Length 451;
Best Local Similarity 61.5%; Pred. No. 5.4e-53;
Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;

QY 10 AGLPKQVQKFSRAQKVLQKLGKAVETKDERFEQASNFYQQQAEHGKLYKDLKNFLS 69
DB 8 AGKIASNVQKLTAKQKVLQKLGKADETKDEQEQCVQNFNKQLTEGTRLOKDLRTYLA 67

QY 70 AVKWHSSKRVSTLQEIYSSWDGHEELKAIVWNNLLWEDYEKADQAVRTMEIYV 129
DB 68 SVKAMHEASKKNECLQEVYEPDPWGRDEANKIAENNDLLWMDYHQKLVQALLTMDTYL 127

QY 130 AQPSEIKERIAKGRKLVVDYSARHLEAVONA-KKDEAKTAKABEEFNKAQTVFEDLNQ 188
DB 128 GQFPDIKSRKAKGRKLVVDYSARHLYESQTAKKDEAKIAKABEELIKAKRVFEEMNV 187

QY 189 ELLEELFILNSRIGCVYTFIFONISNLRDVFYR 221
DB 188 DLOBELPSLNSRVGFYVNTFOSIAGLEENFHK 220

RESULT 9
US-08-630-915A-24
Sequence 24, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-24

Query Match 49.7%; Score 559.5; DB 4; Length 404;
Best Local Similarity 59.1%; Pred. No. 7e-43;
Matches 107; Conservative 30; Mismatches 43; Indels 1; Gaps 1;

QY 42 RFQSSASNFYQQQAEHGKLYKDLKNFLSAVKWHSSKRVSTLQEIYSSWDGHEELKA 101
DB 8 RFQCVQNFNKQLTEGTRLOKDLRTYLASVKAMHEASKKNECLQEVYEPDPWGRDEANK 67

QY 102 IVWNNLLWEDYEKADQAVRTMEIYVAQFSEIKERIAKGRKLVVDYSARHLEAVON 161
DB 68 IAEENNDLLWMDYHQKLVQALLTMDTYLGQFPDIKSRKAKGRKLVVDYSARHLYESQT 127

QY 162 A-KKDEAKTAKABEEFNKAQTVFEDLNQELLEELFILNSRIGCVYTFIFONISNLRDVFY 220
DB 128 AKKDEAKTAKABEELIKAKRVFEEMNVQLELPSLNSRVGFYVNTFOSIAGLEENFHK 187

QY 221 R 221
DB 188 K 188

RESULT 10
US-08-875-435B-3
Sequence 3, Application US/08875435B
Patent No. 6593304
GENERAL INFORMATION:
APPLICANT: Hasegawa, Kazuhide
APPLICANT: Arakawa, Emi
APPLICANT: Oda, Shoji
APPLICANT: Matsuda, Yuzuru
APPLICANT: Takahashi, Katsuhito
APPLICANT: Sugahara, Michihiro
APPLICANT: Ishiyama, Haruo
TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
TITLE OF INVENTION: FOR MYOSIN HEAVY CHAIN SM1 ISOFORM PROTEIN INSERTED INTO
TITLE OF INVENTION: VECTOR DNA, MICROORGANISM CARRYING THE RECOMBINANT DNA, AND
TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
TITLE OF INVENTION: RECOMBINANT DNA
FILE REFERENCE: 07898-013001
CURRENT APPLICATION NUMBER: US/08/875,435B
CURRENT FILING DATE: 1997-07-25
PRIOR APPLICATION NUMBER: PCT/JP96/00134
PRIOR FILING DATE: 1996-01-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1972
TYPE: PRT
ORGANISM: Mus musculus
US-08-875-435B-3

Query Match 10.0%; Score 113; DB 4; Length 1972;
Best Local Similarity 24.8%; Pred. No. 0.23;
Matches 57; Conservative 38; Mismatches 97; Indels 38; Gaps 9;

QY 2 AEGKAGGAA---GLPAKQVQKFSRAQKVLQKLGKAVETKDERFEQASNFY----- 51
DB 1299 AEGKATKADVASJGSQLODTQELLQETROKLN--VSTKRLQLEDERNSLQQLDEEM 1356

QY 52 --QQQAEHG-----KLYKDLKNFLSAVKWHSSKRVSTLQEIYSSWDGHEELKA 97
DB 1357 EAKQNLERHVSNTLQSDSKKQLQDFASTIEVMEGKRLQKEMEGLSQQYBEKAAAYD 1416

QY 98 ELKAIWNNLLWEDYEKAD-----QAVRTMEIYVAQFSEIKERIAKGRKLVVDYSA 152

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Db 1417 KLEK---TKNRLQQLDLDVLDNQRLVSNLEKKKKFQDL---LAEKNTSSKVADE 1470
QY 153 RHLEAVQNAKDEA-KTAKAEFEFNKAQTVFEDLNQELLEELPILYNSR 201
Db 1471 RDAEAREKETKALSARALEEALEAKEELERTNOMLKAEMEDLVSSK 1520

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RESULT 11

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US-09-150-867-1
; Sequence 1, Application US/09150867
; Patent No. 6645748
; GENERAL INFORMATION:
; APPLICANT: Wood, Kenneth W.
; APPLICANT: Sakowicz, Roman
; APPLICANT: Goldstein, Lawrence S.B.
; APPLICANT: Cleveland, Don W.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Plus End-Directed Microtubule Motor Required for
; FILE REFERENCE: 18557C-000110US
; CURRENT APPLICATION NUMBER: US/09/150.867
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: US 60/058,645
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2954
; TYPE: PRT
; ORGANISM: Xenopus sp.
; FEATURE:
; OTHER INFORMATION: Xenopus centromere-associated protein-E (XCENP-E)
; OTHER INFORMATION: member of the kinesin superfamily of microtubule
; OTHER INFORMATION: motor proteins
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(472)
; OTHER INFORMATION: kinesin like motor domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (473)..(2752)
; OTHER INFORMATION: rod domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2753)..(2954)
; OTHER INFORMATION: tail domain
US-09-150-867-1

```

```

Query Match 9.9%; Score 111.5; DB 4; Length 2954;
Best Local Similarity 22.1%; Pred. No. 0.54;
Matches 57; Conservative 46; Mismatches 88; Indels 67; Gaps 10;

QY 13 FAKVQKPSRAQEKVLQKLGKAVETKDERFEQASNFYQQQAFGHKLYKDLNPLSAVK 72
Db 1720 FNEAQQKTTKEQ-----CLINENKELEQSQ---HRLQCEIEELMKALESAL 1767
QY 73 VMHSSKRVSETLQEIYSEWDGHEELK---AIVWNNDLLWEDY----- 113
Db 1768 TLKSEQKVINLQEMVMLE-MEELKNSORTVIAERDQLQDDLRSEVMSIETQDDLR 1826
QY 114 --EKLQADQVRTWEIYVAQFSEIKERIAKGRKLV-----DYDSARHIL- 156
Db 1827 KAQEAQQQKQVQL-TSQISVLQEKISLENQMLYNVATVKETLSERDDLQSQKHLF 1885
QY 157 -----EAVQNAKDEAKTA-KAEFEFNKAQTVFEDLNQELLEELPILY--N 199
Db 1886 SEIETLSLSKEKEFALQAEKQKADAAKTIDITEKISNIEBQLQQAATNLKETLYERE 1945
QY 200 SRIGCVTIFQNISLRD 217
Db 1946 SLIQCKEQLALNTEHLRE 1963

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RESULT 12

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US-08-533-306A-6
; Sequence 6, Application US/08533306A
; Patent No. 5837457
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533.306A
; FILING DATE: September 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36693
; REFERENCE/DOCKET NUMBER: 2115-00869COB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-533-306A-6

```

```

Query Match 9.8%; Score 110; DB 2; Length 816;
Best Local Similarity 22.9%; Pred. No. 0.13;
Matches 52; Conservative 39; Mismatches 104; Indels 32; Gaps 6;

QY 2 AEGKAGGAA---GLFAKQVKPSRAQEKVLQKLGKAVETKDERFEQASNFYQQQAECH 58
Db 177 AEGKAIKADVASLASQLQDTQELLQETRQKLN--VSTKLRQLEERNLSLQDQDEEM 234
QY 59 KLYKDLNPLSAVKVMHSSKRVSETLQEIYSEWDGHEELKAIYWNNDLLWEDYEEKLA 118
Db 235 EAKQNLHERHSTINILQISDSKKLQDPASTVEALEBEGKRFQKEIEN---LTQQVEEKAA 291
QY 119 -----DQAVRTWEIYVAQFSEIKERIAKGRKL-----VDYDSARHH 155
Db 292 AYDKLETKNRLQQLDLDVLDNQRLVSNLEKKKKFQDLAEKNTSSKVADEDR 351
QY 156 LEAVQNAKDEA-KTAKAEFEFNKAQTVFEDLNQELLEELPILYNSR 201
Db 352 AEAREKETKALSARALEEALEAKEELERTNOMLKAEMEDLVSSK 398

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RESULT 13

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US-08-742-923A-6
; Sequence 6, Application US/08742923A
; Patent No. 5869611
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.

```



```
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; TITLE OF INVENTION: Rearrangements
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,923A
; FILING DATE: No. 5869611ember 1, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869DVC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-742-923A-6

Query Match          9.8%; Score 110; DB 2; Length 816;
Best Local Similarity 22.9%; Pred. No. 0.13;
Matches 52; Conservative 39; Mismatches 104; Indels 32; Gaps 6;

QY 2 AEGKAGGAA---GLFAKQVQKFSRAQEKVLQKLGKAVETKDERFQSGASNFYQQQAEGH 58
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 AEGKAIKLAKDVASLSQLOQTQELLQETROKLN--VSTKLQLEERNSLQDQDEEM 234
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 59 KLYDKLKNFLSAVKVHSHSKRVSETLQEIYSEWDGHEELKAIWNNDLMDYEEKLA 118
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 EAKQNLERHISTLNQLSDSKKQLQDPASTVEALEEGKGRFOKEIEN---LTQQYEEKAA 291
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 119 -----DQAVRTWEIYVAQFSEIKERIAKGRKL-----VDYDSARHH 155
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 AYDKLEKTKNRLQQLDLDVLDNQRQLVSNLEKQKQKFDQLLAEKNISSKYADERDR 351
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 156 LEAVONAKKDEA-KTAKAEFEFNKAQTVFEDLNQELLEELPILYNR 201
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 AEAEAREKETKALSARALEALEAKEELERTNKMLKAEMEDLVSK 398
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-08-533-306A-4
; Sequence 4, Application US/08533306A
; Patent No. 5837457
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
```

```
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,306A
; FILING DATE: September 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869COB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 885 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-533-306A-4

Query Match          9.8%; Score 110; DB 2; Length 885;
Best Local Similarity 22.9%; Pred. No. 0.14;
Matches 52; Conservative 39; Mismatches 104; Indels 32; Gaps 6;

QY 2 AEGKAGGAA---GLFAKQVQKFSRAQEKVLQKLGKAVETKDERFQSGASNFYQQQAEGH 58
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 AEGKAIKLAKDVASLSQLOQTQELLQETROKLN--VSTKLQLEERNSLQDQDEEM 303
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 59 KLYDKLKNFLSAVKVHSHSKRVSETLQEIYSEWDGHEELKAIWNNDLMDYEEKLA 118
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 EAKQNLERHISTLNQLSDSKKQLQDPASTVEALEEGKGRFOKEIEN---LTQQYEEKAA 360
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 119 -----DQAVRTWEIYVAQFSEIKERIAKGRKL-----VDYDSARHH 155
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 AYDKLEKTKNRLQQLDLDVLDNQRQLVSNLEKQKQKFDQLLAEKNISSKYADERDR 420
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 156 LEAVONAKKDEA-KTAKAEFEFNKAQTVFEDLNQELLEELPILYNR 201
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 421 AEAEAREKETKALSARALEALEAKEELERTNKMLKAEMEDLVSK 467
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-08-742-923A-4
; Sequence 4, Application US/08742923A
; Patent No. 5869611
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,923A
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; FILING DATE: No. 5869611ember 1, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Dean F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869DVC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 885 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-742-923A-4

Query Match          9.8%; Score 110; DB 2; Length 885;
Best Local Similarity 22.9%; Pred. No. 0.14;
Matches 52; Conservative 39; Mismatches 104; Indels 32; Gaps 6;

QY 2 AEGKAGGAA---GLFAKQVQKFSRAQEKVLQKLGKAVETDERPEOSASNFYQQQAEHG 58
Db 246 AEGKATKLAQVSLSSQLQDTQELLQEBETRQKLN--VSTKLRQLSEERNSLQDLDEEM 303
QY 59 KLYIDLKNFLSAVKVWHSSKRVSETLQEIYSSSEWDGHEELKATVWNNDLLWEDYEKLA 118
Db 304 EAKQNLERHISTINTQLSDSKKQLQDPASTVTEALEEGKKRFQKEIEN---LTQQYEKAA 360
QY 119 -----DQAVRTWEIYVAQFSEIKERIAKGRKL-----VDYDSARHH 155
Db 361 AYDKLEKTKNRLQQLDLDLVLDNQRLVSNLEKKQKQKFDQLAEEKNISSKYADERDR 420
QY 156 LEAVQNAKKDEA-KTAKAEERFNKAQTVFEDLNQELLEELPILYNSR 201
Db 421 ABAAREKETKALSRLALEALEAKELELRTNKKLKAEMEDLVSSK 467
```

Search completed: March 4, 2004, 17:32:27
Job time : 10.2904 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:23:55 ; Search time 10.135 Seconds
(without alignments)
2097.510 Million cell updates/sec

Title: US-10-069-540A-2_COPY_1_221

Perfect score: 1125
Sequence: 1 MAEGKAGAGLPAKQVQKK.....IGCVYTFQINSLRDVFR 221

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	683	60.7	482	2 JC5593	amphiphysin Ii2 - human
2	620.5	55.2	695	2 S62400	amphiphysin (clone 22-2) - human
3	618.5	55.0	682	1 S22700	amphiphysin - chic
4	405	36.0	461	2 T22946	hypothetical prote
5	194.5	17.3	270	2 T43000	RVS161 protein hom
6	192.5	17.1	264	2 T40651	yeast reduced viab
7	129.5	16.0	265	1 S19516	RVS161 protein - y
8	158.5	14.1	466	2 T11684	RVS167 protein hom
9	154.5	13.7	482	1 S40887	RVS167 protein - y
10	129.5	11.5	1992	2 A47297	myosin heavy chain
11	127	11.3	377	2 S52537	eml L15 protein -
12	120.5	10.7	2116	2 A26655	myosin heavy chain
13	118	10.5	399	2 E71169	hypothetical prote
14	116	10.3	1940	2 A59287	myosin heavy chain
15	116	10.3	2401	2 T28676	myosin heavy chain
16	116	10.3	3225	2 I52300	rhoptery protein -
17	116	10.3	3259	1 A56539	giantin - human
18	115	10.2	527	2 S33068	giantin - human
19	114.5	10.2	532	2 S54871	myosin heavy chain
20	114	10.1	226	2 S71108	M protein - Strept
21	114	10.1	1061	2 D98008	hypothetical prote
22	114	10.1	1078	2 T18352	conserved hypothet
23	113.5	10.1	1087	2 T30330	protein P120 - Myc
24	113	10.0	1005	2 A64465	Gelsolin-related p
25	113	10.0	1300	2 T18364	hypothetical prote
26	113	10.0	1938	2 JC5421	ro-3 protein - Neu
27	113	10.0	1972	2 JC5420	smooth muscle myos
28	112.5	10.0	1138	2 T24635	smooth muscle prote
29	112.5	10.0	2245	2 T18278	myosin heavy chain

30 112 10.0 600 2 A45112 major parafagella
31 112 10.0 2007 1 B43402 myosin heavy chain
32 111.5 9.9 1790 2 S67593 transport protein
33 111.5 9.9 2954 2 T14156 kinesin-related pr
34 110.5 9.8 1169 2 A64505 P115 homolog - Met
35 110.5 9.8 1491 2 D82166 cell division prot
36 110 9.8 407 2 S23325 M2 protein precurs
37 110 9.8 841 2 A86188 hypothetical prote
38 110 9.8 1640 2 D86798 prothage p13 prote
39 109.5 9.7 944 2 S26710 spindle pole body
40 109.5 9.7 1225 2 A49464 chromosome segrega
41 109 9.7 281 2 F75216 hypothetical prote
42 109 9.7 520 2 F70350 recombination prot
43 109 9.7 736 2 D64271 protein F16A14.2
44 109 9.7 942 2 A64379 isoleucine-tRNA li
45 109 9.7 1170 2 A56157 chromosome segrega

ALIGNMENTS

RESULT 1

JC5593
amphiphysin Ii2 - human
C:Species: Homo sapiens (man)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jun-2000
C:Accession: JC5593
R:Tsutsui K.; Maeda, Y.; Tsutsui, K.; Seki, S.; Tokunaga, A.
Biochem. Biophys. Res. Commun. 236, 178-183, 1997
A:Title: cDNA cloning of a novel amphiphysin isoform and tissue-specific expression of i
A:Reference number: JC5593; MUID:97366618; PMID:9223448
A:Accession: JC5593
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-482 <TSU>
A:Cross-references: DDBJ:AF001383; NID:g2199534; PIDN:AAB61363.1; PID:g2199535
A:Experimental source: fetal brain
C:Comment: This protein is involved in the synaptic vesicle recycling and in the regulat
C:Superfamily: amphiphysin; RVS161 protein homology
F:16-275/Domain: RVS161 protein homology <RVS>
F:410-481/Domain: SH3 #status predicted <SH3>

Query Match 60.7%; Score 683; DB 2; Length 482;

Best Local Similarity 61.0%; Pred. No. 4.2e-35;

Matches 136; Conservative 32; Mismatches 53; Indels 2; Gaps 2;

Qy 1 MAE-GRAGGAGLPAKQVQKKTSRAQKVLQKLGKAVETKDERFEQSASNFYQQQAGHK 59

Db 1 MAEWSGKVTAGKIANVQKLTQAEKVLQKLGKADETKDEQFCQVQNFNKQLTEGTR 60

Qy 60 LYKDLNFTLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWNNDLLWEDYEELAD 119

Db 61 LQKDLRTYLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIWNNDLLWEDYEELAD 120

Qy 120 QAVRTWEIVVQSFSEIKERIKRGRKLVYDSARHLEAVQNA-KKDAKTAKEEENK 178

Db 121 QALTMDTYUGQFPDIKSRKGRKLVYDSARHLEAVQNA-KKDAKTAKEEELIK 180

Qy 179 AQTVFEDNLQELLEELPILYNSRIGCYVTIFQINSLRDVFR 221

Db 181 AQKVFEMVNDLQELLEELPILYNSRIGCYVTIFQINSLRDVFR 223

RESULT 2

S62400
amphiphysin (clone 22-2) - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S62400; I37165
R:David, C.; Solimena, M.; de Camilli, P.
FEBS Lett. 351, 73-79, 1994
A:Title: Autoimmunity in Stiff-Man Syndrome with breast cancer is targeted to the C-term
A:Reference number: S48686; MUID:94357284; PMID:8076697

A:Accession: S62400
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-695 <DNA>
A:Cross-references: EMBL:U07616; NID:G550449; PIDN:AAA21865.1; PID:G550450
R:Yamamoto, R.; Li, X.; Winter, S.; Francke, U.; Kilmann, M.W.
Hum. Mol. Genet. 4, 265-268, 1995
A:Title: Primary structure of human amphiphysin, the dominant autoantigen of paraneoplasia
A:Reference number: 137166; MUID:95276740; PMID:7757077
A:Accession: 137166
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-695 <RES>
A:Cross-references: EMBL:X81438; NID:G662991; PIDN:CAA57197.1; PID:G662992
C:Genetics:
A:Gene: GDB:AMPH
A:Cross-references: GDB:386990
A:Map position: 7p4-7p13
C:Superfamily: amphiphysin; RVS161 protein homology
F:11-270/Domain: RVS161 protein homology <RVS>
Query Match 55.2%; Score 620.5; DB 2; Length 695;
Best Local Similarity 54.7%; Pred. No. 4.6e-31;
Matches 116; Conservative 49; Mismatches 46; Indels 1; Gaps 1;
QY 11 GLFAKQVQKFRAGQKVLQKLGKAVETKDERFEQASNFYQQOAGHKLKYLKLNFLSA 70
DB 7 GIFAKNVQKRLNRAQKVLQKLGKADETKDEQFEYQVQKQAEQTRQLQRELGLYLA 66
QY 71 VKVMHSSKRVSETLQEIYSSWDGHEELKAIVNNLLWEDYEKLADQAVTMEIYVA 130
DB 67 IKGMEASMKLTESLHEVYEPDYGREDVQKMGKCVLWDFHQKLVGDSLTLDLYLG 126
QY 131 QPSEIKERIAKGRKLVYDVSARHLEAVQNAK-KDEAKTAAEEFNKAQTVFEDLNQ 189
DB 127 QPFDIKNRIAKESKRLVYDVSARHLEALQSSKRSRISKAEERFQKQKVFEEFNVD 186
QY 190 LLEELPILYNSRIGCYTIFONISNLRDVF 221
DB 187 LOELPFLMSRVRGVYVNTFNKVSLEAKFHK 218
RESULT 3
S22700
amphiphysin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S22700
R:Lichte, B.; Veh, R.W.; Meyer, H.E.; Kilmann, M.W.
EMBO J. 11, 2521-2530, 1992
A:Title: Amphiphysin, a novel protein associated with synaptic vesicles.
A:Reference number: S22700; MUID:92331604; PMID:1628617
A:Accession: S22700
A:Molecule type: mRNA
A:Residues: 1-682 <LIC>
A:Cross-references: EMBL:X60422; NID:G62842; PIDN:CAA42953.1; PID:G62843
C:Superfamily: amphiphysin; RVS161 protein homology
F:11-270/Domain: RVS161 protein homology <RVS>
Query Match 55.0%; Score 618.5; DB 1; Length 682;
Best Local Similarity 54.1%; Pred. No. 5.9e-31;
Matches 120; Conservative 47; Mismatches 50; Indels 5; Gaps 2;
QY 1 MAEGKAGGAGAFQKQVQKFRAGQKVLQKLGKAVETKDERFEQASNFYQQOAGHKL 60
DB 1 MADMK-----TGIFAKNVQKRLNRAQKVLQKLGKADETKDEQFEYQVQKQAEGRSL 56
QY 61 YKDLKLNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIVNNLLWEDYEKLADQ 120
DB 57 QRELRAVLAIAKGMQDASKLTESLHEVYEPDYGREDVQKMGKCVLWDFHQKLVG 116
QY 121 AVRTMEIYVAQSEIKERIAKGRKLVYDVSARHLEAVQNAK-KDEAKTAAEEFNKA 179
DB 117 SLLTLDYVLQGPDIKTRIAKRSKRLVYDVSARHLEALQSSKRSRISKAEERFQK 176
QY 180 QTVFEDLNQELLELPILYNSRIGCYTIFONISNLRDVF 221
DB 177 QKVFEENFDTLQELPFLMSRVRGVYVNTFNKVSLEAKFHK 218
RESULT 4
T22946
hypothetical protein F58G6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T22946
R:Lloyd, C.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19641
A:Accession: T22946
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-461 <WIL>
A:Cross-references: EMBL:Z68217; PIDN:CAA92465.1; GSPDB:GN00022; CESP:F58G6.1
C:Genetics:
A:Gene: CESP:F58G6.1
A:Map position: 4
A:Introns: 19/3; 57/3; 96/3; 130/3; 157/3; 186/3; 219/3; 271/3; 302/3; 335/3; 357/3
C:Superfamily: amphiphysin; RVS161 protein homology
Query Match 36.0%; Score 405; DB 2; Length 461;
Best Local Similarity 39.6%; Pred. No. 5.7e-18;
Matches 84; Conservative 52; Mismatches 74; Indels 2; Gaps 2;
QY 10 AGLFQVQKFRAGQKVLQKLGKAVETKDERFEQASNFYQQOAGHKLKYLKLNFLS 69
DB 2 ADLFNKHLKATNRTKELLEGIGKAKATQDEVDFQRAANLNKQSKCEKLNKDVQVSS 61
QY 70 AVKVMHSSKRVSETLQEIYSSWDGHEELKAIVNNLLWEDYEKLADQAVTMEIYV 129
DB 62 ALRTLLSAEQRLDRTIRDAYEPDYGREDVQKMGKCVLWDFHQKLVGDSLTLDLYLG 121
QY 130 AQFSEIKERIAKGRKLVYDVSARHLEAVQNAK-KDEAKTAAEEFNKAQTVFEDLN 187
DB 122 NQFPDLAKKIEKGRKLVYDVSARHLEALQSSKRSRISKAEERFQKQKVFEEFNVD 181
QY 188 QELLELPILYNSRIGCYTIFONISNLRDVF 219
DB 182 NELLEILPAVDFSRITFFVDTLQTLFNANSVY 213
RESULT 5
T43000
RVS161 protein homolog - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
C:Accession: T43000
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722; PMID:9501991
A:Accession: T43000
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-270 <YOS>
A:Cross-references: EMBL:D89200; NID:G1749607; PIDN:BAAL13861.1; PID:G1749608
A:Experimental source: strain PR745
C:Superfamily: RVS161 protein; RVS161 protein homology
F:10-261/Domain: RVS161 protein homology <RVS>
Query Match 17.3%; Score 194.5; DB 2; Length 270;
Best Local Similarity 29.0%; Pred. No. 3e-05;
Matches 56; Conservative 33; Mismatches 93; Indels 11; Gaps 5;
QY 18 QKFSRAQKVLQKLGKAVETKDERFEQASNFYQQOAGHKLKYLKLNFLSAVKVMHES 77

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Db      13 KAVNRAGTSVMKTHGCHVETVDREFETERRRYTMSAAKQKQKAGVLDALRAMTAS 72
QY      78 SKRVSETLOEYI--SSEWDGHEELKAIWVNDLLWEDYEKLADQAVRTMEI-----YVA 130
Db      73 QTRIANITIDAFYDAGSGKGVSAAYRLV-VKDLADTVKE--LDGPFRTVLDPISRFCS 129
QY      131 OFSEIKERIAKRGKLVYDSARHLE-AVQNAKKDEAKTAKAESEFNKAQTTFEDLNQE 189
Db      130 YFPDINAATIKRNHKLHDHAKRAKQVLVDKPSNDTTKLPRTKEGAAMAKEVYETLNNQ 189
QY      190 LLEELPILYNSRI 202
Db      190 LVSELPOLIALRV 202

RESULT 6
T40661
Yeast reduced viability upon starvation protein 161 homolog, implicated in cell growth a
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C:Accession: T40661
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
Submitted to the EMBL Data Library, November 1998
A:Reference number: Z21889
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-264 <LVN>
A:Cross-references: EMBL:AL034352; PIDN:CAA22181.1; GSPDB:GN00067; SPDB:SPBC725.09c
A:Experimental source: strain 972h-; cosmid c725
C:Genetics:
A:Gene: SPDB:SPBC725.09c
A:Map position: 2
A:Introns: 16/3
C:Superfamily: RVS161 protein; RVS161 protein homology
F:4-255/Domain: RVS161 protein homology <RVS>

Query Match      17.1%; Score 192.5; DB 2; Length 264;
Best Local Similarity 27.8%; Pred. No. 3.9e-05;
Matches 54; Conservative 35; Mismatches 92; Indels 13; Gaps 5;

QY      18 OKFSRAQEKVLQKLGAVETKDERPEQASNFYQQAEGHKLKYLKXFLSAVKVMEES 77
Db      7 KAVNRAGTSVMKTHGCHVETVDREFETERRRYTMSAAKQKQKAGVLDALRAMTAS 66
QY      78 SKRVSETLOEYISSEWDGHEELKAIWVNDLLWEDYEE---KLADQAVRTMEI-----YV 129
Db      67 QTRIANITIDAFYDGA--GSKDGVSAAYRQ--VVEDLDADTVKELDGFRTVLDPISRFC 122
QY      130 AQPSEIKERIAKRGKLVYDSARHLE-AVQNAKKDEAKTAKAESEFNKAQTTFEDLNQ 188
Db      123 SYFPDINAATIKRNHKLHDHAKRAKQVLVDKPSNDTTKLPRTKEGAAMAKEVYETLNN 182
QY      189 ELLELPILYNSRI 202
Db      183 QLVSELPOLIALRV 196

RESULT 7
S19516
RVS161 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YCR009c
C:Species: Saccharomyces cerevisiae
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000
C:Accession: S19516; S28651; S28849
R:Goffeau, A.; Purnelle, B.; Skala, J.
submitted to the Protein Sequence Database, March 1992
A:Reference number: S19420
A:Accession: S19516
A:Molecule type: DNA
A:Residues: 1-265 <GOF>
A:Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42326.1; GSPDB:GN00

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R:Crouzet, M.; Urdaci, M.; Dulau, L.; Aigle, M.
Yeast 7, 727-743, 1991
A:Title: Yeast mutant affected for viability upon nutrient starvation: characterization
A:Reference number: S28651; MUID:92133163; PMID:1776363
A:Accession: S28651
A:Molecule type: DNA
A:Residues: 1-94, 'E', 96-265 <CEO>
A:Cross-references: EMBL:X63315; NID:g4417; PIDN:CAA44926.1; PID:g4418
R:Urdaci, M.; Dulau, L.; Aigle, M.; Crouzet, M.
Yeast 6, 173-176, 1990
A:Title: Sequence of the yeast gene RVS161 located on chromosome III.
A:Reference number: S22849; MUID:90224366; PMID:2183524
A:Accession: S22849
A:Molecule type: DNA
A:Residues: 1-94, 'E', 96-265 <URD>
A:Cross-references: EMBL:X63315; NID:g4417; PIDN:CAA44926.1; PID:g4418
R:Skala, J.; Purnelle, B.; Goffeau, A.
Yeast 8, 409-417, 1992
A:Title: The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of c
K genes.
A:Reference number: S25353; MUID:92327849; PMID:1626432
A:Contents: annotation
C:Genetics:
A:Gene: SGP:RVS161; MIPS:YCR009c
A:Cross-references: SGD:S000602; MIPS:YCR009c
A:Map position: 3R
C:Superfamily: RVS161 protein; RVS161 protein homology
F:4-257/Domain: RVS161 protein homology <RVS>

Query Match      16.0%; Score 179.5; DB 1; Length 265;
Best Local Similarity 24.1%; Pred. No. 0.00025;
Matches 52; Conservative 50; Mismatches 87; Indels 27; Gaps 6;

QY      18 OKFSRAQEKVLQKLGAVETKDERPEQASNFYQQAEGHKLKYLKXFLSAVKVMEES 77
Db      7 KAVNRAGTSVMKTHGCHVETVDREFETERRRYTMSAAKQKQKAGVLDALRAMTAS 64
QY      78 SKRVSETLOEYI--SSEW-----DGHEELKAIWVNDLLWEDYEEK-----LADQA 121
Db      65 QTTIAEIVISNLYDSDSKYAGGVNNGVYVLCV-----QDFDSETVKQLDGPLRETV 116
QY      122 VRTMEIYVAQFSEIKERIAKRGKLVYDSARHLL-EAVQNAKKDEAKTAKAESEFNKAQ 180
Db      117 LDPITFTSTFYKFEIEEIAIKGRDHKKQDFDAKAKVRLVDRKPAKASKLPRAEKLSLAK 176
QY      181 TVFEDLNQELLELPILYNSRIGCVYTFIFONTISNLR 216
Db      177 DIFENLNQKLTLPQLVSLRVPYFPDPSFEALIKIQ 212

RESULT 8
T11684
RVS167 protein homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C:Accession: T11684
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z17313
A:Accession: T11684
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-466 <SEE>
A:Cross-references: EMBL:AL031536
A:Experimental source: strain 972h(-)
C:Genetics:
A:Map position: IIR
A:Introns: 444/3
A:Note: SPBC21D10.12
C:Superfamily: RVS167 protein; RVS161 protein homology; SH3 homology
F:4-270/Domain: RVS161 protein homology <RVS>
F:414-463/Domain: SH3 homology <SH3>

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Query Match      14.1%; Score 158.5; DB 2; Length 466;
Best Local Similarity 23.8%; Pred. No. 0.0034;
Matches 57; Conservative 39; Mismatches 99; Indels 45; Gaps 7;

QY 15 KQVKKFSRAQKVLQKLGKAVETKDERFEQSASNYQQAGHKLKYLKXNLSAVKVM 74
DB 4 KGFTKALARTPQTLRSKFNVTGKPIYEDAGRRFKSLTEAKCLAEADAKKYTDALNGL 63

QY 75 HESSKRVSEITQBIY-----SSEWDGH-----BELKAIYVNNLLMEDYEK 116
DB 64 LNHQIGFADACIEIYKIPISGRASDPSEYQEGNAGIEAFAKYEIV-----DIQKN 116

QY 117 LADQAVRTMEIYVAAF-----SEIKERIAKRGKLVYDSARHHLAEVQNAK-- 163
DB 117 LASE-----MDVINTRVNTPTGELLKIVKDVDDKLLKRDHKQLDYDRHRSFCKLQEKDK 172

QY 164 --KDEAKTAKABEEFNKAQTVFEDLNQELBELPILYNSRGICYVITFQNTLSNLR-DVFY 220
DB 173 SLKDEKLYEATFAFQSSQEQEYIYNNMLKEELPKFLAQSFIAPLQFGYNNLVYY 232

RESULT 9
S40887
RVS167 protein - Yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YDR388w
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000
C;Accession: S40887; S69672
Mol. Cell. Biol. 13, 5070-5084, 1993
R;Bauer, F.; Urdick, M.; Aigle, M.; Crouzet, M.
A;Title: Alteration of a yeast SH3 protein leads to conditional viability with defects in
A;Reference number: S40887; MUID:93330299; PMID:836735
A;Accession: S40887
A;Molecule type: DNA
A;Residues: 1-482 <BAU>
A;Cross-references: EMBL:M92092; NID:g172615; PID:AAA35051.1; PID:g172616
R;Dietrich, F. S.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of S. cerevisiae cosmid 9481, 9509, 9926, 9461, and lambda
A;Reference number: S69665
A;Accession: S69672
A;Molecule type: DNA
A;Residues: 1-482 <DIE>
A;Cross-references: EMBL:U32274; NID:g927313; PID:AAB64830.1; PID:g927321; GSPDB:GN0000
C;Genetics:
A;Gene: SGD:RVS167; MIPS:YDR388w
A;Cross-references: SGD:S0002796; MIPS:YDR388w
A;Map position: 4R
C;Superfamily: RVS167 protein; RVS161 protein homology; SH3 homology
C;Keywords: transmembrane protein
F;4-270/Domain: RVS161 protein homology <RVS>
F;292-422/Region: alanine/glycine/proline-rich
F;428-477/Domain: SH3 homology <SH3>

Query Match      13.7%; Score 154.5; DB 1; Length 482;
Best Local Similarity 24.4%; Pred. No. 0.017;
Matches 61; Conservative 38; Mismatches 100; Indels 51; Gaps 8;

QY 15 KQVKKFSRAQKVLQKLGKAVETKDERFEQSASNYQQAGHKLKYLKXNLSAV--- 71
DB 4 KGFTKAVSRAPOSFRQKFMKGQTEDPVYEDARRPQLEQETKLSSESKRYSTAVNGM 63

QY 72 -----KVMHSSKRV-----ETLQEIYSSSEWDGHEELKAIYVNN--NDLLWED--- 112
DB 64 LTHQIGFAKSMEEIFPKISGKSDPNATIPEDNPQIEASQYRAIVAELOETLKPDLAL 123

QY 113 YEKLAQAVRTMEIYVAAFSEIKERIAKRGKLVYDSARHHLAEVQNAKDEAKTAKA 172
DB 124 VEEKIYVTPQESLKI-----ITVIRQVATRNKHKGLDLD---RHLNTYNNKHEKKEPTAKD 176

QY 173 EEEFNKAQTVFEDLNQELBELPIL-----LLELPIL-----YNSRIGCVYTFIQ 210
DB 177 EERLYRAQVQVQAEQYDYNDLLKTLQPLILFSLAEAFVPLFVSYTFMQLNIFYILYN 236

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QY 211 NISNLRDVFY 220
DB 237 RLQDMKPIYF 246

RESULT 10
A47297
myosin heavy chain form B, nonmuscle - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
C;Accession: A47297; A55441
R;Bhatia-Dey, N.; Adelstein, R.S.; David, I.B.
Proc. Natl. Acad. Sci. U.S.A. 90, 2856-2859, 1993
A;Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmuscl
A;Reference number: A47297; MUID:93219383; PMID:8464900
A;Accession: A47297
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1992 <BHA>
A;Cross-references: GB:L09740; NID:g214623; PID:AAA49915.1; PID:g214624
A;Experimental source: XTC cells
A;Note: sequence extracted from NCBI backbone (NCBI:P:128722)
R;Kelley, C.A.; Oberman, P.; Yisraeli, J.K.; Adelstein, R.S.
J. Biol. Chem. 270, 1395-1401, 1995
A;Title: A Xenopus nonmuscle myosin heavy chain isoform is phosphorylated by cyclin-p34 (
A;Reference number: A55441; MUID:95138137; PMID:7836406
A;Accession: A55441
A;Status: preliminary
A;Molecule type: protein
A;Residues: 198-232 <REL>
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: nucleotide binding; P-loop
F;88-787/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)

Query Match      11.5%; Score 129.5; DB 2; Length 1992;
Best Local Similarity 26.0%; Pred. No. 3;
Matches 56; Conservative 44; Mismatches 76; Indels 39; Gaps 9;

QY 16 QVQKKFSRAQKVLQKLGKAVETKDERFEQSASNYQQAGHKLKYLKXNLSAVKVM 74
DB 1331 QLQDTQELLQEBTRQKLNQ--SRIRQLKEEKNLQEQEERARKSLKQLSLQSQL 1388

QY 75 HESSKRVSEITQEIYSSSEWDGHEEL-KAIYVNNLLMEDYEK-----ADQA 121
DB 1389 TEAKKKVDDEVGTI-----EGLEEVKKLLKDTGELGQRLEKIIAYEKLKTRNLQOE 1443

QY 122 VRTMEIYVAFSEIKERIAKRGKLVYD-----SARHLE---AVONAKDEAKT 169
DB 1444 LDDLNVLDLHQRIQVSNLEKKQK--FDQLLAEEKNISARHAEERDRAEDAREKETKA 1500

QY 170 ---AKAEFEFNKAQTVFEDLNQELBELPILYNSR 201
DB 1501 LSLRALDEALEAQDEPERLNKQLRAEMEDLMSSK 1535

RESULT 11
S52537
emm L 15 protein - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 28-May-1999
C;Accession: S52537
R;Katerov, V.; Schalen, C.; Totolian, A.A.
Mol. Gen. Genet. 245, 78-85, 1994
A;Title: Sequencing of genes within the vir regulon of Streptococcus pyogenes type M15
A;Reference number: S52535; MUID:95147851; PMID:7845360
A;Accession: S52537
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <KAT>
A;Cross-references: GB:S75411; NID:g914107; PID:AAB33262.1; PID:g914110
C;Superfamily: M5 protein

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Query Match      11.3%; Score 127; DB 2; Length 377;
Best Local Similarity 24.9%; Pred. No. 0.65; Mismatches 33; Indels 72; Gaps 8;
Matches 55; Conservative 33;

QY 19 KFSRAQEKVLQKLG-----KAVETKDRFPQSASNFYQQAEGHKLKDLNLFSAVK 72
Db 68 EKLKENRYLEKIGQBERQKLEKQERFQVAAADKHQYQVQKQYKQ-----118
QY 73 VMHESKRYSETLOEITYSSEWDGHEELKAIWNNDLLWEDYEELKADQAVTMEIYVQAF 132
Db 119 -EGERKQKQEQERKYQREVE-----KRYOEQLQKQ-----QQ 151
QY 133 SEIKERIAKGRKLVDYDSARHLEAVONAKKD-EAKTAKAEEB-----175
Db 152 LETEKQISEARSKLSRD-----LEASRAAKKQLEAEHQKLEKQISDASREBSRDLE 206
QY 176 --PNKAQTVPEDL-----NQLLELPILYNSRIGCVVTI 208
Db 207 ASRESKRYEADLAALTAHQKLEKQISDASRQGLSVTL 247

RESULT 12
A26655
myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum)
N;Contains: myosin Atpase (EC 3.6.4.1)
C;Species: Dictyostelium discoideum
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 19-Apr-2002
C;Accession: A26655; A24728; S00250
R;Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986
A;Title: Conserved protein domains in a myosin heavy chain gene from Dictyostelium discoideum
A;Reference number: A26655; MUID:87092266; PMID:3540939
A;Accession: A26655
A;Molecule type: DNA
A;Residues: 1-2116 <WAR>
A;Cross-references: GB:M14628; GB:M11938; NID:g167834; PIDN:AAA33227.1; PID:g167835
R;DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985
A;Reference number: A24728; MUID:86016788; PMID:3901008
A;Accession: A24728
A;Molecule type: mRNA
A;Residues: 2035-2116 <DEL>
R;Waggle, G.; Noegel, A.; Scheel, J.; Gerisch, G.
FEBS Lett. 227, 71-75, 1988
A;Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostelium myosin heavy chain
A;Reference number: S00250; MUID:88112226; PMID:2828113
A;Accession: S00250
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1734-1893 <WAG>
C;Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phosphatase
F1-818/Domain: globular head <HED>
F189-747/Domain: myosin motor domain homology <MWOT>
F179-186/Region: nucleotide-binding motif A (P-loop)
F:819-2116/Domain: alpha-helical rod <ROD>

Query Match      10.7%; Score 120.5; DB 2; Length 2116;
Best Local Similarity 22.7%; Pred. No. 12;
Matches 54; Conservative 39; Mismatches 90; Indels 55; Gaps 5;

QY 14 AKQVKQFSRAQEKVLQKGVATKDRFPQSASNFYQQAEGHKLKDLNLFSAVKV 73
Db 1277 AKQALEKKRLGLESLKHNQLEBEKKQESNEKRVLDLEKEVSELKQDIESEVASKKA 1336
QY 74 MHESKRYSETLOEIT-----YSEWDGHEELKAIWNNDLLWEDYEELKADQAVRTME 126
Db 1337 VTEAKNKKSELDIEIKRYADVWSRDKSVFQLATLQAKNEELRNATAEE-----1385
QY 127 IYVAFPSIETKERIAKGRKLVDYDSARHLEAVONAKKDEAKTAKAEEFNKQAVTFED- 185
Db 127 IYVAFPSIETKERIAKGRKLVDYDSARHLEAVONAKKDEAKTAKAEEFNKQAVTFED- 185

Query Match      10.3%; Score 116; DB 2; Length 1940;
Best Local Similarity 26.2%; Pred. No. 20;
Matches 50; Conservative 29; Mismatches 76; Indels 36; Gaps 7;

```


Search completed: March 4, 2004, 17:31:44
Job time : 12.135 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:21:39 ; Search time 5.63057 Seconds
(without alignments)
2043.754 Million cell updates/sec

Title: US-10-069-540A-2_COPY_1_221

Perfect score: 1125

Sequence: 1 MAEGKAGGAGLFAKQVKK.....IGCVTFQINSLRDVFYR 221

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663.5	59.0	588	1 BIN1 MOUSE	O08539 mus musculus
2	663.5	59.0	588	1 BIN1 RAT	O08839 rattus norv
3	657.5	58.4	593	1 BIN1 HUMAN	O00439 homo sapien
4	620.5	55.2	683	1 AMPH RAT	P49418 rattus norv
5	620.5	55.2	695	1 AMPH HUMAN	P50478 homo sapien
6	618.5	55.0	682	1 AMPH CHICK	Q9UUM7 gallus gall
7	192.5	17.1	264	1 HOB3 SCHPO	P25343 schizosacch
8	179.5	16.0	265	1 R161 YEAST	O74352 schizosacch
9	158.5	14.1	466	1 HOB1 SCHPO	P39743 saccharomyc
10	154.5	13.7	482	1 R167 YEAST	Q9QY00 homo sapien
11	143	12.7	253	1 BIN3 HUMAN	O42184 gallus gall
12	122.5	10.9	1433	1 RST CHICK	P08799 dictyostell
13	120.5	10.7	2116	1 MYS2 DICDI	Q8WXH0 homo sapien
14	118.5	10.5	6885	1 SNE2 HUMAN	Q14789 homo sapien
15	116	10.3	3259	1 COB1 HUMAN	O58371 pyrococcus
16	114	10.1	226	1 V637 PYRHO	Q58718 methanococc
17	113	10.0	1005	1 R450 METUA	Q08638 mus musculus
18	113	10.0	1300	1 DINA NEUCR	P54697 dictyostell
19	113	10.0	1972	1 MYH3 MOUSE	O08638 mus musculus
20	112.5	10.0	2245	1 MYSJ DICDI	P25386 saccharomyc
21	111.5	9.9	1790	1 USO1 YEAST	O59037 methanococc
22	110.5	9.8	1169	1 SMC METUA	P24445 caenorhabdi
23	110	9.8	288	1 Y187 CASEL	P30468 streptococc
24	110	9.8	407	1 M21 STRPY	P35749 homo sapien
25	110	9.8	1972	1 MYH8 HUMAN	Q9J1T0 rattus norv
26	109.5	9.7	944	1 NUF1 YEAST	P32908 saccharomyc
27	109.5	9.7	1225	1 SMC1 YEAST	P32908 saccharomyc
28	109.5	9.7	1225	1 SMC1 YEAST	P32908 saccharomyc
29	109	9.7	284	1 TPM ECHMU	O95PUL echinococc
30	109	9.7	520	1 RECN AQUAE	O66834 aquifex aeo
31	109	9.7	942	1 SYL METUA	Q58050 methanococc
32	109	9.7	1170	1 SMC2 YEAST	P38989 saccharomyc
33	109	9.7	2017	1 MYSN_DROME	Q99323 drosophila

34	108.5	9.6	692	1 MYS PODCA	Q05000 podocoryne
35	108.5	9.6	1679	1 YIO9 YEAST	P40457 saccharomyc
36	108	9.6	967	1 SYL PYRHO	O58698 pyrococcus
37	108	9.6	1224	1 DYN4 CHICK	P35458 gallus gall
38	108	9.6	1972	1 MYH8 RABIT	P35748 oryctolagus
39	107.5	9.6	1020	1 CF60 HUMAN	O8nb25 homo sapien
40	107	9.5	975	1 KINH_DROME	P17210 drosophila
41	107	9.5	1360	1 CING_XENLA	Q9Ptd7 xenopus lae
42	107	9.5	1976	1 MYH4 BOVIN	O27991 bos taurus
43	107	9.5	1976	1 MYH4 HUMAN	P35580 homo sapien
44	106.5	9.5	1312	1 RA50 YEAST	P12753 saccharomyc
45	105.5	9.4	248	1 TPM4 RAT	P09495 rattus norv

ALIGNMENTS

RESULT 1					
BIN1_MOUSE					
ID	BIN1_MOUSE	STANDARD;	PRT;	588 AA.	
AC	O08539; Q62434;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Myc box dependent interacting protein 1 (Bridging integrator 1)				
DE	(Amphiphysin-like protein) (Amphiphysin II) (SH3-domain containing protein 9).				
DE					
GN	BIN1 OR AMPHL OR SH3P9.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI TaxID=10090;				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	STRAIN=BALB/c; TISSUE=Brain;				
RX	MEDLINE=97326078; PubMed=9182529;				
RA	Leprince C., Romero F., Cussac D., Vayssi�re B., Berger R.,				
RA	Tavitian A., Canonis J.H.;				
RT	"A new member of the amphiphysin family connecting endocytosis and signal transduction pathways."				
RL	J. Biol. Chem. 272:15101-15105(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	TISSUE=Embryo;				
RX	MEDLINE=98294438; PubMed=9630982;				
RA	Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;				
RT	"Cloning of ligand targets: systematic isolation of SH3 domain-containing proteins."				
RL	Nat. Biotechnol. 14:741-744(1996).				
RN	[3]				
RP	INTERACTION WITH SH3GLB1.				
RX	MEDLINE=22450649; PubMed=12456676;				
RA	Modregger J., Schmidt A.A., Ritter B., Huttner W.B., Plomann M.;				
RT	"Characterization of endophilin B1b, a brain-specific membrane-associated lysophosphatidic acid acyl transferase with properties distinct from endophilin A1."				
RL	J. Biol. Chem. 278:4160-4167(2003).				
CC	- FUNCTION: May be involved in regulation of synaptic vesicle endocytosis. May act as a tumor suppressor and inhibits malignant cell transformation.				
CC	- SUBUNIT: Heterodimer with AMPH (By similarity). Binds to SYNJ1 and DNMI through its SH3 domain, and to clathrin through a region outside of the SH3 domain. Also binds to alpha-adaptin. Interacts with the N-terminal transactivation domain of MYC in a manner requiring the integrity of the conserved MYC box regions 1 and 2. Binds SH3GLB1.				
CC	- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).				
CC	- ALTERNATIVE PRODUCTS:				
CC	Event-Alternative splicing; Named isoforms=2;				
CC	Name=1; Synonyms=BRAMP2;				
CC	IsoId=O08539-1; Sequence=Displayed;				
CC	Name=2; Synonyms=SH3P9;				
CC	IsoId=O08539-2; Sequence=VSP_000254, VSP_000255;				

```

CC -!- TISSUE SPECIFICITY: Isoform 1 is expressed mainly in the
CC brain. Isoform 2 is widely expressed.
CC -!- PTM: Phosphorylated by protein kinase C (By similarity).
CC -!- SIMILARITY: Contains 1 BAR domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U86405; AAC53318.1; -
CC EMBL; U60884; AAC52661.1; -
CC MGd; MG1108092; Bin1.
CC InterPro; IPR003005; Amphiphysin.
CC InterPro; IPR006632; BAR.
CC InterPro; IPR004148; BAR dom.
CC InterPro; IPR001452; SH3.
CC Pfam; PF03114; BAR; 1.
CC Pfam; PF00018; SH3; 1.
CC PRINTS; PR01251; AMPHIPHYSIN.
CC PRINTS; PR00452; SH3DOMAIN.
CC ProDom; PD000066; SH3; 1.
CC SMART; SM00721; BAR; 1.
CC SMART; SM00326; SH3; 1.
CC PROSITE; PS50002; SH3; 1.
CC KW Alternative splicing; SH3 domain; Coiled coil; Endocytosis;
CC Anti-oncogene; Differentiation; Phosphorylation.
CC DOMAIN 15 42
CC FT COILED COIL (POTENTIAL).
CC FT DOMAIN 193 274
CC FT DOMAIN 379 422
CC FT DOMAIN 515 588
CC FT VARSPLIC 174 204
CC FT Missing (in isoform 2).
CC FT VARSPLIC 335 457
CC FT Missing (in isoform 2).
CC FT /FTID=VSP_000255.
CC FT /FTID=VSP_000256.
CC SQ SEQUENCE 588 AA; 64470 MW; 63CA362461500F38 CRC64;

Query Match 59.0%; Score 663.5; DB 1; Length 588;
Best Local Similarity 54.3%; Pred. No. 9.3e-33;
Matches 138; Conservative 30; Mismatches 53; Indels 33; Gaps 3;

QY 1 MAE-GKAGAGLFAKQVQKFSRAQEKVLQKGLKAVETKDRFEQBSANFYQQAGHGK 59
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 LYKDLKNFLSAVKVWHESSKRVSELTQELIYSEWDGHEELKAIWVNDLLWEDYEKLD 119
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 LQDRLTYLASVKAHAEKSLCEQLQSVYEPFPGHGRDEANKIAENNDDLLMDYHQLVD 120
QY 120 QAVRTMEIYVAQFSEIKERIAKRGKLVYDYSARRHLEAVQNA-KDEAKTAK----- 171
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 QALLTMDTVLGQFPDIKSRIAKRGKLVYDYSARRHYESLTQAKKDEAKIAKPSVLEK 190
QY 172 -----AEEFNKAQTVFEDLNQELLEELPILYNRRIGCYVT 207
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 AAPQWCGQKLOHLVAQTNLLRNQAEELIRAKQVFPEMVDLOEELFSLWNSRVGFYN 240
QY 208 IFQNISNLRDVFYR 221
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TFQSIAGLEENPHK 254

RESULT 2
ID BIN1.RAT
AC O08839;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

```

```

DE DE Myc box dependent interacting protein 1 (Bridging integrator 1)
GN GN BIN1 OR AMPH1 OR AMPH2.
OS OS Rattus norvegicus (Rat).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX OX NCBI_TaxID=10116;
RN RN [1]
RP RP SEQUENCE FROM N.A.; SUBUNIT, AND ALTERNATIVE SPLICING.
RC RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex, and Kidney;
RX RX MEDLINE=98009145; PubMed=9348539;
RA RA Wigge P., Kohler K., Hunt S., Doyle C., McMahon H.T.;
RT "Amphiphysin heterodimers: potential role in clathrin-mediated
RT endocytosis".
RL RL Mol. Biol. Cell 8:2003-2015 (1997).
RN RN [2]
RP RP SEQUENCE FROM N.A. (ISOFORM AMPH2-1).
RC RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex;
RX RX MEDLINE=97424383; PubMed=9280305;
RA RA McMahon H.T., Wigge P., Smith C.;
RT "Clathrin interacts specifically with amphiphysin and is displaced by
RT dynamin.".
RL RL FEBS Lett. 413:319-322 (1997).
RN RN [3]
RP RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 506-588, FUNCTION, AND
RP INTERACTION WITH DNM1.
RX RX MEDLINE=98409533; PubMed=9736607;
RA RA Owen D.J., Wigge P., Vallis Y., Moore J.D.A., Evans P.R.,
RA McMahon H.T.;
RT "Crystal structure of the amphiphysin-2 SH3 domain and its role in the
RT prevention of dynamin ring formation.".
RL RL EMBO J. 17:5273-5285 (1998).
CC CC -!- FUNCTION: May be involved in regulation of synaptic vesicle
CC endocytosis. May act as a tumor suppressor and inhibits
CC malignant cell transformation.
CC -!- SUBUNIT: Heterodimer with AMPH. Binds SH3GLB1 (By similarity).
CC Binds to SYNJ1 and DNM1 through its SH3 domain, and to clathrin
CC through a region outside of the SH3 domain. Also binds to alpha-
CC adaptin. Interacts with the N-terminal transactivation domain of
CC MYC in a manner requiring the integrity of the conserved MYC box
CC regions 1 and 2.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=AMPH2-1;
CC IsoId=O08839-1; Sequence=Displayed;
CC Name=AMPH2-2;
CC IsoId=O08839-2; Sequence=VSP_000260;
CC Name=AMPH2-3;
CC IsoId=O08839-3; Sequence=VSP_000258;
CC Name=AMPH2-4;
CC IsoId=O08839-4; Sequence=VSP_000257;
CC Name=AMPH2-5;
CC IsoId=O08839-5; Sequence=VSP_000259;
CC Name=AMPH2-6;
CC IsoId=O08839-6; Sequence=VSP_000256, VSP_000259;
CC -!- TISSUE SPECIFICITY: Isoform AMPH2-1 is expressed in brain,
CC concentrated at nerve terminals. Isoform AMPH2-2 is widely
CC expressed.
CC -!- PTM: Phosphorylated by protein kinase C.
CC -!- SIMILARITY: Contains 1 BAR domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
CC EMBL; Y13380; CAA73807.1; -
CC PDB; 1BB9; 17-JUN-98.

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DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
KW Alternative splicing; SH3 domain; Coiled coil; Endocytosis;
KW Anti-oncogene; Differentiation; Phosphorylation; 3D-structure.
FT DOMAIN 15 42
FT COILED COIL (POTENTIAL).
FT DOMAIN 193 274
FT COILED COIL (POTENTIAL).
FT DOMAIN 379 422
FT CLATHRIN-BINDING (BY SIMILARITY).
FT DOMAIN 515 588
FT SH3.
FT VARSPLIC 173 205
FT Missing (in isoform AMPH2-4 and isoform
FT AMPH2-6).
FT FTID=VSP 000256.
FT Missing (in isoform AMPH2-4).
FT VARSPLIC 253 588
FT FTID=VSP 000257.
FT Missing (in isoform AMPH2-3).
FT VARSPLIC 335 588
FT FTID=VSP 000258.
FT Missing (in isoform AMPH2-5 and isoform
FT AMPH2-6).
FT FTID=VSP 000259.
FT Missing (in isoform AMPH2-2).
FT VARSPLIC 423 460
FT FTID=VSP 000260.
SQ SEQUENCE 588 AA; 64533 MW; 164AC90E9547F1A CRC64;

Query Match 59.0%; Score 663.5; DB 1; Length 588;
Best Local Similarity 54.3%; Pred. No. 9.3e-33;
Matches 138; Conservative 30; Mismatches 53; Indels 33; Gaps 3;

QY 1 MAE-GKAGAGLPAKQVOKFSPRAQKVLQKAVETKDERPEQASNYFOQQAEGHK 59
DB 1 MAEMSGKGTAGKIASNVQKLTAKQAEKVLQKAGADETKDEQECQVQNFQKLTGTR 60

QY 60 LYKDLKFLSAVKVNHSSKVSFETLQIYSSEWDGHEELKAIWNNDLLWEDYEKLAD 119
DB 61 LQDLRTYLSAKVMEHASKLSCLQVYEPFEPFGDEANKAENNDLLWMDYHOKLVD 120

QY 120 QAVRTMEIYVAQSFSEIKRIARGRKLVYDPSARHHLAVQNA-KKDEAKTAK----- 171
DB 121 QALLTMDTYLGQFPDIKSRIARGRKLVYDPSARHLYESSLTAKKDEAKIAPVSLLEK 180

QY 172 -----AEEFNKAQTVFEDLNQELLEKLPILYNSRIGCYVT 207
DB 181 AAPQVQCKQLQHLVAQNTLNRQAEBELIKAKVFEMNVDLQELFSLWNSRVGFYN 240

QY 208 IFQINSLNRDVPYR 221
DB 241 TFQSIAGLEENFHK 254

RESULT 3
BIN1_HUMAN
ID BIN1_HUMAN STANDARD; PRT; 593 AA.
AC O00499; O00297; O00545; O43867; O60552; O60553; O60554; O60555;
AC O75514; O75515; O75516; O75517; O75518; O92944; Q99688;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Myc box dependent interacting protein 1 (Bridging integrator 1)
DE (Amphiphysin-like protein) (Amphiphysin II) (Box-dependent myc-
DE interacting protein-1).
GN BIN1 OR AMPHL
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

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RN RP SEQUENCE FROM N.A. (ISOFORM IIA).
RC TISSUE=Brain;
RX MEDLINE=97341217; PubMed=9195986;
RA Ramjaun A.R., Micheva K.D., Bouchelet I., McPherson P.S.;
RT "Identification and characterization of a nerve terminal-enriched
RT amphiphysin isoform.";
RL J. Biol. Chem. 272:16700-16706 (1997).
RN RP SEQUENCE FROM N.A. (ISOFORMS IIA AND BIN1).
RC TISSUE=Brain, and skeletal muscle;
RX MEDLINE=97327761; PubMed=9182667;
RA Butler M.H., David C., Ochoa G.-C., Freyberg Z., Daniell L., Grabs D.,
RA Crenona O., De Camilli P.;
RT "Amphiphysin II (SH3P9; BIN1), a member of the amphiphysin/Rvs family,
RT is concentrated in the cortical cytomatrix of axon initial segments
RT and nodes of ranvier in brain and around T tubules in skeletal
RT muscle.";
RL J. Cell Biol. 137:1355-1367 (1997).
RN RP SEQUENCE FROM N.A. (ISOFORM BIN1).
RC TISSUE=Skeletal muscle;
RX MEDLINE=96376973; PubMed=8782822;
RA Sakamuro D., Elliott K.J., Wechsler-Reya R., Prendergast G.C.;
RT "BIN1 is a novel Myc-interacting protein with features of a tumour
RT suppressor.";
RL Nat. Genet. 14:69-76 (1996).
RN RP REVISIONS TO N-TERMINUS.
RA Sakamuro D., Elliott K.J., Wechsler-Reya R., Prendergast G.C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE FROM N.A. (ISOFORMS IIB; IIC1; IIC2 AND IID).
RC TISSUE=Brain;
RX MEDLINE=98264340; PubMed=9603201;
RA Ramjaun A.R., McPherson P.S.;
RT "Multiple amphiphysin II splice variants display differential clathrin
RT binding: identification of two distinct clathrin-binding sites.";
RL J. Neurochem. 70:2369-2376 (1998).
RN RP SEQUENCE FROM N.A. (ISOFORMS I12 AND I13).
RC TISSUE=Brain;
RX MEDLINE=97366618; PubMed=9223448;
RA Tsutsui K., Maeda Y., Tsutsui K., Seki S., Tokunaga A.;
RT "cDNA cloning of a novel amphiphysin isoform and tissue-specific
RT expression of its multiple splice variants.";
RL Biochem. Biophys. Res. Commun. 236:178-183 (1997).
RN RP SEQUENCE FROM N.A. (ISOFORMS I13; I13; BIN1-10-13; BIN1-13 AND
RN BIN1+12A).
RC TISSUE=Fibroblast;
RX MEDLINE=98058932; PubMed=9395479;
RA Wechsler-Reya R.J., Sakamuro D., Zhang J., DuHadaway J.,
RA Prendergast G.C.;
RT "Structural analysis of the human BIN1 gene. Evidence for tissue-
RT specific transcriptional regulation and alternate RNA splicing.";
RL J. Biol. Chem. 272:31453-31458 (1997).
RN RP SEQUENCE FROM N.A. (ISOFORM I12).
RA Zhang J., Du W., Wechsler-Reya R.J., DuHadaway J., Sakamuro D.,
RA Prendergast G.C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN RP SEQUENCE OF 133-593 FROM N.A.
RC TISSUE=Brain;
RA Yu W., Gibbs R.A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN RP CHARACTERIZATION.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98078712; PubMed=9418903;
RA Wechsler-Reya R.J., Elliott K.J., Prendergast G.C.;
RT "A role for the putative tumor suppressor Bin1 in muscle cell

```

RT differentiation.":
 RL Mol. Cell. Biol. 18:566-575(1998).
 CC -!- FUNCTION: May be involved in regulation of synaptic vesicle
 CC endocytosis. May act as a tumor suppressor and inhibits
 CC malignant cell transformation.
 CC -!- SUBUNIT: Heterodimer with AMPH. Binds SH3GLB1 (By similarity).
 CC Binds to SYNJ1 and DNMI1 through its SH3 domain, and to clathrin
 CC through a region outside of the SH3 domain. Also binds to alpha-
 CC adaptin. Interacts with the N-terminal transactivation domain of
 CC MYC in a manner requiring the integrity of the conserved MYC box
 CC regions 1 and 2.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Isoform Ila is
 CC found in the cytoplasm while isoform BIN1 is nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=11;
 CC Comment=Additional isoforms seem to exist;
 CC Name=Ila;
 CC IsoId=O00499-1; Sequence=Displayed;
 CC Name=IIB;
 CC IsoId=O00499-2; Sequence=VSP_000246, VSP_000252;
 CC Name=IIC1;
 CC IsoId=O00499-3; Sequence=VSP_000249;
 CC Name=IIC2;
 CC IsoId=O00499-4; Sequence=VSP_000246, VSP_000249;
 CC Name=IID;
 CC IsoId=O00499-5; Sequence=VSP_000248;
 CC Name=II2;
 CC IsoId=O00499-6; Sequence=VSP_000246, VSP_000253;
 CC Name=II3;
 CC IsoId=O00499-7; Sequence=VSP_000246, VSP_000250;
 CC Name=BIN1;
 CC IsoId=O00499-8; Sequence=VSP_000246, VSP_000247, VSP_000250;
 CC Name=BIN1-10-13;
 CC IsoId=O00499-9; Sequence=VSP_000246, VSP_000251;
 CC Name=BIN1-13;
 CC IsoId=O00499-10; Sequence=VSP_000246, VSP_000247, VSP_000251;
 CC Name=BIN1-12A;
 CC IsoId=O00499-11; Sequence=VSP_000246, VSP_000247, VSP_000253;
 CC TISSUE SPECIFICITY: ISOFORM IIA IS EXPRESSED ONLY IN THE BRAIN
 CC WHERE IT IS CONCENTRATED IN AXON INITIAL SEGMENTS AND NODES OF
 CC RANVIER. ISOFORM BIN1 IS WIDELY EXPRESSED WITH HIGHEST EXPRESSION
 CC IN SKELETAL MUSCLE.
 CC -!- PTM: Phosphorylated by protein kinase C (By similarity).
 CC -!- SIMILARITY: Contains 1 BAR domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC -----
 CC EMBL; AF004015; AAC51345.1; -
 CC EMBL; AF070576; AAC28646.1; -
 CC EMBL; U68485; AAC17461.1; -
 CC EMBL; AF001383; BAB61363.1; -
 CC EMBL; AF043898; AAC39710.1; -
 CC EMBL; AF043899; AAC39711.1; -
 CC EMBL; AF043900; AAC39712.1; -
 CC EMBL; AF043901; AAC39713.1; -
 CC EMBL; U87558; AAB63263.1; -
 CC EMBL; AF068914; AAC24126.1; -
 CC EMBL; AF068915; AAC24127.1; -
 CC EMBL; AF068916; AAC24128.1; -
 CC EMBL; AF068917; AAC23750.1; -
 CC EMBL; AF068918; AAC23751.1; -
 CC EMBL; U84004; AAC23440.1; -
 CC EMBL; U83999; AAC23440.1; JOINED.
 CC EMBL; U84001; AAC23440.1; JOINED.
 CC EMBL; U84002; AAC23440.1; JOINED.
 CC EMBL; U84003; AAC23440.1; JOINED.

DR EMBL; U84004; AAC23441.1; ALT INIT.
 DR EMBL; U83999; AAC23441.1; JOINED.
 DR EMBL; U84001; AAC23441.1; JOINED.
 DR EMBL; U84002; AAC23441.1; JOINED.
 DR EMBL; U84003; AAC23441.1; JOINED.
 DR PIR; JC5593; JC5593.
 DR TRANSFAC; T03490; -
 DR Genew; HGNC:1052; BIN1.
 DR MIM; 601248; -
 DR GO; GO:0015629; C:actin cytoskeleton; TAS.
 DR GO; GO:0008283; P:cell proliferation; TAS.
 DR GO; GO:0006899; P:nonspecific vesicle transport; TAS.
 DR GO; GO:0000074; P:regulation of cell cycle; TAS.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR004148; BAR_dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYGIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.
 DR ProSITE; PS00002; SH3; 1.
 KW Alternative splicing; SH3 domain; Coiled coil; Endocytosis;
 KW Anti-oncogene; Differentiation; Phosphorylation.
 FT DOMAIN 15 42
 FT COILED COIL (POTENTIAL).
 FT DOMAIN 193 267
 FT COILED COIL (POTENTIAL).
 FT DOMAIN 378 421
 FT CLATHRIN-BINDING.
 FT DOMAIN 520 592
 FT SH3.
 FT VARSPLIC 174 204
 FT Missing (in isoform IIB, isoform IIC2,
 FT isoform II2, isoform II3, isoform BIN1,
 FT isoform BIN1-12A, isoform BIN1-10-13 and
 FT isoform BIN1-13).
 FT /FTId=VSP_000246.
 FT VARSPLIC 285 285
 FT P -> PRKSKLFSRLRRKN (in isoform BIN1,
 FT isoform BIN1-12A and isoform BIN1-13).
 FT /FTId=VSP_000247.
 FT VARSPLIC 335 377
 FT Missing (in isoform IID).
 FT /FTId=VSP_000248.
 FT VARSPLIC 335 421
 FT Missing (in isoform IIC1 and isoform
 FT IIC2).
 Query Match 58.4%; Score 657.5; DB 1; Length 593;
 Best Local Similarity 53.5%; Pred. No. 2.1e-32;
 Matches 136; Conservative 32; Mismatches 53; Indels 33; Gaps 3;
 QY 1 MAE-GKAGAGLFAKQVKKFRAQEKVLQKLGKAVETKDERFEQASNFYQQAGHKK 59
 DB 1 MAEMSGKVTAGKLASNVQKKLTRAQEKVLQKLGKADETKDEQECVQNFNKLTEGTR 60
 QY 60 LYKDKKFLSAVKVHSSKRVSETLQETYSSEWDGHEELKALVWNDLLWEDYEKLAD 119
 DB 61 LQKDLRTYLASVKAMHEASKKLNCEIQEVTEPDPWGRDEANKIAENNDLLWMDYHQLVD 120
 QY 120 QAVRTMEIYVAQFSEIKERIAKGRKLVVDYSARHHEAVQNA-KDEAKTAK----- 171
 DB 121 QALLTMDTLGQPPDIKRIAKGRKLVVDYSARHHEYSLSQTAKKDKAKIAPVSLLEK 180
 QY 172 -----AEEFNKAQTVFEDLNQELLEELPLINSRIGCVTV 207
 DB 181 AAPQWCCQKLQAHVLAQTNLLRNQAEELIKAKQVFENNVDLQELPSELNRSRVGYVN 240
 QY 208 IFQNISNLRVFVYR 221
 DB 241 TFQSIAGLEENFHK 254
 RESULT 4
 AMPH RAT STANDARD; PRT; 683 AA.
 ID AMPH RAT
 AC O08838;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

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DE Amphiphsyn.
GN AMPH OR AMPH1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=98009145; PubMed=9348539;
RA Wigge P., Kohler K., Vallis Y., Owen D., Hunt S.P., McMahon H.T.;
RT "Amphiphysin heterodimers: potential role in clathrin-mediated
RL endocytosis.";
RT Mol. Biol. Cell 8:2003-2015 (1997).
CC -1- FUNCTION: May participate in mechanisms of regulated exocytosis in
CC synapses and certain endocrine cell types. May control the
CC properties of the membrane associated cytoskeleton (By
CC similarity).
CC -1- SUBUNIT: Heterodimer with BIN1. Binds SH3GLB1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Peripheral membrane protein associated with
CC the cytoplasmic surface of synaptic vesicles (By similarity).
CC -1- SIMILARITY: Contains 1 BAR domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DE EMBL; Y13381; CAA73808.1; -
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR003017; Amphiphysin_1.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PRO1251; AMPHIPHYSIN.
DR PRINTS; PRO0452; SH3DOMAIN.
DR ProDom; PD003208; Amphiphysin_1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR Cytoskeleton; SH3 domain; Coiled coil.
FT DOMAIN 10 83 COILED COIL (POTENTIAL).
FT DOMAIN 144 191 COILED COIL (POTENTIAL).
FT DOMAIN 610 683 SH3.
SQ SEQUENCE 683 AA; 74877 MW; 7FEA4A9B5A1F6631 CRC64;

Query Match
Best Local Similarity 55.2%; Score 620.5; DB 1; Length 683;
Matches 116; Conservative 49; Mismatches 46; Indels 1; Gaps 1;

QY 11 GLFAQVQKFSRAQEKVLOKLGAVETKDERFEQASNFYQQAGHKLYKDLXNFLSA 70
Db 7 GIFAQVQKLNRAQEKVLOKLGAVETKDERFEQASNFYQQAGHKLYKDLXNFLSA 66
QY 71 VYVHESKRVSELTQBIYSSEWDGHEELKAIYVNNDDLWEDYEELADQAVRTWEIYVA 130
Db 67 IKGQASMKLTESLHEVEYFPDWMYGRDVKVNGEKDVLWEDPHQKLVGSLTLDYLG 126
QY 131 QFSIKRIAKRGKLVYDSARHLEAVQNAK-KDEAKTAKAEFPNKAQVTFEDLNQEB 189
Db 127 QFPDIKNRIAKRGKLVYDSARHLEALQSSRRKDESRKAEBFQKAQKVFPEFNV 186
QY 190 LLEELPILYNSRGICYVTTFQNTISNLRDVFYR 221
Db 187 LQELPSLWRRGVFYNTFNKVSLEAKFKH 218

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RESULT 5
AMPH_HUMAN
ID AMPH_HUMAN STANDARD; PRT; 695 AA.
AC P49418; O43538;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amphiphysin.
GN AMPH OR AMPH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Cerebellum;
RX MEDLINE=94357284; PubMed=8076697;
RA David C., Solimena M., de Camilli P.;
RT "Autoimmunity in stiff-man syndrome with breast cancer is targeted to
RT the C-terminal region of human amphiphysin, a protein similar to the
RT yeast proteins, Rvs167 and Rvs161.";
RT FEBS Lett. 351:73-79 (1994).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=95276740; PubMed=7757077;
RA Yamamoto R., Li X., Winter S., Francke U., Kilian M.W.;
RT "Primary structure of human amphiphysin, the dominant autoantigen of
RT paraneoplastic stiff-man syndrome, and mapping of its gene (AMPH) to
RT chromosome 7p13-p14.";
RT Hum. Mol. Genet. 4:265-268 (1995).
RL [3]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Breast;
RX MEDLINE=98174372; PubMed=9513187;
RA Floyd S.R., Butler M.H., Cremona O., David C., Freyberg Z., Zhang X.,
RA Solimena M., Tokunaga A., Ishizu H., Tsutsui K., De Camilli P.V.;
RT "Expression of amphiphysin I, an autoantigen of paraneoplastic
RT neurological syndromes, in breast cancer.";
RT Mol. Med. 4:29-39 (1998).
CC -1- FUNCTION: May participate in mechanisms of regulated exocytosis in
CC synapses and certain endocrine cell types. May control the
CC properties of the membrane associated cytoskeleton.
CC -1- SUBUNIT: Heterodimer of AMPH and AMPH1 (By similarity).
CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC SURFACE OF
CC SYNAPTIC VESICLES.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=128 kDa;
CC IsoId=P49418-1; Sequence=Displayed;
CC Name=2; Synonyms=108 kDa;
CC IsoId=P49418-2; Sequence=VSP_000245;
CC -1- TISSUE SPECIFICITY: Neurons, certain endocrine cell types and
CC spermatocytes.
CC -1- DISEASE: Patients with stiff-man syndrome, a rare disease of the
CC central nervous system characterized by progressive rigidity of
CC the body musculature with superimposed painful spasms, have
CC antibodies against AMPH.
CC -1- SIMILARITY: Contains 1 BAR domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
DE EMBL; U07616; AAA1865.1; -
DR EMBL; X81438; CAA57197.1; -
DR EMBL; AF034996; AAC02977.1; -

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DR PIR; S62400; S62400.
DR PDB; 1KV7; 12-JUN-02.
DR Genew; HGNC:471; AMPH.
DR MIM; 600418; -.
DR GO; GO:0015629; C:actin cytoskeleton; TAS.
DR GO; GO:0006021; C:synaptic vesicle; TAS.
DR GO; GO:0006897; P:endocytosis; TAS.
DR GO; GO:0007268; P:synaptic transmission; TAS.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR003017; Amphiphysin_1.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD003208; Amphiphysin_1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00721; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR Cytoskeleton; SH3 domain; Coiled coil; Alternative splicing;
KW 3D-structure.
FT DOMAIN 10 83 COILED COIL (POTENTIAL).
FT DOMAIN 144 191 COILED COIL (POTENTIAL).
FT DOMAIN 622 695 SH3.
FT VARSPIC 425 466 Missing (in isoform 2).
FT VARSPIC 425 466 /FTID=VSP_000245.
SQ SEQUENCE 695 AA; 76256 MW; 78B4F75AB759A357 CRC64;

Query Match 55.2%; Score 620.5; DB 1; Length 695;
Best Local Similarity 54.7%; Pred. No. 4e-30;
Matches 116; Conservative 49; Mismatches 46; Indels 1; Gaps 1;

QY 11 GLFAKQVQKFRSAQEKVLQKLGKAVETKDRFFQSASNFYQQAEGHLYKDKLNFSLA 70
DB 7 GIFAQNVQKRLNRAQEKVLQKLGKADETKDSQFEYVQNFQKQAECTRLQRELGYLAA 66.
QY 71 VKVHESKRVSEITLQEIYSSWDGHEELKAIWNNDLLWEDYEELKADQAVTMEIYA 130
DB 67 IKGQEAQSKKTESLHEVYEPDYGREDYKGVGKCVLWEDFHOKLVDSGLTLDTYLG 126

QY 131 QFSEIKERIAKGRKLVYDYSARHLEAVQNAK-KDEAKTAKAEFEFNKAQTVFEDLNOR 189
DB 127 QPFDIKNRIAKESKLVYDYSARHLEALQSSKDESRISKAEFEFNKAQTVFEDNVD 186

QY 190 LLEELPILNSRIGCVTTFIFONISNLRDVFYR 221
DB 187 LQEEPLSLWSRRVGFYVNTFNVSSEAKFHK 218

RESULT 6
AMPH CHICK
ID AMPH CHICK STANDARD; PRT; 682 AA.
AC P50478;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amphiphysin.
GN AMPH
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RC STRAIN-Tetra-hybrid; TISSUE=Forebrain;
RX MEDLINE=92331604; PubMed=1628617;
RA Lichte B., Veh R.W., Meyer H.R., Kilmann M.W.;
RT "Amphiphysin, a novel protein associated with synaptic vesicles.";
RL EMBO J. 11:2521-2530(1992).

-!- FUNCTION: May participate in mechanisms of regulated exocytosis in
synapses and certain endocrine cell types. May control the
properties of the membrane associated cytoskeleton.
-!- SUBUNIT: Heterodimer with BIN1. Binds SH3GLB1 (By similarity).
-!- SUBCELLULAR LOCATION: Peripheral membrane protein associated with
the cytoplasmic surface of synaptic vesicles.
-!- TISSUE SPECIFICITY: Is abundant in the forebrain and cerebellum.
It is also found in the adrenal gland, anterior and posterior
pituitary.
-!- SIMILARITY: Contains 1 BAR domain.
-!- SIMILARITY: Contains 1 SH3 domain.

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or send an email to license@isb-sib.ch).

EMBL; X60422; CAA42953.1; -.
DR PIR; S22700; S22700.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR003017; Amphiphysin_1.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD003208; Amphiphysin_1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR Cytoskeleton; SH3 domain; Coiled coil.
FT DOMAIN 10 84 COILED COIL (POTENTIAL).
FT DOMAIN 144 191 COILED COIL (POTENTIAL).
FT DOMAIN 609 682 SH3.
SQ SEQUENCE 682 AA; 61617F494F38EB20 CRC64;

Query Match 55.0%; Score 618.5; DB 1; Length 682;
Best Local Similarity 54.1%; Pred. No. 5.2e-30;
Matches 120; Conservative 47; Mismatches 50; Indels 5; Gaps 2;

QY 1 MAEGKAGAGLFAKQVQKFRSAQEKVLQKLGKAVETKDRFFQSASNFYQQAEGHKL 60
DB 1 MADMK---TGIFAKNVQKRLNRAQEKVLQKLGKADETKDSQFEYVQNFQKQAESESL 56

QY 61 YKDLKFNLSAVKVMHESKRVSEITLQEIYSSWDGHEELKAIWNNDLLWEDYEELKADQ 120
DB 57 QRELRLAYLAIKGVQDASKKLTESLHEVYEPDYGREDYKGVGKCVLWEDFHOKLVG 116

QY 121 AVRTMEIYVAQFSEIKERIAKGRKLVYDYSARHLEAVQNAK-KDEAKTAKAEFEFNKA 179
DB 117 SLTLDTYLGQFPDIKTRAKSRKLVYDYSARHLEALQSSKDESRISKAEFEFNKA 176

QY 180 QTVFEDLNQELLEELPILNSRIGCVTTFIFONISNLRDVFYR 221
DB 177 QKVFEFNTDQLEELPSLWSRRVGFYVNTFNVSSEAKFHK 218

RESULT 7
HOB3 SCHPO
ID HOB3 SCHPO STANDARD; PRT; 264 AA.
AC Q9UUM7; P78950;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein hob3 (Homolog of Bin3).
GN HOB3 OR SPBC725.09C.
OS Schizosaccharomyces pombe (Fission yeast).

```


Eukaryota, Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
[1]
SEQUENCE FROM N.A., AND FUNCTION.
RP MEDLINE=21293007; PubMed=11274158;
RX Routhier E.L., Burn T.C., Abbezeade I., Summers M., Albright C.F.,
RA Prendergast G.C.;
RT "Human BIN3 complements the F-actin localization defects caused by
FT loss of Hob3p, the fission yeast homolog of Rvs161p.";
RL J. Biol. Chem. 276:21670-21677(2001).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Scouras K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volktaert G., Aert R., Robben J., Grynoprez B.,
RA Weltjens I., Vanscreire E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garçon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrall B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RN Nature 415:871-880(2002).
[3]
SEQUENCE FROM N.A.
RP STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNAs";
RN DNA Res. 4:363-369(1997).
CC -!- FUNCTION: Involved in cytokinesis and septation where it has a
CC role in the localization of F-actin.
CC -!- SIMILARITY: Contains 1 BAR domain.
CC
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CC
CC EMBL; AF275638; AAF86459.1; -.
CC EMBL; AL034352; CAA22181.1; -.
CC EMBL; D89200; BAA13861.1; ALT_INIT.
CC FIR; T40661; T40661.
CC GenedB_Spombe; SPBC725.09c; -.
CC InterPro; IPR003005; Amphiphysin.
CC InterPro; IPR006632; BAR.
CC InterPro; IPR004148; BAR_dom.
CC Pfam; PF03114; BAR; 1.
CC PRINTS; PR01251; AMPHIPHYSIN.
CC SMART; SM00721; BAR; 1.

1

Db 64 LNHQIGFADACIEIYKPIGRASDPESVEQGNAGIEBAEAYKEIYV-----DLQKN 116
 QY 117 LADQAVRTMEIYVAF-----SEIKERIAKRGKLVVDVDSARHLEAVONAK-- 163
 Db 117 LASE-----MDVINTRIVNPTGELLKIVKDVLDKLRHDKLDYDRHRSFKLQEKQK 172
 QY 164 --KDEAKTAAEEFNKAQTVFEDLNQELLEPLFYNSRIGCVTVTFQNTSNLR-DVFFY 220
 Db 173 SLKDEKKLYEATAEQSSQVEYENMLKEELPKLPALAQSFIAPLFQGYVQLNVY 232

RESULT 10
 R167_YEAST
 ID R167_YEAST STANDARD; PRT; 482 AA.
 AC F39743;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reduced viability upon starvation protein 167.
 GN RVS167 OR YDR388W OR D9509.8.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE=93330299; PubMed=8336735;
 RA Bauer F., Urdaci M., Aigle M., Crouzet M.;
 RT "Alteration of a yeast SH3 protein leads to conditional viability
 with defects in cytoskeletal and budding patterns.";
 RL Mol. Cell. Biol. 13:5070-5084(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97313263; PubMed=9169867;
 RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G.,
 RA Barques M., Baron L., Becker N., Bileau N., Bloeker H., Bugnon C.,
 RA Boskovic J., Brandt P., Bruckner M., Buitrago M.J., Coster F.,
 RA Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,
 RA Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T.,
 RA Hohnel J.D., Jaeger W., Jimenez A., Joniaux J.-L., Kraemer C.,
 RA Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S.,
 RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,
 RA Paulin L., Perez J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
 RA Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Revuelta J.J.,
 RA Rieger M., Salom D., Saluz H.P., Salz J.E., Saren A.-M., Schaefer M.,
 RA Scharfe M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,
 RA Urrutazu L.A., Verhaesselt P., Vissers S., Voet M., Volckaert G.,
 RA Wagner G., Wambutt R., Wedler E., Wedler H., Wolfel S., Harris D.E.,
 RA Bowman S., Brown D., Churcher C.M., Connor R., Dedman K., Gentles S.,
 RA Hamlin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D.,
 RA Odell C., Oliver K., Rajandream M.A., Richards C., Shore L.,
 RA Walsh S.V., Barrall B.G., Dietrich F.S., Mulligan J.T., Allen E.,
 RA Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M.,
 RA Chung E., Duncan M., Hunnicke-Smith S., Hyman R.W., Komp C.,
 RA Laskhari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A.,
 RA Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M.,
 RA Shogren T., Shroff N., Winant A., Yelton M.A., Botstein D.,
 RA Davis R.W., Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,
 RA Du Z., Favell A., Fulton L., Gattung S., Greco T., Hallsworth K.,
 RA Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L.,
 RA Kirsten J., Kucaba T., Langston Y., Latreille P., Le T., Mardis E.,
 RA Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifkin L.,
 RA Riles L., Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P.,
 RA Vaudin M., Wilson R., Waterston R., Albermann K., Hani J., Heumann K.,
 RA Kleine K., Mewes H.-W., Zollner A., Zaccaria P.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IV.";
 RL Nature 387:75-78(1997).
 RN [3]
 RP ACTIN-BINDING.
 RX MEDLINE=95236199; PubMed=7719850;
 RA Amberg D.C., Basart E., Botstein D.;
 RT "Defining protein interactions with yeast actin in vivo.";

RL Nat. Struct. Biol. 2:28-35(1995).
 CC -!- FUNCTION: Component of a cytoskeletal structure that is required
 CC for the formation of endocytic vesicles at the plasma membrane
 CC level. Could be implicated in cytoskeletal reorganization in
 CC response to environmental stresses and could act in the budding
 CC site selection mechanism. Binds to actin.
 CC -!- SIMILARITY: Contains 1 BAR domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC
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 CC
 CC EMBL; M92092; AAA35051.1; -;
 CC EMBL; U32274; AAB64830.1; -;
 CC PIR; S40887; S40887.
 CC HSSP; P19174; 2HSP.
 CC GerMOnline; 140880; -;
 CC SGD; S0002796; RVS167.
 CC DR GO; GO:0005857; C:actin cortical patch (sensu Saccharomycetes); IDA.
 CC DR GO; GO:0008092; F:cytoskeletal protein binding; IPI.
 CC DR GO; GO:0006897; P:endocytosis; IMP.
 CC DR GO; GO:0007121; P:polar budding; IMP.
 CC DR GO; GO:0006970; P:response to osmotic stress; IMP.
 CC DR InterPro; IPR000632; BAR.
 CC DR InterPro; IPR004148; BAR_dom.
 CC DR InterPro; IPR001452; SH3.
 CC DR Pfam; PF03114; BAR; 1.
 CC DR Pfam; PF00018; SH3; 1.
 CC DR PRINTS; PR00452; SH3DOMAIN.
 CC DR ProDom; PD000066; SH3; 1.
 CC DR SMART; SM00721; BAR; 1.
 CC DR SMART; SM00326; SH3; 1.
 CC DR PROSITE; PS50002; SH3; 1.
 CC KW Cytoskeleton; SH3 domain; Coiled coil; Transmembrane; Actin-binding.
 FT DOMAIN 31 64
 FT DOMAIN 174 204
 FT DOMAIN 292 427
 FT TRANSMEM 344 367
 FT DOMAIN 421 482
 FT SEQUENCE 482 AA; 52774 MW; 3FOAB53EBCC95A5B CRC64;
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 Query Match 13.7%; Score 154.5; DB 1; Length 482;
 Best Local Similarity 24.4%; Pred. No. 0.015;
 Matches 61; Conservative 38; Mismatches 100; Indels 51; Gaps 8;
 QY 15 KQVKFSRAQEKVLQKLGAVETKDERFQSSNFYQQQAGHKLYKDLKXFLSAV--- 71
 Db 4 KGFTKVASRAPOSFROKFMGEQTPVVEDARRRFOELEQETKQLSESKRYSTAVNGM 63
 QY 72 -----KWHSSSKSVS-----ETLQEIYSSMDGHEELKAVWN-NDLLMED--- 112
 Db 64 LTHQIGFAKSEHIFKPIGSGMSDPNATIPENPQGEASEQYRAIVAELOETLPDLAL 123
 QY 113 YEEKLADQAVRTMEIYVAFSEIKERIAKRGKLVVDVDSARHLEAVONAKDEAKTAKA 172
 Db 124 VEEKIVTPCQELKLI-----ITYRKMATKGNKGLDLD---RLHNTYKHEKKKEPTAKD 176
 QY 173 EESFNKAQTVFEDLNQ-----LLEELPIL-----YNSRIGCVTVTFQ 210
 Db 177 EERYLQAQAVQVVAQOEYDYNDLLKTLQTLPIFLSLEAEFVKPLFVSFYFMQLNIFITLYN 236
 QY 211 NISNLRDVFFY 220
 Db 237 RLQDMKIPYF 246

RESULT 11
 BIN3_HUMAN

ID BIN3 HUMAN STANDARD; PRT; 253 AA.
AC OSNOYO;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bridging integrator 3.
GN BIN3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21293007; PubMed=11274158;
RA Routhier E.L., Burn T.C., Abbaszade I., Summers M., Albright C.F.,
RA Prendergast G.C.;
RT "Human BIN3 complements the F-actin localization defects caused by
RT loss of Hob3p, the fission yeast homolog of Rvs161p.";
RL J. Biol. Chem. 276:21670-21677 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Makamatsu A., Nakamura Y., Nagahari K., Maeuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NED0 human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22389557; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Involved in cytokinesis and septation where it has a
CC role in the localization of F-actin.
CC -!- SIMILARITY: Contains 1 BAR domain.
CC
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CC
CC EMBL; AF217132; RAF76218.1; -;
CC EMBL; AK023980; BAB14751.1; -;
CC EMBL; BC009824; AAH09824.1; -;
CC Genbank; HGNC:1054; BIN3.
CC MIM; 606396; -;
CC InterPro; IPR006632; BAR.
CC InterPro; IPR004148; BAR_dom.

DR Pfam: PF03114; BAR; 1.
DR SMART; SM00721; BAR; 1.
KW Septation; Cytoskeleton; Coiled coil.
FT DOMAIN 12 208 BAR.
FT DOMAIN 18 51 COILED COIL (POTENTIAL).
FT DOMAIN 120 152 COILED COIL (POTENTIAL).
FT DOMAIN 231 247 COILED COIL (POTENTIAL).
SQ SEQUENCE 253 AA; 29665 MW; 254CC7113749C584 CRC64;
Query Match 12.7%; Score 143; DB 1; Length 253;
Best Local Similarity 22.7%; Pred. No. 0.037;
Matches 48; Conservative 49; Mismatches 96; Indels 18; Gaps 5;
QY 20 KFSRAQKVLQKLGKAVETDERFEQSASNYQQQAEGHKLKYNFLSAVKVMHESK 79
Db 7 KIGPKQKIVPK-----TVERDFEYKGLQLESTRELQKMKKSTADLANSAV 60
QY 80 RVSETLQELVSSSEWDGHEELKAIWNNDLL---WEDYEKLADQAVRT-----MEIVVAF 132
Db 61 KISLDLSNPLCEQD--QDLLNMVTALDTAMKMDAFNQEKVNQIQKTVIEPLKKGVSFV 118
QY 133 SEIKERIAKRGKLVDSARHLEAVONAKDE---AKTAKAEFEFNKAQTVFEDLNOE 189
Db 119 PSLNAYKVRQEQALQDYRRLOAKVEKYEKEKTPVLAKLHQARELRPVREDFAKVRQ 178
QY 190 LLEELPILYNSRICGYVTIFQNISNLRDVPY 220
Db 179 LLEMPFPGSRDLYFQPSFSLRAQVYVY 209
RESULT 12
REST_CHICK
ID REST_CHICK STANDARD; PRT; 1433 AA.
AC 042184; 042228; 057563; 057564;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Restin (Cytoplasmic linker protein-170) (CLIP-170).
GN RSN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RX MEDLINE=98137792; PubMed=9469933;
RA Gripatic L., Volosky J.M., Keller T.C. III;
RT "Cloning and expression of chicken CLIP-170 and restin isoforms.";
RL Gene 206:195-208 (1998).
RN [2]
RP SEQUENCE OF 17-1139 FROM N.A. (ISOFORMS 3 AND 4).
RC TISSUE=pectoralis muscle;
RX MEDLINE=99002898; PubMed=9784600;
RA Gripatic L., Keller T.C. III;
RT "Identification and expression of two novel CLIP-170/restin isoforms
RT expressed predominantly in muscle.";
RL Biochim. Biophys. Acta 1405:35-46 (1998).
CC -!- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN
CC THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
CC CYTOSKELETON (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=042184-1; Sequence=Displayed;
CC Name=2;
CC IsoId=042184-2; Sequence=VSP_000761;
CC Name=3; Synonyms=CLIP-170(11);
CC IsoId=042184-3; Sequence=VSP_000762, VSP_000763;
CC Name=4; Synonyms=CLIP-170(11+35);
CC IsoId=042184-4; Sequence=VSP_000764;

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CC -1- SIMILARITY: Contains 2 CAP-Gly domains.
CC -----
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CC -----
DR EMBL: AF014012; AAC60344.1; -
DR EMBL: AF020764; AAC60345.1; -
DR EMBL: AF045650; AAC03547.1; -
DR EMBL: AF045651; AAC03548.1; -
DR InterPro: IPR000938; CAP-Gly.
DR InterPro: IPR001878; Znf CCHC.
DR Pfam: PF01302; CAP GLY; 2.
DR SMART: SM00343; Znf C2HC; 1.
DR PROSITE: PS00845; CAP_GLY_1; 2.
DR PROSITE: PS02445; CAP_GLY_2; 2.
KW Cytoskeleton; Microtubule; Coiled coil; Repeat; Alternative splicing.
FT DOMAIN 79 121
FT DOMAIN 144 207
FT DOMAIN 235 277
FT DOMAIN 305 332
FT DOMAIN 351 1353
FT DOMAIN 1414 1427
FT VARSPPLIC 458 492
FT VARSPPLIC 458 492
FT VARSPPLIC 803 803
FT VARSPPLIC 458 458
FT VARSPPLIC 458 458
FT CONFLICT 309 309
FT CONFLICT 440 440
FT SEQUENCE 1433 AA; 161026 MW; 5631CE8683498E23 CRC64;
Query Match 10.9%; Score 122.5; DB 1; Length 1433;
Best Local Similarity 27.1%; Pred. No. 3.6;
Matches 58; Conservative 37; Mismatches 74; Indels 45; Gaps 10;
QY 15 KQVKKFSRAQKVLKLGKAVETKQKRFQESANFVQQAQGH-KLYKDLKNFLSAVKV 73
Db 943 EQIQELTKANEKAVQ-LQKNVBTQAQAEQS-----QQETLKTHQBELKQMDQDQDMKK 997
QY 74 MHESSKRVSETLQETYSSE-----WDGHEELKAVVNDLLWEDYE 114
Db 998 QWETSQNYKDLQAKYKESKEMTKHDADIKGPKQNLDAEALKAQKNDLETOAE 1057
QY 115 E-----KLADQAVRTMEIYVAFSEI-KERIAKGRKLVVDYSARHLEAVQNA 162
Db 1058 ELKQAEQAKADKRAEEVLTQMEKVTKEKDAIHOEKI-----ETLASLENSRQTNKQLN- 1112
QY 163 KQDEAK--TAAEEFNKAQVFDLNOELLEEL 194
Db 1113 ELDMLKQNNLQNEBELTKSKELL-NLENKKVEEL 1145
RESULT 13
ID_MYS2_DICDI STANDARD; PRT; 2116 AA.
AC P08739;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Myosin II heavy chain, non muscle.
GN MHCA.
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;

```

```

RN RP SEQUENCE FROM N.A.
RX MEDLINE=87092266; PubMed=3540939;
RA Warlick H.M., de Lozanne A., Leinwand L.A., Spudich J.A.;
RT "Conserved protein domains in a myosin heavy chain gene from
RT Dictyostelium discoideum."
RL Proc. Natl. Acad. Sci. U.S.A. 83:9433-9437 (1986).
RN RP
RX PHOSPHORYLATION SITES, AND MUTAGENESIS.
RC STRAIN=AX2;
RX MEDLINE=90353583; PubMed=2387408;
RA Lueck-Vielmeier D., Schleicher M., Grabatin B., Wippler J.,
RA Gerisch G.;
RT "Replacement of threonine residues by serine and alanine in a
RT phosphorylatable heavy chain fragment of Dictyostelium myosin II."
RL FEBS Lett. 269:239-243 (1990).
RN RP
RX PHOSPHORYLATION SITES.
RX MEDLINE=88112226; PubMed=2828113;
RA Wagie G., Noegel A., Scheel J., Gerisch G.;
RT "Phosphorylation of threonine residues on cloned fragments of the
RT Dictyostelium myosin heavy chain."
RL FEBS Lett. 227:71-75 (1988).
RN RP
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762.
RX MEDLINE=95345066; PubMed=7619795;
RA Fisher A.J., Smith C.A., Thoden J.B., Smith R., Sutcho K., Holden H.M.,
RA Rayment I.;
RT "X-ray structures of the myosin motor domain of Dictyostelium
RT discoideum complexed with MgADP.BefX and MgADP.ALIF4."
RL Biochemistry 34:8960-8972 (1995).
RN RP
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-762.
RX MEDLINE=95345067; PubMed=7619796;
RA Smith C.A., Rayment I.;
RT "X-ray structure of the magnesium (II)-pyrophosphate complex of the
RT truncated head of Dictyostelium discoideum myosin to 2.7-A
RT resolution."
RL Biochemistry 34:8973-8981 (1995).
RN RP
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
RX MEDLINE=96206189; PubMed=8611530;
RA Smith C.A., Rayment I.;
RT "X-ray structure of the magnesium (II).ADP.vanadate complex of the
RT Dictyostelium discoideum myosin motor domain to 1.9-A resolution."
RL Biochemistry 35:5404-5417 (1996).
RN RP
RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1-762.
RX MEDLINE=97452580; PubMed=9305951;
RA Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
RT "X-ray structures of the MgADP, MgATPgammA, and MgAMPPNP complexes
RT of the Dictyostelium discoideum myosin motor domain."
RL Biochemistry 36:11619-11628 (1997).
RN RP
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
RX MEDLINE=98070605; PubMed=9405148;
RA Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;
RT "X-ray crystal structure and solution fluorescence characterization
RT of Mg.2'(3')-O-(N-methylanthraniloyl) nucleotides bound to the
RT Dictyostelium discoideum myosin motor domain."
RL J. Mol. Biol. 274:394-407 (1997).
CC -1- FUNCTION: Myosin is a protein that binds to actin and has ATPase
CC activity that is activated by actin.
CC -1- SUBUNIT: Myosin II heavy chain is two-headed. It self-assembles
CC into filaments. Hexamer of 2 heavy chain subunits (MHC), 2 alkali
CC light chain subunits (MLC) and 2 regulatory light chain subunits
CC (MLC-2).
CC -1- SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL
CC CORTEX.
CC -1- DOMAIN: Each myosin heavy chain can be split into 1 light
CC meromyosin (LMM) and 1 heavy meromyosin (HMM). It can be further
CC split into 2 globular subfragments (S1) and 1 rod-shaped
CC subfragment (S2).

```

-1- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
-1- PTM: Phosphorylation inhibits thick filament formation and reduces the actin-activated ATPase activity.
-1- MISCELLANEOUS: Dictyostelium myosin II has no K(2)EDTA ATPase activity, perhaps correlated with the absence of a Cys at the SH-1 position (688).
-1- SIMILARITY: Contains 1 myosin-like globular head domain.
-1- SIMILARITY: Contains 1 IQ domain.

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10-OCT-2003 (Rel. 42, Last annotation update)
 DT Nespriin 2 (Nuclear envelope spectrin repeat protein 2) (Synne-2)
 DE (Synaptic nuclear envelope protein 2) (Nucleus and actin connecting
 DE element protein) (NUANCE protein).
 GN SYNE2 OR NUA OR KIAA1011.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 9), FUNCTION, CHARACTERIZATION, AND
 RP INTERACTION WITH F-ACTIN.
 RX MEDLINE=22113122; PubMed=11792814;
 RX Zhen Y.-Y., Libotte T., Munk M., Noegel A.A., Korenbaum E.;
 RT "NUANCE, a giant protein connecting the nucleus and actin
 RT cytoskeleton.";
 RL J. Cell Sci. 115:3207-3222 (2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 4; 5 AND 7).
 RX MEDLINE=2152858; PubMed=11792814;
 RX Zhang Q., Skepper J.N., Yang F., Davies J.D., Hegyi L., Roberts R.G.,
 RA Weisberg P.L., Ellis J.A., Shanahan C.M.;
 RT "Nesprins: a novel family of spectrin-repeat-containing proteins that
 RT localize to the nuclear membrane in multiple tissues.";
 RL J Cell Sci. 114:4485-4498 (2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22296983; PubMed=12408964;
 RX Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.;
 RT "The nesprins are giant actin-binding proteins, orthologous to
 RT Drosophila melanogaster muscle protein MSP-300.";
 RL Genomics 80:473-481 (2002).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RX Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX PubMed=12508121;
 RX Heilig R., Eckenberg R., Petit J.-L., Fonknechten N., Da Silva C.,
 RA Cattolico L., Levy M., Barbe V., De Berardinis V., Ureta-Vidal A.,
 RA Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,
 RA Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C.,
 RA Buelts T., Jallouin O., Friedlander L., Samson G., Brottier P.,
 RA Cure S., Segurens B., Aniere F., Samain S., Crespeau H., Abbasi N.,
 RA Alich N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C.,
 RA Guyyenoux M., James R., Madan A., Mairrey-Estrada B., Mangenot S.,
 RA Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Traak B.,
 RA Vacherie B., Bellemere C., Belser C., Beaudard-Comnet M.,
 RA Bartsch-Navel D., Bourard M., Bries-Silla S., Combette S.,
 RA Dufosse-Laurent V., Ferron C., Lechaplais C., Lousse C., Muselet D.,
 RA Magdegnat G., Pateau E., Petit E., Sirvain-Trukniewicz P., Trybou A.,
 RA Vega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M.,
 RA Dumont C., Guerin T., Hatray S., Hammadi R., Muanga J., Pellouin V.,
 RA Robert D., Wundler E., Gauguier G., Roy A., Sainte-Marthe L.,
 RA Verdier J., Verdier-Discala C., Hillier L.W., Fulton L., McPherson J.,
 RA Matsuda F., Wilson R., Scarpelli C., Gypay G., Wincher P., Saurin W.,
 RA Quetier F., Waterston R., Hood L., Weissbach J.;
 RT "The DNA sequence and analysis of human chromosome 14.";
 RL Nature 421:601-607 (2003).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 8).
 RP TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Ioshizuka S., Carninci P., Frange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 1-956 AND 5133-6885
 RP FROM N.A.
 RX TISSUE=Spleen, and Tongue;
 RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.,
 RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
 RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
 RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
 RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 5709-6885 FROM N.A. (ISOFORM 2).
 RX TISSUE=Brain;
 RX MEDLINE=9924063; PubMed=10231032;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:63-70 (1999).
 RN [9]
 RP REVISIONS.
 RX TISSUE=Brain;
 RX MEDLINE=22158633; PubMed=12168954;
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual
 RT curation of 330 KIAA cDNA clones.";
 RL DNA Res. 9:99-105 (2002).
 RN [10]
 RP SEQUENCE OF 5754-6885 FROM N.A.
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
 RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435 (2001).
 CC -!- FUNCTION: Involved in the maintenance of nuclear organization and
 CC structural integrity. Probable anchoring protein which tethers the
 CC nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton
 CC by interacting with the nuclear envelope and with F-actin in the
 CC cytoplasm.
 CC -!- SUBUNIT: Interacts with F-actin via its N-terminal domain.
 CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (potential). The
 CC largest part of the protein is cytoplasmic, while its C-terminal
 CC part is associated with the nuclear envelope, most probably the
 CC outer nuclear membrane. Remains associated with the nuclear
 CC envelope during its breakdown in mitotic cells.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=9;
 CC Name=1;
 CC IsoId=Q8WXH0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8WXH0-2; Sequence=VSP_007164, VSP_007166;

CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q8WXH0-3; Sequence=VSP_007155;
 CC Note=Produced by exon skipping that results in a frameshift. No
 CC experimental confirmation available;
 CC Name=4; Synonyms=Beta;
 CC IsoId=Q8WXH0-4; Sequence=VSP_007156;
 CC Name=5; Synonyms=Alpha;
 CC IsoId=Q8WXH0-5; Sequence=VSP_007157, VSP_007164, VSP_007165;
 CC Name=6;
 CC IsoId=Q8WXH0-6; Sequence=VSP_007158, VSP_007165, VSP_007166;
 CC Note=No experimental confirmation available;
 CC Name=7; Synonyms=Gamma;
 CC IsoId=Q8WXH0-7; Sequence=VSP_007154, VSP_007163;
 CC Name=8;
 CC IsoId=Q8WXH0-8; Sequence=VSP_007161, VSP_007162;
 CC Note=No experimental confirmation available;
 CC Name=9; Synonyms=Nuance-N-33;
 CC IsoId=Q8WXH0-9; Sequence=VSP_007159, VSP_007160;
 CC TISSUE SPECIFICITY: Widely expressed, with higher level in kidney,
 CC adult and fetal liver, stomach and placenta. Weakly expressed in
 CC skeletal muscle and brain. Isoform 5 is highly expressed in
 CC pancreas, skeletal muscle and heart.
 CC -!- DOMAIN: The Klarsicht domain mediates the nuclear envelope
 CC targeting.
 CC -!- SIMILARITY: Belongs to the nesprin family.
 CC -!- SIMILARITY: Contains 1 actin-binding domain.
 CC -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
 CC -!- SIMILARITY: Contains 1 Klarsicht domain.
 CC -!- SIMILARITY: Contains 13 leucine-rich (LRR) repeats.
 CC -!- SIMILARITY: Contains 9 spectrin repeats.
 CC -----
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 CC EMBL: AF435010; AAL33547.1; -
 CC EMBL: AF435011; AAL33548.1; -
 CC EMBL: AY061757; AAL33800.1; -
 CC EMBL: AY061758; AAL33801.1; -
 CC EMBL: AY061759; AAL33802.1; -
 CC EMBL: AF495911; AAG60443.1; -
 CC EMBL: AL117404; CAB55905.1; -
 CC EMBL: AL162832; -; NOT_ANNOTATED_CDS.
 CC EMBL: AL355094; -; NOT_ANNOTATED_CDS.
 CC -----
 CC Query Match 10.5%; Score 118.5; DB 1; Length 6885;
 CC Best Local Similarity 24.0%; Pred. No. 31;
 CC Matches 52; Conservative 33; Mismatches 73; Indels 59; Gaps 10;
 CC
 CC QY 26 EKVQLKGLKAVENKRRPQCSASNFQQAGHGKLYKDLKFLSAV-KVMHSSKRVSET 84
 CC Db 3658 ESQVECRKALEDIDKESIKVNLKSPSYAMERKI-BEINNGHLNVERKLOOKSKNT-EK 3715
 CC
 CC QY 85 LQIYISSEWD---GHEELKAIWNNDLWEEKLDQAVRTWE---IVVAQFSEIKE 137
 CC Db 3716 AQEIQKKWDELDTWISKNEL-----DSEVDIVQDPQAGQWMDNLMIFFQVQVSQ 3771
 CC
 CC QY 138 RIARGRKL-----VDYDSAR---HHLEAVQNAK 163
 CC Db 3772 RAECRTSOLNKAIVKVMEEYSDLLKSTEAWIENTSHLANPADYSLRTLSHASTVQVAL 3831
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 CC QY 164 KDEAKTAKAEERFKAQTVFEDLNQELLEELILYNS 200
 CC Db 3832 ED-----SEQXNLHISFMD-----LEDLSIIFET 3857
 CC
 CC RESULT 15
 CC GOB1_HUMAN

GOB1_HUMAN STANDARD; PRT; 3259 AA.
 AC Q14789; Q14398;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Golgi autoantigen, golgin subfamily B member 1 (Giantin) (Macroglin)
 DE (Golgi complex-associated protein, 372-kDa) (GCP372).
 GN GOLGB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94187728; PubMed=7511208;
 RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
 RA Renz M.;
 RT "Molecular genetic analyses of a 376-kilodalton Golgi complex membrane
 RT protein (Giantin).";
 RL Mol. Cell. Biol. 14:2564-2576(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94257116; PubMed=8198703;
 RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
 RA Renz M.;
 RT "Macroglin -- a new 376 kD Golgi complex outer membrane protein as
 RT target of antibodies in patients with rheumatic diseases and HIV
 RT infections.";
 RL J. Autoimmun. 7:67-91(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95100974; PubMed=7802676;
 RA Schoda M., Misumi Y., Fujiwara T., Nishioka M., Ikehara Y.;
 RT "Molecular cloning and sequence analysis of a human 372-kDa protein
 RT localized in the Golgi complex.";
 RL Biochem. Biophys. Res. Commun. 205:1399-1408(1994).
 CC -!- FUNCTION: May participate in forming interstitial cross-bridges
 CC of the Golgi complex.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Golgi; membrane-associated.
 CC -!- DISEASE: Antigen in chronic rheumatoid arthritis and in the
 CC autoimmune disease Sjogren's syndrome.
 CC -!- SIMILARITY: Belongs to the golgin family.
 CC -----
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 CC EMBL: X75304; CAA53052.1; -
 CC EMBL: D25542; BAA05025.1; -
 CC FIR; A56539; A56539.
 CC FIR; I52300; I52300.
 CC Genew; HGNC:4429; GOLGB1.
 CC MIM; 602500; -
 CC GO; GO:0000139; C:Golgi membrane; TAS.
 CC GO; GO:0005795; C:Golgi stack; TAS.
 CC GO; GO:0016021; C:Integral to membrane; TAS.
 CC GO; GO:0007030; P:Golgi organization and biogenesis; TAS.
 CC Golgi stack; Antigen; Coiled coil; Transmembrane.
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 1 3235
 CC TRANSMEM 3236 3256
 CC POTENTIAL.
 CC LUMENAL (POTENTIAL).
 CC COILED COIL (POTENTIAL).
 CC COILED COIL (POTENTIAL).
 CC COILED COIL (POTENTIAL).
 CC COILED COIL (POTENTIAL).
 CC COILED COIL (POTENTIAL).
 CC POLY-GLU.
 CC POLY-SER.
 CC DOMAIN 2993 2996

Search completed: March 4, 2004, 17:28:22
Job time : 7.63057 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:22:14 ; Search time 21.3962 Seconds
(without alignments)
3258.971 Million cell updates/sec

Title: US-10-069-540A-2_COPY_1_221
Perfect score: 1125
Sequence: 1 MAEGKAGAGLFAKQVOKK.....IGCVITFQNISNLRDVFYR 221

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp archaea:*
 - 2: sp bacteria:*
 - 3: sp fungi:*
 - 4: sp human:*
 - 5: sp invertebrate:*
 - 6: sp mammal:*
 - 7: sp mhc:*
 - 8: sp organelle:*
 - 9: sp phage:*
 - 10: sp plant:*
 - 11: sp rodent:*
 - 12: sp virus:*
 - 13: sp vertebrate:*
 - 14: sp unclassified:*
 - 15: sp virus:*
 - 16: sp bacteriap:*
 - 17: sp archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1125	100.0	564	Q9UKN4	Q9UKN4 homo sapien
2	1114.5	99.1	565	Q86VW0	Q86VW0 homo sapien
3	1111.5	98.8	565	Q8UBW5	Q8UBW5 homo sapien
4	782.5	69.6	524	Q803I3	Q803I3 brachydanio
5	683	60.7	439	Q8ETH3	Q8ETH3 homo sapien
6	683	60.7	490	Q8WH99	Q8WH99 homo sapien
7	662.5	58.9	478	Q7ZWP5	Q7ZWP5 xenopus lae
8	625.5	55.6	250	Q8BXH2	Q8BXH2 mus musculus
9	625.5	55.6	686	Q7TGF7	Q7TGF7 mus musculus
10	620.5	55.2	385	Q8NFI3	Q8NFI3 homo sapien
11	620.5	55.2	695	Q8N4G0	Q8N4G0 homo sapien
12	449	35.9	414	Q8WQ54	Q8WQ54 geodia cydo
13	429.5	38.2	602	Q8Y092	Q8Y092 drosophila
14	405	36.0	461	Q21004	Q21004 caenorhabdi
15	228.5	20.3	273	Q8X0D7	Q8X0D7 neurospora
16	171.5	15.2	499	Q8NJ03	Q8NJ03 neurospora

17	149	13.2	823	4	Q8IVY3	Q8IVY3 homo sapien
18	149	13.2	1315	4	Q8Y2L3	Q8Y2L3 homo sapien
19	146	13.0	606	11	Q8R0Y2	Q8R0Y2 mus musculu
20	144	12.8	253	11	Q8J108	Q8J108 mus musculu
21	141	12.5	137	4	Q8UQI2	Q8UQI2 homo sapien
22	129.5	11.5	1992	13	Q04834	Q04834 xenopus lae
23	127	11.3	217	2	Q8R5X5	Q8R5X5 streptococc
24	127	11.3	377	2	Q53475	Q53475 streptococc
25	120.5	10.7	639	4	Q86B40	Q86B40 homo sapien
26	120.5	10.7	652	4	Q8P2B4	Q8P2B4 homo sapien
27	120	10.7	400	16	Q8N279	Q8N279 streptococc
28	119	10.6	1175	16	Q8XNW6	Q8XNW6 clostridium
29	118.5	10.5	650	4	Q8N9W4	Q8N9W4 homo sapien
30	118	10.5	399	17	Q58288	Q58288 pyrococcus
31	118	10.5	1186	16	Q895M7	Q895M7 clostridium
32	117.5	10.4	899	3	Q8NI20	Q8NI20 neurospora
33	116.5	10.4	1486	2	Q93IE8	Q93IE8 actinobacil
34	116	10.3	471	2	Q93SL9	Q93SL9 streptococc
35	116	10.3	1940	5	Q02456	Q02456 schistosoma
36	116	10.3	2771	5	Q26216	Q26216 plasmodium
37	115.5	10.3	2029	4	Q9C014	Q9C014 homo sapien
38	115.5	10.3	2069	4	Q9C013	Q9C013 homo sapien
39	115.5	10.3	2073	4	Q9C012	Q9C012 homo sapien
40	115	10.2	528	5	Q26589	Q26589 schistosoma
41	115	10.2	3641	13	Q7ZTH4	Q7ZTH4 fugu rubrip
42	114.5	10.2	532	2	Q55098	Q55098 streptococc
43	114.5	10.2	1320	11	Q9JK25	Q9JK25 rattus norv
44	114	10.1	1056	16	Q8REF7	Q8REF7 fusobacteri
45	114	10.1	1061	16	Q8DPM8	Q8DPM8 streptococc

ALIGNMENTS

RESULT 1
Q9UKN4
ID Q9UKN4 PRELIMINARY; PRT; 564 AA.
AC Q9UKN4
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Bridging integrator-2.
GN BIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=20366138; PubMed=10903846;
RX Ge K., Prendergast G.C.;
RA "Bin2, a Functionally Nonredundant Member of the BAR Adaptor Gene
RT Family";
RL Genomics 67:210-220 (2000).
RR EMBL; AF145531; X0542271; .
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 564 AA; 61747 MW; 3CB3791A56CE53CB CRC64;

Query Match 100.0%; Score 1125; DB 4; Length 564;
Best Local Similarity 100.0%; Pred. No. 5.8e-64;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEGKAGAGLFAKQVOKKFKSRAQKVKLQKLGKAVETKDERFEQASNFYQQAEGHKL 60
DB 1 MAEGKAGAGLFAKQVOKKFKSRAQKVKLQKLGKAVETKDERFEQASNFYQQAEGHKL 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:22:14 ; Search time 54.6038 Seconds
(without alignment)
3258.971 Million cell updates/sec

Title: US-10-069-540A-2
Perfect score: 2855
Sequence: 1 MAEGKAGGAAGLFAKQVQK.....NNLTAPBPQEVSTSENQQL 564

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315519202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL.25.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mhc.*
- 8: sp_mhc.*
- 9: sp_mhc.*
- 10: sp_mhc.*
- 11: sp_mhc.*
- 12: sp_mhc.*
- 13: sp_mhc.*
- 14: sp_mhc.*
- 15: sp_mhc.*
- 16: sp_mhc.*
- 17: sp_mhc.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2851	99.9	564	Q9UKN4	Q9UKN4 homo sapien
2	2840.5	99.5	565	Q86VW0	Q86VW0 homo sapien
3	2837.5	99.4	565	Q2UBW5	Q2UBW5 homo sapien
4	1721	60.3	342	Q9NWK4	Q9NWK4 homo sapien
5	986	34.5	524	Q803I3	Q803I3 brachydanio
6	873	30.6	490	Q8WH9	Q8WH9 homo sapien
7	818.5	28.7	686	Q7TQF7	Q7TQF7 mus musculus
8	805.5	28.2	439	Q8ETH3	Q8ETH3 mus musculus
9	804.5	28.2	695	Q8N4G0	Q8N4G0 homo sapien
10	786.5	27.5	478	Q7ZWP5	Q7ZWP5 xenopus lae
11	743.5	26.0	385	Q8NFK3	Q8NFK3 homo sapien
12	705.5	24.7	250	Q8BXH2	Q8BXH2 mus musculus
13	555.5	19.5	602	Q9Y092	Q9Y092 drosophila
14	535.5	18.8	414	Q8WQ34	Q8WQ34 geodia cydo
15	463	16.2	461	Q21004	Q21004 caenorhabdi
16	256.5	9.0	137	Q9UQ12	Q9UQ12 homo sapien

17.	251	8.8	904	4	Q8IYB3	Q8IYB3 homo sapien
18	243	8.5	897	11	O70495	O70495 mus musculus
19	241.5	8.5	499	3	Q8NJO3	Q8NJO3 neurospora
20	233	8.2	820	4	O60585	O60585 homo sapien
21	232	8.1	770	2	Q9K37	Q9K37 streptococc
22	231	8.1	1200	5	O25388	Q25388 loligo peal
23	229.5	8.0	273	3	Q8X0D7	Q8X0D7 neurospora
24	228	8.0	769	2	Q9K24	Q9K24 streptococc
25	223.5	7.8	639	4	Q96B40	Q96B40 homo sapien
26	223.5	7.8	652	4	Q9P2B4	Q9P2B4 homo sapien
27	223.5	7.8	769	2	Q9FDO1	Q9FDO1 streptococc
28	219	7.7	638	11	Q9LJ70	Q9LJ70 mus musculus
29	218	7.6	763	2	Q9K25	Q9K25 streptococc
30	217	7.6	638	11	Q8BSV1	Q8BSV1 mus musculus
31	214	7.5	763	10	Q9SUA1	Q9SUA1 arabidopsis
32	213	7.5	1110	13	Q91255	Q91255 petromyzon
33	213	7.5	1560	5	O26644	O26644 strongyloce
34	212.5	7.4	1135	6	Q8HW3	Q8HW3 canis famil
35	212	7.4	769	2	Q9K40	Q9K40 streptococc
36	212	7.4	885	5	Q9TX39	Q9TX39 caenorhabdi
37	212	7.4	908	5	Q8X0J1	Q8X0J1 caenorhabdi
38	212	7.4	930	5	O17339	O17339 caenorhabdi
39	211	7.4	1315	4	Q9Y2L3	Q9Y2L3 homo sapien
40	210.5	7.4	1505	12	Q8JKF9	Q8JKF9 heliothis z
41	210	7.4	823	4	O8IYV3	O8IYV3 homo sapien
42	208	7.3	759	10	Q9FW72	Q9FW72 arabidopsis
43	206	7.2	971	5	Q9XU54	Q9XU54 caenorhabdi
44	206	7.2	1268	4	O75046	O75046 homo sapien
45	206	7.2	1318	16	Q7UG24	Q7UG24 rhodopirell

ALIGNMENTS

RESULT 1
Q9UKN4
ID Q9UKN4 PRELIMINARY; PRT; 564 AA.
AC Q9UKN4
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2003 (TREMBLrel. 13, Last sequence update)
DE Bridging integrator-2.
GN BIN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20366138; PubMed=10903846;
RA Ge K., Prendergast G.C.,
RT "Bin2, a Functionally Nonredundant Member of the BAR Adaptor Gene Family."
RL Genomics 67:210-220(2000).
DR EMBL; AF146531; AF54227.1;
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR Pfam; PF03114; BAR_1.
DR PRINTS; PR01251; AMPHIPHYLIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 564 AA; 61747 MW; 3CB3791A56CE53CB CRC64;

Query Match
Best Local Similarity 99.9%; Score 2851; DB 4; Length 564;
Matches 563; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAEGKAGGAAGLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQSASNFYQQQAEHGKL 60
DB 1 MAEGKAGGAAGLFAKQVQKFSRAQKVLQKLGKAVETKDERFEQSASNFYQQQAEHGKL 60


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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Miki Y., Saito H.;
RT "Genomic structure and chromosome location of the BRP1 gene.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032710; BAA88125.1; JOINED.
DR EMBL; AB032699; BAA88125.1; JOINED.
DR EMBL; AB032700; BAA88125.1; JOINED.
DR EMBL; AB032701; BAA88125.1; JOINED.
DR EMBL; AB032702; BAA88125.1; JOINED.
DR EMBL; AB032703; BAA88125.1; JOINED.
DR EMBL; AB032704; BAA88125.1; JOINED.
DR EMBL; AB032705; BAA88125.1; JOINED.
DR EMBL; AB032706; BAA88125.1; JOINED.
DR EMBL; AB032707; BAA88125.1; JOINED.
DR EMBL; AB032708; BAA88125.1; JOINED.
DR EMBL; AB032709; BAA88125.1; JOINED.
DR EMBL; AB032698; BAA88108.1; -.
DR Genew; HGNC:1053; BIN2.
DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 565 AA; 61902 MW; 28D1FB89A7779860 CRC64;

Query Match 99.4%; Score 2837.5; DB 4; Length 565;
Best Local Similarity 99.5%; Pred. No. 1.3e-138;
Matches 562; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAEGKAGGAGLFAKQVQKFSRAQKVLQKLGKAVETKDRFRFQSASNFYQQAEGHKL 60
DB 1 MAEGKAGGAGLFAKQVQKFSRAQKVLQKLGKAVETKDRFRFQSASNFYQQAEGHKL 60
QY 61 YKDLNLFSAVKVMHESKRVSETLQEIYSSEWDGHEELKAIWNNDLLMEDYEELADQ 120
DB 61 YKDLNLFSAVKVMHESKRVSETLQEIYSSEWDGHEELKAIWNNDLLMEDYEELADQ 120
QY 121 AVRTMEIYVAQSEIKERIAKGRKLVVDYDARHHLAVQNA-KDDEAKTAKAEENFKA 179
DB 121 AVRTMEIYVAQSEIKERIAKGRKLVVDYDARHHLAVQNA-KDDEAKTAKAEENFKA 180
QY 180 QTVFEDLNQELLEELPILYNSRIGCYVTIFQNIENLRDVFYREMSKLNHLYEVMKLEK 239
DB 181 QTVFEDLNQELLEELPILYNSRIGCYVTIFQNIENLRDVFYREMSKLNHLYEVMKLEK 240
QY 240 QHSNKVFVVKGLSSRSRLVISPVRTATVSSPLTSPSTSLKSESESVSATEDLA 299
DB 241 QHSNKVFVVKGLSSRSRLVISPVRTATVSSPLTSPSTSLKSESESVSATEDLA 300
QY 300 PDAAGQEDNSETKELLEEEIEKEGSEASSEEDDPLPACNGPAQAPSPPTTERAKSQEE 359
DB 301 PDAAGQEDNSETKELLEEEIEKEGSEASSEEDDPLPACNGPAQAPSPPTTERAKSQEE 360
QY 360 VLPSTTSPGALSPGQSPSSATEVVLRTTASSEGSEQPKKASTQRTASPPSPPPP 419
DB 361 VLPSTTSPGALSPGQSPSSATEVVLRTTASSEGSEQPKKASTQRTASPPSPPPP 420
QY 420 RATASPRSSGNIIPSSPTASGGGSPSPRASLGTGTASPTSLSEVSNPPEPKPVRTPE 479
DB 421 RATASPRSSGNIIPSSPTASGGGSPSPRASLGTGTASPTSLSEVSNPPEPKPVRTPE 480
QY 480 AKENENINQNPPEELCTSPMLTQVASEPGEAKMEDKONKLI SADSEGDQLQVS 539
DB 481 AKENENINQNPPEELCTSPMLTQVASEPGEAKMEDKONKLI SADSEGDQLQVS 540
QY 540 MYPENNNTAPEPQEVSTSENPOL 564
DB 541 MYPENNNTAPEPQEVSTSENPOL 565

RESULT 4
Q9NWK4 PRELIMINARY; PRT; 342 AA.
ID Q9NWK4;
AC Q9NWK4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ20776.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isegai T., Sugano S.;
RT "NEO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK000783; BAA31376.1; -.
KW Hypothetical protein.
SQ SEQUENCE 342 AA; 35986 MW; 8DD6B908D9A28DBD CRC64;

Query Match 60.3%; Score 1721; DB 4; Length 342;
Best Local Similarity 99.7%; Pred. No. 2.6e-81;
Matches 341; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 223 MSKLNHNLYEVMKLEKQHSNKVFVVKGLSSRSRLVISPVRTATVSSPLTSPST 282
DB 1 MSKLNHNLYEVMKLEKQHSNKVFVVKGLSSRSRLVISPVRTATVSSPLTSPST 60
QY 283 LSLKSESESVSATEDLADPAQAQEDNSEIKELLEEEIEKEGSEASSEEDDPLPACNGP 342
DB 61 LSLKSESESVSATEDLADPAQAQEDNSEIKELLEEEIEKEGSEASSEEDDPLPACNGP 120
QY 343 AAQAPSPPTTERAKSQEVLFPSSITPPGALSPGQSPSSATEVVLRTTASSEGSEQPKK 402
DB 121 AAQAPSPPTTERAKSQEVLFPSSITPPGALSPGQSPSSATEVVLRTTASSEGSEQPKK 180
QY 403 RASTQRTASPPSPPPRATASPPSSGNTSPSSGNTSPSSGNTSPSSGNTSPSSGNTSP 462
DB 181 RASTQRTASPPSPPPRATASPPSSGNTSPSSGNTSPSSGNTSPSSGNTSPSSGNTSP 240
QY 463 EVSPNPPEPKPVRTPEAKENENINQNPPEELCTSPMLTQVASEPGEAKMEDKON 522
DB 241 EVSPNPPEPKPVRTPEAKENENINQNPPEELCTSPMLTQVASEPGEAKMEDKON 300
QY 523 KLISADSEGDQLQVSNPENNNTAPEPQEVSTSENPOL 564
DB 301 KLISADSEGDQLQVSNPENNNTAPEPQEVSTSENPOL 342

RESULT 5
Q803I3 PRELIMINARY; PRT; 524 AA.
ID Q803I3;
AC Q803I3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to bridging integrator 2.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCB1_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044473; AAH44473.1; -.

```

DR GO: GO:0006897; P: endocytosis; IEA.
 DR GO: GO:0007268; P: synaptic transmission; IEA.
 DR InterPro: IPR003005; Amphiphysin.
 DR InterPro: IPR006632; BAR.
 DR InterPro: IPR004148; BAR_dom.
 DR Pfam: PF03114; BAR; 1.
 DR PRINTS: PR01251; AMPHIPHYSIN.
 DR SMART: SM00721; BAR; 1.
 SQ SEQUENCE 524 AA; 59280 MW; F4A2988732D153FF CRC64;

Query Match 34.5%; Score 986; DB 13; Length 524;
 Best Local Similarity 47.1%; Pred. No. 3.4e-430;
 Matches 218; Conservative 73; Mismatches 120; Indels 52; Gaps 11;

QY 1 MAEGK-----AGGAAGLFAKQVKFSRAQEKVLQKLGKAVETKDERFEQASNFYQ 52
 DB 1 MADGKLTGNTGNGAGAGILAKFKQSMNRAQEKVLQKLGKAVETKDERFEQASNFYQ 60
 QY 53 QQAEGHKLKDLNPLSAKVWHSESKRSETLQEIYSSWDGHEELKAIWNNDLILWED 112
 DB 61 QQTDGIRLVKDVKAYNVAKVWHSESKRLSQTLDIYEPDWHGVEDLTVMESDILLND 120
 QY 113 YEEKLADQAVRTMEIYVAQFSIKERIAKGRKLVYDSARHHLAEVONAKK-DEAKTAK 171
 DB 121 YEEKLADQAVRTMEIYVAQFSIKERIAKGRKLVYDSARHHLAEVONAKK-DEAKTAK 180
 QY 172 ABEFKAQVTFEDLNQELLELPILYNSRICYVTFITONISNRDVPYREMSKLNINLY 231
 DB 181 ABEFKAQVTFEDLNQELLELPILYNSRICYVTFITONISNRDVPYREMSKLNINLY 240
 QY 232 EVMSKLEKHSNKVFVVKGLSSS---SRSLVISPVRTAT-----VSPLTSP 277
 DB 241 NMUKLEDOHSTKPFIVKGLNSKSKKSVTISAPICVNTAFPTDHPMSKLSMPTLA 300
 QY 278 TSPSTLSKSESVSATLADPAAGQDENSEIKELLEEEIEKEG-SEASSSEEDDPL 336
 DB 301 HTDTRHTSKSTEISESES---DSFDPSPNTPKQSL--CSVRSDGASENTSGTTDEI 355
 QY 337 PACNGPAQAPSPPTERRAKSQEVLPSSTPPFGALSPGQSPSSATTEVVLRTASEG 396
 DB 356 VQANG-QEIQDVSVERQEER-----SKSQASSED-----AHNASTDG 395
 QY 397 SEQPKKRAIQRTSAPSPPPPPPRATASPRSSGNIPSPSTAS 439
 DB 396 DQTKLLSADEKPAE---IPTPRSSSTSKDEGTENTKGS 435

RESULT 6

Q8WH9 PRELIMINARY; PRT; 490 AA.
 AC Q8WH9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Amphiphysin Iib-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Kim K.-C., Kim T.-S., Kang K.-H., Choi K.-H.;
 RT "Amphiphysin Iib-1, a novel splicing variant of amphiphysin II,
 RT regulates p73b function through protein-protein interactions.";
 RL Oncogene 0:0-0(2002).
 DR EMBL: AF411606; AAL38509.1; -
 DR GO: GO:0006897; P: endocytosis; IEA.
 DR GO: GO:0007268; P: synaptic transmission; IEA.
 DR InterPro: IPR003005; Amphiphysin.
 DR InterPro: IPR006632; BAR.
 DR InterPro: IPR004148; BAR_dom.
 DR InterPro: IPR001452; SH3.

DR Pfam: PF03114; BAR; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR01251; AMPHIPHYSIN.
 DR Prodom: PD000066; SH3; 1.
 DR SMART: SM00721; BAR; 1.
 DR SMART: SM00326; SH3; 1.
 SQ SEQUENCE 490 AA; 53167 MW; 8F50F36F7B6E9690 CRC64;

Query Match 30.6%; Score 873; DB 4; Length 490;
 Best Local Similarity 39.5%; Pred. No. 2.1e-37;
 Matches 206; Conservative 73; Mismatches 165; Indels 78; Gaps 11;

QY 1 MAE-OKAGAGLFAKQVKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQAEGHK 59
 DB 1 MAEMSGKVTAGKLTASNQKLTQAEKVLQKLGKAVETKDERFEQASNFYQQAEGHK 60
 QY 60 LYKDLKNTLSAVKVMHSESKRSETLQEIYSSWDGHEELKAIWNNDLILWEDYEKLAD 119
 DB 61 LQDRLTILASVKAHSESKRSETLQEIYSSWDGHEELKAIWNNDLILWEDYEKLAD 120
 QY 120 QAVRTMEIYVAQFSIKERIAKGRKLVYDSARHHLAEVONAKK-DEAKTAKAEEFNK 178
 DB 121 QALLTMDTLYGQFPDIKSRIAKGRKLVYDSARHHLAEVONAKK-DEAKTAKAEEFNK 180
 QY 179 AQTVEDLNQELLELPILYNSRICYVTFITONISNRDVPYREMSKLNINLYEYMSKLE 238
 DB 181 AQTVEDLNQELLELPILYNSRICYVTFITONISNRDVPYREMSKLNINLYEYMSKLE 240
 QY 239 KQHSNKVFWKGLSSSRRSLVISPVRTATVSPSTPSSTLSKSESVSATLAD 298
 DB 241 KQHSNKVFWKGLSSSRRSLVISPVRTATVSPSTPSSTLSKSESVSATLAD 291
 QY 299 APDAAQDENSEIKELLEEEIEKEGSEASSSEEDDPLACNGPAQAPSPPTERRAKSQE 358
 DB 292 TFGATLPKSPQLAK-----GPFVPPPPKHTPSKVKQE 325
 QY 359 EVL-----PSSTTPSGALSPGQSPSS---ATEVVLRTASEGSEOPK 401
 DB 326 QILSLFEDTFTVEISVTPSOPTSPAGSL-PSGEPAAEGTFAVSWPQTAFGPAQPA 384
 QY 402 KRAIQRTSAPSPPPPPPRATASPRSSGNIPSPSTAS-----SPTASGGSPSPASL 451
 DB 385 EASEVAGGTQPAAGAQEPGETAASEAASSLFAVWETPVTAVGTVEGSG--AGRLDL 442
 QY 452 GTG-----TASPRTSLEVPNPEPEKPVRTPEAKE 482
 DB 443 PPGFMFKVQAQHDXTATDTDELQKAGDVVLVTFQNPPEEQD 484

RESULT 7

Q7TOF7 PRELIMINARY; PRT; 686 AA.
 AC Q7TOF7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=23389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

Db	247	GAPSDSGPLRIAKTSPPEEPSPFPTSPPTASNNHTLAPAPAPARPPSPSQT-----	297
Qy	301	DAAQGSDNSEIKELLESEIEKGESEASSSEDPLP--ACNGPAQAQPSPTTERAKSOE	358
Db	298	--RKGGPVPLPKVPTKELQE--NIISPEDNFVFEISVTTPSQNE----VPEVKGE	349
Qy	359	EVL-----PSSTTPSPGALSPSQPSS-----SATEVVLRTTASEGS-----	400
Db	350	TLLDLDFDPKPEVTPAGSAGVTHSPMSQTLPMWDLWTITDLV---QPASGGSGFNGT	406
Qy	401	KKRASI-----ORTSAPPRPPPRATASPRESSGNIPSSPTASGGSGPTSP	447
Db	407	QDTSLTFTWQDOSMICNLAESEQAPTPEPAEPLAAVPAVG-----	449
Qy	448	RASLTGTGTSAPRTSLEVPNPEPPEKPVRTPEAKENININONPELCTSPTLMTSOVAS	507
Db	450	-LDLGMNDTRA-----BEPVEEAVIIPGADADAAGVT-----LVSAAGS	486
Qy	508	EPGEAKKVEDK-----EKDNKLISADSSGODQLQVSMVPENNNLTAPEPQEEVST	559
Db	487	AFGEAEAEATATVPAGEGVSLAEAKIGITETTEGASQAQ-----PEABEATVPQEK	542
RESULT 10			
Q7ZWPS			
ID	Q7ZWPS	PRELIMINARY;	PRT; 478 AA.
AC	Q7ZWPS;		
DT	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Similar to bridging integrator 1.		
OC	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxId=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Embryo;		
RA	Klein S., Strausberg R.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC046852; AAA46852.1; -.		
DR	GO; GO:0006897; P:endocytosis; IEA.		
DR	GO; GO:0007269; P:synaptic transmission; IEA.		
DR	InterPro; IPR003005; Amphiphysin.		
DR	InterPro; IPR006632; BAR.		
DR	InterPro; IPR004148; BAR dom.		
DR	InterPro; IPR001452; SH3.		
DR	Pfam; PF03114; BAR; 1.		
DR	Pfam; PF00018; SH3; 1.		
DR	PRINTS; PR01251; AMPHIPHYSIN.		
DR	PRINTS; PR0452; SH3DOMAIN.		
DR	SMART; SM00721; BAR; 1.		
DR	SMART; SM00326; SH3; 1.		
DR	PROSITE; PS50002; SH3; 1.		
SQ	SEQUENCE 478 AA; 53445 MW; 042A1A94D59095A8 CRC64;		
Query Match			
Best local Similarity 27.5%; Score 786.5; DB 13; Length 478;			
Matches 190; Conservative 59; Mismatches 128; Indels 69; Gaps 11			
Qy	1	MAEGKAGGAAGLFAKQVQKFSRAQKVLOKIGAVETKDERFESANFYQQQAEHGKL	60
Db	1	MAELKGVSAGKLASNNQKLLTAQEKVLQKLGKADETDEQFESCVQNFNKLTEGSKL	60
Qy	61	YKDLKNFLSAVKVNHSSKRVSTLOEIVYSSEWDGHEELKATVWNNDLLWDEYEEKLADQ	120
Db	61	QKDLAYLATVKAMHEASKLLTECLLDVTEPDWPGREETNKIAENNDLLWTYHQKLVQDQ	120
Qy	121	AVRTWEIYVAQFSIEKRIARGRKLVYDYSAPHHLEAVQNA-KKDEAKTAAEEFNKA	179
Db	121	ALLTMDTVLGQFPDKSIARGRKLVDFDSARHHPFESLQNAKKGOETKIAAEEDLLKS	180

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QY 180 QTVFEDLNOELLELPILYNSRIGCVYTFIFONISNLRDVFYREMSKLNHLYEVMWKLK 239
Db 181 QKVFEEMVNDLQEEPLSLWNSRVGYVYTFQSIAGLENFHKMGKHLQMLNVMWKLK 240
QY 240 Q-----HSNKVYVVKGL--SSSSRRSLV-----GPPVRTATVSSPLT 275
Db 241 EOGNLSNSSSVKQVPSLKHNTSNRKNKWLFSRLRIKKGSHCHISESTPTKNTNPPSPA 300
QY 276 SPTSSTLSLKSESSVSATEDL-APDAAQGEDNSEIKELLEEEIEKEGSEASSSEEDD 334
Db 301 SDGPVAV-----SETKVNHDFEAPSA-----VEETSVSAISKSPSOPVE 341
QY 335 PIPACNGPAQAQSPPTTERAKSQEVLPSSTPSPGGLSPGSSGQSSSATEVLRTRTAS 394
Db 342 PAPA-----PVSVNEPAKETEVPESAPPEEVPDKSPSSSLPA-----VVVEIFSA 388
QY 395 -EGSQPKKRAIORTSAPPSRPPPP 419
Db 389 VNGTVE-----SSPPKPEMP 404

RESULT 11
Q8NFL3
ID Q8NFL3 PRELIMINARY; PRT; 385 AA.
AC Q8NFL3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Amphiphysin I variant N22 (Fragment).
GN AMPH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22017878; PubMed=12023042;
RA Terada Y., Teutsui K., Sano K., Hosoya O., Ohtsuki H., Tokunaga A.,
RA Tsutsui K.;
RT "Novel splice variants of amphiphysin I are expressed in retina.";
RL FEBS Lett. 519:185-190(2002).
DR EMBL; AF498097; AA04811.1; -.
DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR003017; Amphiphysin_1.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYYSIN.
DR ProDom; PD003208; Amphiphysin_1; 1.
DR SMART; SM00721; BAR; 1.
FT NON_TER 385
SQ SEQUENCE 385 AA; 43753 MW; 499AB0A3136711AA CRC64;

Query Match 26.0%; Score 743.5; DB 4; Length 385;
Best Local Similarity 41.9%; Pred. No. 7.4e-31;
Matches 164; Conservative 77; Mismatches 113; Indels 37; Gaps 9;

QY 11 GLPAQVQKKFSRAQEKVLQKLGKAVETKDERPEQSASNFYQQAGHKLKXDLKNFLSA 70
Db 7 GIFAKVQKLNRAQEKVLQKLGKADETKDEQFEYVQNFKQEAETRLQRELGYLAA 66
QY 71 VVMHESKRVSETLQETYSSEWDGHEELKAIWNNDDLWEDYEKLADQAVRTMEIYVA 130
Db 67 IKGQEAEMKLTESLHEVPEWDYGRDVKVWGKCDVLWEDFHQKLVDSLLTDTYIG 126
QY 131 QFSEIKERIAKRGKLVNVDYSARHLEAVQNAK-KDEAKTAKAEFEFNKAQTVFEDLNQE 189
Db 127 QFPDKNRIAKRSKLVNVDYSARHLEALQSSKEDSRISKAEEFFQKAQKVFEEFNVD 186
QY 190 LLEELPILYNSRIGCVYTFIFONISNLRDVFYREMSKLNHLYEVMWKLKQHSNKVYVVK 249
Db 187 LQEEPLSLWNSRVGYVYTFQSIAGLENFHKMGKHLQMLNVMWKLKQHSNKVYVVK 246
QY 250 G 250
Db 247 G 247

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Db 187 LQEEPLSLWNSRVGYVYTFQSIAGLENFHKMGKHLQMLNVMWKLKQHSNKVYVVK 246
QY 250 GLSSSSRRSLVISPVRTATVSSPLTSPSTLSKSESVSATEDLAP----- 300
Db 247 G-----APMRCDGSLRIAKTPSP---PEPSPSL-----PSPTASPNHTLAPASPAPAPR 295
QY 301 --DAAQGEDNSEIKELLEEEIEKEGSEASSSEEDDPLP--ACNGPAQAQSPPTTERAK 355
Db 296 SPSQTRKGPVPPPLPKVPTFKELQOE--NIISFEENFVFEISVITPSPQNE-----VPEVK 349
QY 356 SQEEVL-----PSSTTPSPGALSPSGQPS 381
Db 350 KEETILLDLDFFPKPEVTPAGSAGVTHSPMS 380

RESULT 12
Q8BXH2
ID Q8BXH2 PRELIMINARY; PRT; 250 AA.
AC Q8BXH2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to MYC box dependent interacting protein 1.
GN AMPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK047144; BAC32971.1; -.
DR MGD; MGI:103574; Amph.
DR GO; GO:0006897; P:endocytosis; IEA.
DR GO; GO:0007268; P:synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 250 AA; 29125 MW; 568A3D55CC6C37CE CRC64;

Query Match 24.7%; Score 705.5; DB 11; Length 250;
Best Local Similarity 54.8%; Pred. No. 4e-29;
Matches 132; Conservative 56; Mismatches 52; Indels 1; Gaps 1;

QY 11 GLPAQVQKKFSRAQEKVLQKLGKAVETKDERPEQSASNFYQQAGHKLKXDLKNFLSA 70
Db 7 GIFAKVQKLNRAQEKVLQKLGKADETKDEQFEYVQNFKQEAETRLQRELGYLAA 66
QY 71 VVMHESKRVSETLQETYSSEWDGHEELKAIWNNDDLWEDYEKLADQAVRTMEIYVA 130
Db 67 IKGQEAEMKLTESLHEVPEWDYGRDVKVWGKCDVLWEDFHQKLVDSLLTDTYIG 126
QY 131 QFSEIKERIAKRGKLVNVDYSARHLEAVQNAK-KDEAKTAKAEFEFNKAQTVFEDLNQE 189
Db 127 QFPDKNRIAKRSKLVNVDYSARHLEALQSSKEDSRISKAEEFFQKAQKVFEEFNVD 186
QY 190 LLEELPILYNSRIGCVYTFIFONISNLRDVFYREMSKLNHLYEVMWKLKQHSNKVYVVK 249
Db 187 LQEEPLSLWNSRVGYVYTFQSIAGLENFHKMGKHLQMLNVMWKLKQHSNKVYVVK 246
QY 250 G 250
Db 247 G 247

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RESULT 13
 QY092 PRELIMINARY; PRT; 602 AA.
 AT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-JUN-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Amphiphysin protein (LID19810P).
 GN AMPH OR CGS604.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Phyllophoridae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flosser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Talali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Follard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20076404; PubMed=10607911;
 RA Razaq A., Su Y., Mehren J.E., Mizuguchi K., Jackson A.P., Gay N.J.,
 RA O'Kane C.J.;
 RT "Characterization of the gene for Drosophila amphiphysin."
 RL Gene 241:167-174 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Zhang Y.Q., Xue H., Broadie K.S.;
 RT "Dissecting the functions of amphiphysin."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nurco J., Pacleb J., Parsgas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMEL; AF171225; AAF58486.1; -;
 DR EMEL; AF171225; AAD46684.1; -;
 DR EMEL; AJ242855; CAB45188.1; -;
 DR EMEL; AY061278; AAL28826.1; -;
 DR HSPF; P27986; 1EHT.
 DR Flybase; FBgn0027356; Amph.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR GO; GO:0045202; C:synaptic junction; IDA.
 DR GO; GO:0007269; P:neurotransmitter secretion; NAS.
 DR GO; GO:0008104; P:protein localization; IMP.
 DR GO; GO:0006937; P:regulation of muscle contraction; IMP.
 DR GO; GO:0045313; P:rhabdosome membrane biogenesis; IMP.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYSIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SMO0721; BAR; 1.
 DR SMART; SMO0326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR SH3 domain.
 KW SH3 domain.
 SQ SEQUENCE 602 AA; 65901 MW; 86D1D4CBAE1B8F31 CRC64;
 Query Match 19.5%; Score 555.5; DB 5; Length 602;
 Best Local Similarity 28.4%; Pred. No. 6.3e-21;
 Matches 169; Conservative 90; Mismatches 240; Indels 97; Gaps 15;
 QY 12 LFAQVQKSKRAQKVLQKLGKAVETQERFQSSASNFVQQAEGHKLKDLKXFLSAV 71
 DB 8 MLAKSVQKHAGRAKELQNLGKVDRTADEIFDHLNFRNQQAASNRLOKGFNNYIRCV 67
 QY 72 KVMHESKRVSETTQETYSSEWDGHEKLAIVWNLLMEDYEKLADQAVTMEIYVAQ 131
 DB 68 RAAQAASKLWDSVCEIYEPQWSSYDALQATQASSELWADPAHKLGDQVLPLNTYTCQ 127
 QY 132 FSEIKERIAGKRLVDYDSARH---HLEAVQAKQDEAKTAKAEFEKNAQVTFEDLNQ 188
 DB 128 FPEKKVKEKRNKLDYDQGRHSFQNLQANAKRDXDKLTGKREQLSEARTYEILNT 187
 QY 189 ELLEELPLTLYNSRIGCVVTTFQINSLRDVVFREMSKLNHLYEVVMKL--EKQHSNKVF 246
 DB 188 ELHDELPAIDYDRLFLVTLVQLTFLATEQVFNHETAKIYSELEAIVDKLATESQSGSNT- 246
 QY 247 VYKGLSSSSRRSLVISPPVR-----TATVSSPLTPTPTPTPTSLSKSESE 290
 DB 247 LRKQTSNPIKTSPPQSPVFNKLNANINSYQNIITNGSSLSANSTPTSSLSQEPFRFD 306
 QY 291 SVSATEDLAPDA-----AQGEDNSEIKELLEEEIEKEGSEASSSEDDPLPACNGPAQA 345
 DB 307 SVSPTPSPESPAALVSVATSPSPV-----ENGVTTKSLERFELSGLNASAKA 355
 QY 346 ----QPSFTTERAKSQBEVLPSSTTTPPGGALSPGQSSSSATTEVLRTRT-----ASEG 396
 DB 356 TTTTTSPTEDKAVVSAVKPSET---EGAAVAASVTPAPPATPAQINGNNNEPSIVKEG 412
 QY 397 SEQPKKASQRTSAPPSPPPPRATASPPSGNIPSSPTAGGSGSPSPRAS-----450
 DB 413 GKQPKEL-----PSTTSNAEAAEAANNGNSIEEHKQKGLGNDTIVTATETVTVT 463
 QY 451 ----LGTTG-----ASPTSLSEVSPNPEPEKVPRTPEAKENENIENQNPPE-----493
 DB 464 QHSVTSTDTNIVTISDTNTDTTKTSTGTSQKRPVFPVVRNHSVNNL--NKKPFEDDDDR 522

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QY 494 -----LCTSPITMTSQVASEPCEAKMEDKEKN-----KLISADSEGOQ 535
Db 523 IYEVPADANTADLPQVLYRVTATGYAKEDVDLSFGLIRVIEYDDPEDOEE 578

RESULT 14
ID Q8WQ54 PRELIMINARY; PRT; 414 AA.
AC Q8WQ54;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Putative aggregation factor.
GN GEOCYAF.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA Schuetze J., Krasko A., Diehl-Seifert B., Mueller W.B.G.;
RT "Cloning and Expression of the Putative Aggregation Factor from the
RT Marine Sponge Geodia cydonium";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ311598; CAC83970.1; -.
DR GO; GO:0008697; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 414 AA; 46558 MW; 90CABDAB20152310 CRC64;

Query Match 18.8%; Score 535.5; DB 5; Length 414;
Best Local Similarity 29.4%; Pred. No. 4.3e-20;
Matches 150; Conservative 84; Mismatches 150; Indels 127; Gaps 15;

QY 1 MAE-----GKAGGAALFAQVQKFSRAQEKVLQKLGKAVETKDERFEQASNFYQ 53
Db 1 MAERHDGGAGGGGKGKILSMTVKRAQVQKXMKQKLGKSDQTRDEVEEFVNFHKQ 60
QY 54 QAEGHLYKDLNKLNFSAVKVWHSESKRVSETLQIYSSEWDGHEELKAIYVNDLLWEDY 113
Db 61 NASAIKLOKELMKYNSIRVLYQNTKMSDTLKSLEYBEDWDGCEKQRELMEQRIILWEDL 120
QY 114 EKLADQAVRTMEIYVAQSFBIKRIAGRKLVYDYSARHLE-AVONAKDEAKTAKA 172
Db 121 LTLSTRTVEPMYNIYSFSDVKTRIQKREKMDYDLRRRELEHAKSKAKVNDQKVOQA 180
QY 173 EEFNKAAQTVFEDLNQELLELPILYNSRICGYVTIIFONISNLRDVFYREMSKLNHLYE 232
Db 181 EDTHQAKOLYDEITDLEYELPLTYDSRIQFYQCFQSIATAAEFTHAEISKVDEDLAR 240
QY 233 VMSKLEKQHSNKFVVKGLSSSSRSRLVSPPVRTATVSSPLTSPTSLSKSSESV 292
Db 241 VND-----GLAEATGVHSTKKQVNSNAP-----SEEDS-----EGTESQP---TS 291
QY 293 SATEDLAPDAQGEDNSIKELLBEEIEKEGSEASSSEEDDPLPACNGPAQAPSPTTE 352
Db 268 -----KLLSRPEE-----SEEDS-----EGTESQP---TS 291
QY 353 RAKSOEEVLPSTTSPGALSPSQSPSSSATEVVLTRTASGSGOPKKRASIQTSPAP 412
Db 292 RSPSLKQ---SHLSFSP-----PEPNQNNIDQDTSTSSDVAVDP-----AP 329
QY 413 ---PSRPPPPRATASPRPSSGNIPSSPTASGGGSPT--SPRASLTGTGTASPRTSLEYSPN- 467
Db 330 GQPKPKPPPPFR-----SPDHSETAETGTGEAEKGTEDQOQEL 367
QY 468 PEPPEKPVRTPEAKENENIHQNEBELCTSP 498

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Db 368 QENQTAVESPPANE-ELLTDEDEQNVASP 397

RESULT 15
ID Q21004 PRELIMINARY; PRT; 461 AA.
AC Q21004;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE F58G6.1 protein.
GN F58G6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RT Science 282:2012-2018(1998).
CC 1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; Z68217; CAA92465.1; -.
DR PIR; T22946; T22946.
DR WormPep; F58G6.1; CE03428.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00346; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 461 AA; 51910 MW; 771C89E21EF7BEC8 CRC64;

Query Match 16.2%; Score 463; DB 5; Length 461;
Best Local Similarity 26.9%; Pred. No. 2.7e-16;
Matches 144; Conservative 96; Mismatches 175; Indels 120; Gaps 18;

QY 10 AGLPAQVQKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQAEGHLYKDLNKLNF 69
Db 2 ADLFNKHLKXATNRTEKLEGIGKAKATQDFVDQHAANLNKQSKCEKLHKDKVKNYSS 61
QY 70 AVKWHSESKRVSETLQIYSSEWDGHEELKAIYVNDLLWEDYBEKLADQAVRTMEIYV 129
Db 62 ALRLLSAEQQLDTRDAYEPENPDREHLTAIFNLDTQTNELEKTVCDLPTQVTVQV 121
QY 130 AQFSEIKERIAKGRKLVYDYSARHLEAVO-NAKXD-EAKTAKAEFEFNKAAQTVFEDLN 187
Db 122 NQFDDKKTEKGRKLVYDYSKNSFNVSFKASSKNDPFLAKATWELQAAEQMTENN 181
QY 188 QELLEEPILYNSRICGYVTIIFONISNLRDVFYREMSKLNHLYEYMSKLEKQHSNKFV 247
Db 182 NELLEILPAFVDSRITFFVDTLQTLFNANSVYQTDASKFHK---QIVMQLDK----- 230
QY 248 VKGLSSSSRSRLVSPPVRTATV--SSPLTSPTSLSKSSESVSATEDLAPDAQG 305
Db 231 ---LGSNDYLRVARFARALTIDITSLASSDAPAT-----PDQNK- 269
QY 306 EDNSEIKELLEEEIEKEGSEASSSEEDDPLPACNGPAQAPSPTTERAKSQEVLPSST 365

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Db 270 SDNSSLRQ-----TPSPS-----VLPS-- 286
QY 366 TPSPGALSPSQPSSSATEVVLRTETATSEGEQPKKEASIQRTSAPSPRPPPRATASP 425
Db 287 -FVP-----APMAKPREVVVSMANSTNPPDDDDDAEHDKAT-----PTDVEEKFEAKVYP 335
QY 426 RPSSGNIPSPSTASGGSPSPRASLGITGATSP-----RTSLEVSP---NPEPPEKPV 475
Db 336 KLNAAQOTAAAEQAIAAAKKEKKEAS-----NPPDDEDESTEVEEAPKKKDPPTPKPL 389
QY 476 RTEAKENENIHQNPEEL--CTS-----PTLMTSQVASEPGEAKKQEDKXKNKL 524
Db 390 -----DGITNEKRTLYFVTSTHNYKAVDTDELSFEQGVQIKVIEANEDDQL 436

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Search completed: March 4, 2004, 17:29:50
 Job time : 58.6038 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:19:24 ; Search time 72.5656 Seconds
(without alignments)
2196.038 Million cell updates/sec

Title: US-10-069-540A-2
Perfect score: 2855
Sequence: 1 MAEGKAGAGLFAKQVKK.....NNLTAPQBEVSTENPQL 564

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2855	100.0	564	AAB62100	Aab62100 Human bri
2	2794.5	97.9	594	ABG20887	Abg20887 Novel hum
3	2794.5	97.9	594	ABG20324	Abg20324 Novel hum
4	2787.5	97.6	594	ABG22457	Abg22457 Novel hum
5	2765.5	96.9	572	ABG21411	Abg21411 Novel hum
6	1988.5	63.6	414	ABG13005	Abg13005 Novel hum
7	1846	64.7	425	ABG22456	Abg22456 Novel hum
8	1788	62.6	960	ABG20886	Abg20886 Novel hum
9	1788	62.6	960	ABG20323	Abg20323 Novel hum
10	858	30.1	588	ADD45951	Add45951 Rat Prote
11	858	30.1	588	ADE60848	Ade60848 Rat Prote
12	858	30.1	588	ADE60840	Ade60840 Rat Prote
13	858	30.1	588	ADE60844	Ade60844 Rat Prote
14	858	30.1	588	ADE60852	Ade60852 Rat Prote
15	851.5	29.8	593	ADE60842	Ade60842 Human Pro
16	851.5	29.8	593	ADD45953	Add45953 Human Pro
17	851.5	29.8	593	ADE60850	Ade60850 Human Pro
18	851.5	29.8	593	ADE60846	Ade60846 Human Pro
19	851.5	29.8	593	ADE60854	Ade60854 Human Pro
20	829	28.0	482	ABU87771	Abu87771 Protein d
21	815.5	28.6	434	AAW05391	Aaw05391 Mouse SH3
22	815.5	28.6	683	ADD44887	Add44887 Rat Prote
23	804.5	28.2	695	AAU75110	Aau75110 Synaptic
24	804.5	28.2	695	ADD44889	Add44889 Human Pro
25	803.5	28.1	695	AAE22091	Aae22091 Human amp

ALIGNMENTS

RESULT 1
AAB62100
ID AAB62100 standard; protein; 564 AA.

XX AC AAB62100;
XX DT 29-MAY-2001 (first entry)
XX DE Human bridging integrator-2 (Bin2) protein.
XX KW Bridging integrator-2 protein; Bin2; cancer; leukemia; blood disorder;
XX KW hyperplastic disease; cytostatic; cell growth regulator;
XX KW Chromosome 4q22.1.
XX OS Homo sapiens.
XX FH Key
FT Peptide Location/Qualifiers
FT Peptide 23..35
FT Peptide /note= "specifically claimed fragment"
FT Peptide 138..155
FT Peptide /note= "specifically claimed fragment"

PN WO200116158-A2.

PD 08-MAR-2001.

PF 30-AUG-2000; 2000WO-US023723.

PR 31-AUG-1999; 99US-0151554P.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.

PI Prendergast GC, Ge K;

XX WPI; 2001-235087/24.

DR N-PSDB; AAF57268.

XX New bridging integrator-2 (Bin2) protein and nucleic acid molecules,
PT useful for regulating cell growth, and for diagnosing or treating
PT conditions associated with inappropriate expression of Bin2, e.g. cancers
PT or hepatocarcinoma.

PS Claim 1; Fig 1A-C; 62pp; English.

XX This represents a human bridging integrator-2 (Bin2) protein. The Bin2
CC protein can be expressed by standard recombinant methodology. The Bin2
CC proteins or peptides are useful in regulating cell growth, cell survival,
CC differentiation, endocytosis and actin organization. These peptides or

Aaw47295 Human Bin
Aaw94504 Human Bin
Aaw06602 Human Box
Aab36881 Human Bin
Aab62101 Bar domain
Abg22453 Novel hum
Abg20321 Novel hum
Abg20884 Novel hum
Abg20884 Novel hum
Abr69631 Human CGD
Abg2454 Novel hum
Aaw05392 Human SH3
Abg22449 Novel hum
Abg20881 Novel hum
Abg21407 Novel hum
Abg20318 Novel hum
Abg63948 Drosophila
Aab33907 Human sec
Abb06161 Human NS
Abg21410 Novel hum
Abg20317 Novel hum

26 793.5 27.8 451 2 AAW47295
27 793.5 27.8 451 2 AAW94504
28 792 27.7 451 2 AAW06602
29 792 27.7 451 2 AAB36881
30 767 26.9 252 4 AAB62101
31 763.5 26.7 721 4 ABG22453
32 763.5 26.7 721 4 ABG20321
33 763.5 26.7 721 4 ABG20884
34 720.5 25.2 453 6 ABR69631
35 712 24.9 233 4 ABG22454
36 675 23.6 404 2 AAW05392
37 625.5 21.9 130 4 ABG22449
38 625.5 21.9 130 4 ABG20881
39 625.5 21.9 130 4 ABG21407
40 625.5 21.9 130 4 ABG20318
41 555.5 19.5 602 4 ABB63948
42 546 19.1 106 3 AAB33907
43 527 18.5 108 5 ABB06161
44 527 18.5 137 4 ABG21410
45 367.5 12.9 82 4 ABG20317

CC proteins are also useful for diagnosing or treating conditions associated
 CC with inappropriate expression of Bin2, e.g. liver cancer, breast cancer,
 CC hepatocarcinoma, myeloid and lymphoid leukemias or blood disorders. The
 CC peptides, nucleic acid sequences or anti-Bin2 antibodies are useful for
 CC diagnosing inappropriate expression of Bin2. Bin2 is also useful for
 CC treating disorders associated with excessive Bin1 levels, e.g. liver,
 CC colorectal, prostate or breast cancers, epithelia cell cancers, melanoma,
 CC or hyperplastic disease states.

XX
 SQ Sequence 564 AA;

Query Match 100.0%; Score 2855; DB 4; Length 564;
 Best Local Similarity 100.0%; Pred. No. 9.1e-167;
 Matches 564; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEGKAGGAGLPAKQVQKFSRAQKVLQKLGKAVETKDERFQCSANFYQQQAEHGKL 60
 DB 1 MAEGKAGGAGLPAKQVQKFSRAQKVLQKLGKAVETKDERFQCSANFYQQQAEHGKL 60

QY 61 YKDLKNFLSAVKVMHSSKRVSETLQETYSSEWDGHEELKAIWVNDLLWEDYEELADQ 120
 DB 61 YKDLKNFLSAVKVMHSSKRVSETLQETYSSEWDGHEELKAIWVNDLLWEDYEELADQ 120

QY 121 AVRTMEIYVAQSEIKERIAKRGKLVYDSARHLEAVQNAKDEAKTAKAEFEFNKA 180
 DB 121 AVRTMEIYVAQSEIKERIAKRGKLVYDSARHLEAVQNAKDEAKTAKAEFEFNKA 180

QY 181 TVFEDLNQELLELPILYNSRIGCVYTFQNTISNLRDVFYREMSKLNHLYEVMSKLEKQ 240
 DB 181 TVFEDLNQELLELPILYNSRIGCVYTFQNTISNLRDVFYREMSKLNHLYEVMSKLEKQ 240

QY 241 HSNKVFVVKGLSSSRSLVSPVETATVSSPLTSPSTLSKSESVSATDELAP 300
 DB 241 HSNKVFVVKGLSSSRSLVSPVETATVSSPLTSPSTLSKSESVSATDELAP 300

QY 301 DAAQGEDNSEIKELLEEEIEKEGSEASSEDDEPLPACNGPAQAQSPPTTERAKSQEEV 360
 DB 301 DAAQGEDNSEIKELLEEEIEKEGSEASSEDDEPLPACNGPAQAQSPPTTERAKSQEEV 360

QY 361 LPSSTTSPGGLSPSGQSSGATEVLRTRTASGSGQPKKRASIORASAPPSPPPPPR 420
 DB 361 LPSSTTSPGGLSPSGQSSGATEVLRTRTASGSGQPKKRASIORASAPPSPPPPPR 420

QY 421 ATASPRPSSGNTPSSPTASGSGSPTRASLGTGTASPRTSLEVPKPEKPVRTPEA 480
 DB 421 ATASPRPSSGNTPSSPTASGSGSPTRASLGTGTASPRTSLEVPKPEKPVRTPEA 480

QY 481 KENENIHQNPELCTSPMTSQVASEPGEAKMEDKEKDKNLISADSSGQDLQVSM 540
 DB 481 KENENIHQNPELCTSPMTSQVASEPGEAKMEDKEKDKNLISADSSGQDLQVSM 540

QY 541 VPENNNLTAPEQEEVSTSENPL 564
 DB 541 VPENNNLTAPEQEEVSTSENPL 564

RESULT 2
 ID ABG20887 standard; protein; 594 AA.
 AC ABG20887;
 DT 13-FEB-2002 (first entry)
 DE Novel human diagnostic protein #20878.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 XX WO200175067-A2.
 XX

PD 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 PF 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 PA (HYSE-) HYSEQ INC.
 XX Dmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS85074.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 51246; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have application in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 594 AA;

Query Match 97.9%; Score 2794.5; DB 4; Length 594;
 Best Local Similarity 98.1%; Pred. No. 5e-163;
 Matches 554; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MAEGKAGGAGLPAKQVQKFSRAQKVLQKLGKAVETKDERFQCSANFYQQQAEHGKL 60
 DB 30 MAEGKAGGAGLPAKQVQKFSRAQKVLQKLGKAVETKDERFQCSANFYQQQAEHGKL 89

QY 61 YKDLKNFLSAVKVMHSSKRVSETLQETYSSEWDGHEELKAIWVNDLLWEDYEELADQ 120
 DB 90 YKDLKNFLSAVKVMHSSKRVSETLQETYSSEWDGHEELKAIWVNDLLWEDYEELADQ 149

QY 121 AVRTMEIYVAQSEIKERIAKRGKLVYDSARHLEAVQNA-KDEAKTAKAEFEFNKA 179
 DB 150 AVRTMEIYVAQSEIKERIAKRGKLVYDSARHLEAVQNAKDEAKTAKAEFEFNKA 209

QY 180 QTVFEDLNQELLELPILYNSRIGCVYTFQNTISNLRDVFYREMSKLNHLYEVMSKLEK 239
 DB 210 QTVFEDLNQELLELPILYNSRIGCVYTFQNTISNLRDVFYREMSKLNHLYEVMSKLEK 269

QY 240 QHSNKVFVVKGLSSSRSLVSPVETATVSSPLTSPSTLSKSESVSATDEL 299
 DB 270 QHSNKVFVVKGLSSSRSLVSPVETATVSSPLTSPSTLSKSESVSATDEL 329

QY 300 PDAAQGEDNSEIKELLEEEIEKEGSEASSEDDEPLPACNGPAQAQSPPTTERAKSQEE 359
 DB 330 PDAAQGEDNSEIKELLEEEIEKEGSEASSEDDEPLPACNGPAQAQSPPTTERAKSQEE 389

QY 360 VLPSTTTPSGGALSPGSSSEVTLRTTASGSEOPKKEASTORTSAPSRPPPP 419
 DB 390 VLPSTTTPSGGALSPGSSSEVTLRTTASGSEOPKKEASTORTSAPSRPPPP 449
 QY 420 RATASPRSSGNIPSSPTASGGGSPTSRASLTGTGTASPRTSLEVSFNPPEPKPVRTPE 479
 DB 450 RATASPRSSGNIPSSPTASGGGSPTSRASLTGTGTASPRTSLEIXNPPEPKPVRTPE 509
 QY 480 AKENENIHONPEELCTSPTLMTSOVASEPGEAKMEDKEKNKLISADSSGQDQLQVS 539
 DB 510 AKENENIHONPEELCTSPTLMTSOVASEPGEAKMEDKEKNKLISADSSGQDQLQVS 569
 QY 540 MYPENNLTAPPEQEVSTSENPOL 564
 DB 570 MYPENNLTAPPEQEVSTSENPOL 594

RESULT 3
 ABG20324
 ID ABG20324 standard; protein; 594 AA.
 AC ABG20324;
 XX
 DT 13-FEB-2002 (first entry)
 DE
 XX
 XX Novel human diagnostic protein #20315.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 XX Homo sapiens.
 XX
 XX WO200175067-A2.
 PN
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 XX
 XX 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS84511.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 XX Claim 20; SEQ ID NO 50683; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridization probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (I). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 594 AA;
 Query Match 97.98; Score 2794.5; DB 4; Length 594;
 Best Local Similarity 98.18; Pred. No. 5e-163; 6; Indels 1; Gaps 1;
 Matches 554; Conservative 4; Mismatches 4;
 QY 1 MAEGKAGGAAGLFAKQVKKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQAGHKL 60
 DB 30 MAEGKAGGAAGLFAKQVKKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQAGHKL 89
 QY 61 YKDLKNFLSAVKVWHSSKVSETIQEISSEWDGHEELKAIWNNDLLWEDYEELADQ 120
 DB 90 YKDLKNFLSAVKVWHSSKVSETIQEISSEWDGHEELKAIWNNDLLWEDYEELADQ 149
 QY 121 AVRTWEIYVAQFSEIKERIAKRGKLVYDSARHLEAVQNA-KKDEAKTAAEEFENKA 179
 DB 150 AVRTWEIYVAQFSEIKERIAKRGKLVYDSARHLEAVQNA-KKDEAKTAAEEFENKA 209
 QY 180 QTVFEDLNQELLBELPILYNSRIGCVYTFQNIISNRDVFYREMSKLNHNLVEVMSKLEK 239
 DB 210 QTVFEDLNQELLBELPILYNSRIGCVYTFQNIISNRDVFYREMSKLNHNLVEVMSKLEK 269
 QY 240 QHSNKFVVKGLSSSSRRSLVISPVRTATVSSPLTSPSTLSLKSSSESVSATEDLA 299
 DB 270 QHSNKFVVKGLSSSSRRSLVISPVRTATVSSPLTSPSTLSLKSSSESVSATEDLA 329
 QY 300 PDAAGEDNSEIKELLEEEIEKEGSEASSEDDPLPACNGPAQAQPSPTTERAKSQE 359
 DB 330 PDAAGEDNSEIKELLEEEIEKEGSEASSEDDPLPACNGPAQAQPSPTTERAKSQE 389
 QY 360 VLPSTTTPSGGALSPGSSSEVTLRTTASGSEOPKKEASTORTSAPSRPPPP 419
 DB 390 VLPSTTTPSGGALSPGSSSEVTLRTTASGSEOPKKEASTORTSAPSRPPPP 449
 QY 420 RATASPRSSGNIPSSPTASGGGSPTSRASLTGTGTASPRTSLEVSFNPPEPKPVRTPE 479
 DB 450 RATASPRSSGNIPSSPTASGGGSPTSRASLTGTGTASPRTSLEIXNPPEPKPVRTPE 509
 QY 480 AKENENIHONPEELCTSPTLMTSOVASEPGEAKMEDKEKNKLISADSSGQDQLQVS 539
 DB 510 AKENENIHONPEELCTSPTLMTSOVASEPGEAKMEDKEKNKLISADSSGQDQLQVS 569
 QY 540 MYPENNLTAPPEQEVSTSENPOL 564
 DB 570 MYPENNLTAPPEQEVSTSENPOL 594

RESULT 4
 ABG22457
 ID ABG22457 standard; protein; 594 AA.
 XX
 AC ABG22457;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22448.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 PF
 XX 31-MAR-2000; 2000US-00540217.
 PR

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PR 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Dmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS86644.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 20; SEQ ID NO 52816; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (II) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 594 AA;
XX
XX Query Match 97.6%; Score 2787.5; DB 4; Length 594;
XX Best Local Similarity 97.9%; Pred. No. 1.3e-162;
XX Matches 553; Conservative 3; Mismatches 8; Indels 1; Gaps 1;
XX
XX QY 1 MAEGKAGAGAGLFAKOVOKKESRAQKVLQKLGAVETKDERFQSSASNYQQAGHKL 60
XX Db 30 MAEGKAGAGAGLFAKOVOKKESRAQKALXKLGAVETKDERFQSSASNYQQAGHKL 89
XX
XX QY 61 YKDLNFLSAVKVHSESKRVSITLQETIYSSSEMDGHEELKAIYVNNDDLWEDYEELADQ 120
XX Db 90 YKDLNFLSAVKVHSESKRVSITLQETIYSSSEMDGHEELKAIYVNNDDLWEDYEELADQ 149
XX
XX QY 121 AVRTWEIYVAQSEIKERIAKRGKLVYDSARHHLAVQNA-KQDAKTAKEEFNKA 179
XX Db 150 AVRTWEIYVAQSEIKERIAKRGKLVYDSARHHLAVQNAKQDAKTAKEEFNKA 209
XX
XX QY 180 QTVFEDLNQELLELPILYNSKIGCYVTIFONISNLRDVFYREMSKLNHLYEVMKLEK 239
XX Db 210 QTVFEDLNQELLELPILYNSKIGCYVTIFONISNLRDVFYREMSKLNHLYEVMKLEK 269
XX
XX QY 240 QHSNKFVVKGLSSRRSLVSPVPTATVSSPLTSPSTLSLKSESESVATEDLA 299
XX Db 270 QHSNKFVVKGLSSRRSLVSPVPTATVSSPLTSPSTLSLKSESESVATEDLA 329
XX
XX QY 300 PDAAGDENSETKELLEETKEGSEASSSEEDPLPACNGPAQAQPSPTTAKSQEE 359
XX Db 330 PDAAGDENSETKELLEETKEGSEASSSEEDPLPACNGPAQAQPSPTTAKSQEE 389
XX
XX QY 360 VLPSSSTTSPGALSFGSQPSSSATEVVLRTTASGEQPKKRASTQRTSAPSPRPFP 419
XX Db 390 VLPSSSTTSPGALSFGSQPSSSATEVVLRTTASGEQPKKRASTQRTSAPSPRPFP 449
XX
XX QY 420 RATASPRSSGNIPSSPTASGGGSPTRASLGTTGTSAPRTSLEVPNPEPPKPVRTPE 479

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Db 450 RATASPRSSGNIPSSPTASGGGSPTRASLGTTGTSAPRTSLEVPNPEPPKPVRTPE 509
QY 480 AKENENIHQNPELCTSPILMTSQVASEPGEAKKVEDKEKKNKLIADSSSQDQLOYS 539
Db 510 AKENENIHQNPELCTSPILMTSQVASEPGEAKKVEDKEKKNKLIADSSSQDQLOYS 569
QY 540 MYPENNNLTAPEQEEVSTSENPOL 564
Db 570 MYPENNNLTAPEQEEVSTSENPOL 594
XX
XX RESULT 5
XX ID ABG21411
XX ID ABG21411 standard; protein; 572 AA.
XX AC ABG21411;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #21402.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS85598.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 20; SEQ ID NO 51770; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 572 AA;

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Query Match      96.9%; Score 2765.5; DB 4; Length 572;
Best Local Similarity 97.5%; Pred. No. 2.9e-161;
Matches 551; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 1 MAEGKAGGAGAGLFAKQVOKFESRAQEKVLQKLGKAVETKDERFEQSASNFYQQQAGHKL 60
DB 8 MAEGKAGGAGAGLFAKQVOKFESRAQEKVLQKLGKAVETKDERFEQSASNFYQQQAGHKL 67
QY 61 YKDLKNFLSAVKVWHSESKRVSETLQEIYSEWDGHEELKAIWVNDLLMEDYEEKLADQ 120
DB 68 YKDLKNFLSAVKVWHSESKRVSETLQEIYSEWDGHEELKAIWVNDLLMEDYEEKLADQ 127
QY 121 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKA 179
DB 128 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKA 187
QY 180 QTVFEDLNQELLEELPILYNSRIGCVYTIQFONISNLRDVFYREMSKLNHNLYEVMKLEK 239
DB 188 QTVFEDLNQELLEELPILYNSRIGCVYTIQFONISNLRDVFYREMSKLNHNLYEVMKLEK 247
QY 240 QHSNKFVFWKGLSSSRSLVISPVRTATVSSPLTSPSTLSLKSESESVSATDEL 299
DB 248 QHSNKFVFWKGLSSSRSLVISPVRTATVSSPLTSPSTLSLKSESESVSATDEL 307
QY 300 PDAAQGEDNSEIKELLEEEIEKESGSEASSEDPLPACNGPAQAQPSPTTERAKSOEE 359
DB 308 PDAAQGEDNSEIKELLEEEIEKESGSEASSEDPLPACNGPAQAQPSPTTERAKSOEE 367
QY 360 VLPSTTSPGGALSPGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQ 419
DB 368 VLPSTTSPGGALSPGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQ 427
QY 420 RATASPRSSGNIPSSPTASGGSGPTSPRASLGTTGTSAPRTSLEVSFNPPEPKVPTPE 479
DB 428 RATASPRSSGNIPSSPTASGGSGPTSPRASLGTTGTSAPRTSLEVSFNPPEPKVPTPE 487
QY 480 AKENENIHNONPEELCTSPTLMTSQVASEPGEAKKMDKDNKLI.SADSSEGGDQLQVS 539
DB 488 AKENENIHNONPEELCTSPTLMTSQVASEPGEAKKMDKDNKLI.SADSSEGGDQLQVS 547
QY 540 MVPENNNLTAPPEQEVSTSENPOL 564
DB 548 MVPENNNLTAPPEQEVSTSENPOL 572

RESULT 6
ABG13005
ID ABG13005 standard; protein; 414 AA.
XX AC ABG13005;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #12996.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
```

XX WPI; 2001-639362/73.
DR N-PSDB; AAS77192.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX Claim 20; SEQ ID NO 43364; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC responsible for genetic disorders or other traits to assess biodiversity
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 414 AA;

Query Match 69.8%; Score 1988.5; DB 4; Length 414;
Best Local Similarity 99.0%; Pred. No. 8.4e-114;
Matches 399; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 MAEGKAGGAGAGLFAKQVOKFESRAQEKVLQKLGKAVETKDERFEQSASNFYQQQAGHKL 60

DB 1 MAEGKAGGAGAGLFAKQVOKFESRAQEKVLQKLGKAVETKDERFEQSASNFYQQQAGHKL 60

QY 61 YKDLKNFLSAVKVWHSESKRVSETLQEIYSEWDGHEELKAIWVNDLLMEDYEEKLADQ 120

DB 61 YKDLKNFLSAVKVWHSESKRVSETLQEIYSEWDGHEELKAIWVNDLLMEDYEEKLADQ 120

QY 121 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKA 179

DB 121 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAKAEFEFNKA 180

QY 180 QTVFEDLNQELLEELPILYNSRIGCVYTIQFONISNLRDVFYREMSKLNHNLYEVMKLEK 239

DB 181 QTVFEDLNQELLEELPILYNSRIGCVYTIQFONISNLRDVFYREMSKLNHNLYEVMKLEK 240

QY 240 QHSNKFVFWKGLSSSRSLVISPVRTATVSSPLTSPSTLSLKSESESVSATDEL 299

DB 241 QHSNKFVFWKGLSSSRSLVISPVRTATVSSPLTSPSTLSLKSESESVSATDEL 300

QY 300 PDAAQGEDNSEIKELLEEEIEKESGSEASSEDPLPACNGPAQAQPSPTTERAKSOEE 359

DB 301 PDAAQGEDNSEIKELLEEEIEKESGSEASSEDPLPACNGPAQAQPSPTTERAKSOEE 360

QY 360 VLPSTTSPGGALSPGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQ 402

DB 361 VLPSTTSPGGALSPGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQPSGQ 403

RESULT 7

ABG22456

ID ABG22456 standard; protein; 425 AA.

XX AC ABG22456;

XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #22447.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN W0200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI: 2001-639362/73.
 XX DR N-PSDB; AAS86643.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 XX PT diagnostics, forensics, gene mapping, identification of mutations
 XX PT responsible for genetic disorders or other traits and to assess
 XX PT biodiversity.
 XX PS Claim 20; SEQ ID NO 52815; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 425 AA;
 Query Match 64.7%; Score 1846; DB 4; Length 425;
 Best Local Similarity 79.0%; Pred. No. 4.8e-105;
 Matches 381; Conservative 6; Mismatches 13; Indels 82; Gaps 3;
 QY 51 YQQQAGHKLKLDLKNFLSAVKVHSESKRVSSETLQETIYSSEWPDGHEELKAIYVNDLLW 110
 Db 10 FITQAECHLKFVKNFLNFIAGGVHSESKRVSXTLQFIYSEWYGHHEELKAIYVNDLLW 69
 QY 111 EYEEKLADQAVRTWEIYVQSEIYKRIKRGKLDVYDSARHLEAVQNA-KDEAKT 169
 Db 70 EYEEKLADQAVRTWEIYVQSEIYKRIKRGKLDVYDSARHLEAVQNAKDEAKT 129
 QY 170 AKAEFEFNKAQTVFEDLQELLEELPILYNSRIGCYVTIFQINSLRDVYREMSKLNHN 229
 Db 130 AKAEFEFNKAQTVFEDLQELLEELPILYNSRIGCYVTIFQINSLRDVYREMSKLNHN 199

QY 230 LYEVMSKLEKOHKNKVFVWKGLSSSSRSRLVISPVPRTATVSSPLTSPSPSTLSLKSES 289
 Db 190 LYEVMSKLEKOHKNKVFVWKGLS-----SPSTLSLKSES 223
 QY 290 ESVSATEDLAPDAAQGEDNSEIKELLEEEIEKEGSEASSEEDDPLPACNGPAQAQPSF 349
 Db 224 ESVSATEDLAPDAAQGEDNSEIKELLEEEIEKEGSEASSEEDDPLPACNGPAQAQPSF 283
 QY 350 TTERAKSQEEVLPSSTTTPSPGGALSPGQSSSATEVVLTRTASGSGSQPKKRASIORT 409
 Db 284 TTERAKSQEEVLPSSTTTPSPGGALSPGQSSSATEVVLTRTASGSGSQPKKRASIORT 343
 QY 410 SAPPSRPPPPRATASPRPSSGNIPSSPTASGGGSP*SPRASLGTGTASPTSLSEVSPNPE 469
 Db 344 SAP-----PK 348
 QY 470 PPEKPVRTPEAKENENIHNONPEELCTSP*TLMTSQAASPEGEAKQVEDKKNKLISANS 529
 Db 349 PPEKPVRTPEAKENENIHNONPEELCTSP*TLMTSQAASPEGEAKQVEDKKNKLISANS 408
 QY 530 SE 531
 Db 409 SE 410
 RESULT 8
 ABG20886
 ID ABG20886 standard; protein; 960 AA.
 XX AC ABG20886;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #20877.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN W0200175067-A2.
 PD 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI: 2001-639362/73.
 XX DR N-PSDB; AAS85073.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 XX PT diagnostics, forensics, gene mapping, identification of mutations
 XX PT responsible for genetic disorders or other traits and to assess
 XX PT biodiversity.
 XX PS Claim 20; SEQ ID NO 51245; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging

of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 960 AA;

Query Match 62.6%; Score 1788; DB 4; Length 960;
Best Local Similarity 79.7%; Pred. No. 4.8e-101;
Matches 369; Conservative 5; Mismatches 5; Indels 84; Gaps 4;

QY 46 SASNF--YQQAEGHKLKDLNFKLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAV 103
DB 144 SAFHFTYKCRAGHKLKDLNFKLSAVKVMHSSKRVSETLQFIYSEWYGHLEKAV 203

QY 104 WNDLLMEDYEEKLADQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA- 162
DB 204 WNDLLMEDYEEKLADQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA 263

QY 163 KQDAKTAKEEFNKATQVFEDLNQELLELPILYNSRIGCVYVTFQINSLRDVFYRE 222
DB 264 KQDAKTAKEEFNKATQVFEDLNQELLELPILYNSRIGCVYVTFQINSLRDVFYRE 323

QY 223 MSKLNHLNLYEVMKLEKQHSNKVYVVKGLSSRRSLVSPVRTATVSSPLTSPST 282
DB 324 MSKLNHLNLYEVMKLEKQHSNKVYVVKGLS-----SPST 357

QY 283 LSLKSESESVSATDLAPDAQGEDNSEIKELLEEEIEKEGSEASSSEDDPLPACNGP 342
DB 358 LSLKSESESVSATDLAPDAQGEDNSEIKELLEEEIEKEGSEASSSEDDPLPACNGP 417

QY 343 AQAPSPPTTERRAKSQEVLPSSTTPSPGGALSPSGQPSSTATEVVLRTTASEGSEQPK 402
DB 418 AQAPSPPTTERRAKSQEVLPSSTTPSPGGALSPSGQPSSTATEVVLRTTASEGSEQPK 477

QY 403 RASIQRTSAPPSPPPPRATASPRSSGNIPSSPTASGGSPSPRASLGCTASPTSL 462
DB 478 RASIQRTSAP----- 487

RESULT 9

ABG20323
ID ABG20323 standard; protein; 960 AA.
XX AC ABG20323;
XX AC
XX AC
DT 13-FEB-2002 (first entry)
DE Novel human diagnostic protein #20314.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS84510.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 50682; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 960 AA;

Query Match 62.6%; Score 1788; DB 4; Length 960;
Best Local Similarity 79.7%; Pred. No. 4.8e-101;
Matches 369; Conservative 5; Mismatches 5; Indels 84; Gaps 4;

QY 46 SASNF--YQQAEGHKLKDLNFKLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAV 103
DB 144 SAFHFTYKCRAGHKLKDLNFKLSAVKVMHSSKRVSETLQFIYSEWYGHLEKAV 203

QY 104 WNDLLMEDYEEKLADQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA- 162
DB 204 WNDLLMEDYEEKLADQAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA 263

QY 163 KQDAKTAKEEFNKATQVFEDLNQELLELPILYNSRIGCVYVTFQINSLRDVFYRE 222
DB 264 KQDAKTAKEEFNKATQVFEDLNQELLELPILYNSRIGCVYVTFQINSLRDVFYRE 323

QY 223 MSKLNHLNLYEVMKLEKQHSNKVYVVKGLSSRRSLVSPVRTATVSSPLTSPST 282
DB 324 MSKLNHLNLYEVMKLEKQHSNKVYVVKGLS-----SPST 357

QY 283 LSLKSESESVSATDLAPDAQGEDNSEIKELLEEEIEKEGSEASSSEDDPLPACNGP 342
DB 358 LSLKSESESVSATDLAPDAQGEDNSEIKELLEEEIEKEGSEASSSEDDPLPACNGP 417

QY 343 AQAPSPPTTERRAKSQEVLPSSTTPSPGGALSPSGQPSSTATEVVLRTTASEGSEQPK 402
DB 418 AQAPSPPTTERRAKSQEVLPSSTTPSPGGALSPSGQPSSTATEVVLRTTASEGSEQPK 477

QY 403 RASIQRTSAPPSPPPPRATASPRSSGNIPSSPTASGGSPSPRASLGCTASPTSL 462
DB 478 RASIQRTSAP----- 487

QY 463 EVSPNPPEPKPVRTPEAKENENIHNONPEELCTSPTLMTSQV 505

CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 588 AA;
SQ
Query Match 30.1%; Score 858; DB 7; Length 588;
Best Local Similarity 37.9%; Pred. No. 2.8e-44;
Matches 230; Conservative 76; Mismatches 179; Indels 122; Gaps 20;
QY 1 MAE-GKAGAGAGLFAKQVQKFSRAQEKVLQKAVETKDERPESASNFYQQAGHGH 59
Db 1 MAEMSGKGVTAGKIASNVQKLTAKQEKVLQKGADETKDEQFCQVQNFQKLTGTR 60
QY 60 LYKDLKNFLSAVKVWHSESKSVSETLQEIYSSEWDGHEELKAIWNNDLLWEDYEKLAD 119
Db 61 LQKDLRTYLASVKAMHEASKLSECLQEYVEPEPFGDEANKIAENNDLLWMDYHQLVD 120
QY 120 QAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAK----- 171
Db 121 QALLTMDYTLGQFPDIKSIARGRKLVYDSARHLYESLQTKAKKDEAKIAPVSLLEK 180
QY 172 -----AEEFNKAQTVFEDLNQELLEEPLIYNRSICYYT 207
Db 181 AAPQWCQKQLAHLVAQTNLLRNQAEELIKQAVFEMVNDLQELPLSNWSEVGFYV 240
QY 208 IFQNISLRNDFVREMSKLNENLYEVMKLEKQHSNKVFVVKGLSSSS---RSLVISPP 264
Db 241 TFQSIAGLEENPHKEMSKLNQNLNDVLSLEKQHSNTFTVKAQPSDSAPEKGNKSPSP 300
QY 265 VRTATVSPSLTSPSTLSKSESVSATEDAPAAQGENSEI----- 311
Db 301 -----PDGSPAATPEIRVNHPEFEPASGA---SPGATIPKSPQLRKGPPVPPPKHT 349
QY 312 ---KELLEEE-----EIEKEG---SEASSSEED-DPLPACNGPAQAO 346
Db 350 PSKEMKQQLSLPDDAFVPSIVTSPQFAPGFSEQASLDDLDEPLPVPVAPVKA- 408
QY 347 PSPTTERAKSQEVLVLP---SSTTSPGALSPSQSPSS---ATEVWLRTTASEGEQPK 401
Db 409 PTPSQQS-----IPWDLWEPTESQAGVL-PSGEPSSAEGSFAPVWPSQTAEPGPAQA 460
QY 402 KEASIQRTSAPPSRPPPRATASPPSGNTPSSPTASGG--GSPTSPLASLTG----- 454
Db 461 EASEVVGQTQPGETAASEATSSSLPAAVVVTFATVNGAVEGSGTITGRDLPLPGFMKV 520
QY 455 -----TASPTSLEVSPPPEPKPVRTPEAKE-----NENINQNPE-ELCTS--P 498
Db 521 QAQHDYATDDELQKAGDVVLVIFQNPQEQEGWLMGVKESDNQHKLEKCRGVFP 580
QY 499 TMTSQV 505
Db 581 ENFTERV 587
RESULT 13
ID ADE60844
XX ADE60844 standard; protein; 588 AA.
XX AC ADE60844;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein O08839, SEQ ID NO 6757.
XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-031247P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GCHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; O08839.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
CC
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 588 AA;

Query Match 30.1%; Score 858; DB 7; Length 588;
Best Local Similarity 37.9%; Pred. No. 2.8e-44;
Matches 230; Conservative 76; Mismatches 179; Indels 122; Gaps 20;
QY 1 MAE-GKAGAGAGLFAKQVQKFSRAQEKVLQKAVETKDERPESASNFYQQAGHGH 59
Db 1 MAEMSGKGVTAGKIASNVQKLTAKQEKVLQKGADETKDEQFCQVQNFQKLTGTR 60
QY 60 LYKDLKNFLSAVKVWHSESKSVSETLQEIYSSEWDGHEELKAIWNNDLLWEDYEKLAD 119
Db 61 LQKDLRTYLASVKAMHEASKLSECLQEYVEPEPFGDEANKIAENNDLLWMDYHQLVD 120
QY 120 QAVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNA-KKDEAKTAK----- 171
Db 121 QALLTMDYTLGQFPDIKSIARGRKLVYDSARHLYESLQTKAKKDEAKIAPVSLLEK 180

QY 172 -----ABEFNKATQVFDLNOELLELPILYNSRIGCYVT 207
 Db 181 AAPQWCGKLOAHLVAQTNLLRNQAEELIKAKVFEEMVNDLOELPSLWNSRVGFVN 240
 QY 208 IFONISLRDVFVREMSKLNHNLVEVMSKLEKQHSNKVFWVKGSLSSSS---RRSLVISPP 264
 Db 241 TFQSIAGLEENFHKEMSKLNQNLNDVLVLSLEKQHSNTFTVKAQPSDSAPEKGNKSPSP 300
 QY 265 VRTATVSSLTPTSPSTLSKSESVSATDLAPDAQGEDNSEI----- 311
 Db 301 -----PDGSPAATPEIRVNHEPEPASGA---SPGATIPKSPQLKRGPPVPPPKHT 349
 QY 312 ---KELLEEE-----EIEKEG---SEASSSED-DPLPACNGPAQAQ 346
 Db 350 PSKEMKQKQILSLFDADFVPEISVTTQFPAEPFSEQAQLLDLDLDFELPPVAPVKA- 408
 QY 347 PSPTTERAKSQEVLV-----SSTTPSGGALSPSGQSSS---ATEVLRTRTASEGSPK 401
 Db 409 PTPSGQS-----IPWDLWEPTESQAGVL-PSGEPSSAEGSFVAVWPSQTAEPGPAQA 460
 QY 402 KRASIQTSAAPSPRPPPRATASPRSSGNIPSSPTASGG---GSPTSPRASLGTG----- 454
 Db 461 EASEVVGTOEPGTAASEATSSSLPAVVVETTSATVNGAVEGTTTGRDLDPGFMFKV 520
 QY 455 -----TASPRTSLEVPNPEPEKPVRTPEAKE-----NENIHQNPE-ELCTS--P 498
 Db 521 QAQHDYATDTDELQKAGDVVLVTFQNPPEQDEGLMGVKSQWQHKLEKCRGVFP 580
 QY 499 TLMTSQV 505
 Db 581 ENFTERV 587

RESULT 14

ID ADE60852
 XX ADE60852 standard; protein; 588 AA.

AC ADE60852;

DT 29-JAN-2004 (first entry)

XX Rat Protein O08839, SEQ ID NO 6765.

DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0345382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Belfort K, Costigan M;

XX WPI: 2003-268312/26.

XX GENBANK; O08839.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIDO at
 CC ftp.wido.int/pub/published_pct_sequences.

XX Sequence 588 AA;

QY Query Match 30.1%; Score 858; DB 7; Length 588;
 Db Best Local Similarity 37.9%; Pred. No. 2.8e-44;
 Matches 230; Conservative 76; Mismatches 179; Indels 122; Gaps 20;

QY 1 MAE-CKAGGAGLEAKOVOKKFSRAQKVLQKGAKEVHKDEPEQASNFYQOQEGHK 59
 Db 1 MAEMSGKGVTAGKIASNVQKLTFAQKVLQKGADETKDEQFQCVQNFNQLTEGTR 60
 QY 60 LYKDLKNFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIVMNDLLWEDYEKLD 119
 Db 61 LQDLRTVLSAVKAMHEASKLSECLQEVYEPWPGRDEANKIAENNDLLWMDYQKLV 120
 QY 120 QAVTMEIYVAQFSEIEXERIAKGRKLVYDSARHLEAVQNA-KDEAKTAK----- 171
 Db 121 QALLTMDTYLGQFPDIKSRIAKGRKLVYDSARHHVYESLQTAKKDEAKIAPVSLLEK 180
 QY 172 -----ABEEFNKAQTVFEDLNQELLELPILYNSRIGCYVT 207
 Db 181 AAPQWCGKLOAHLVAQTNLLRNQAEELIKAKVFEEMVNDLOELPSLWNSRVGFVN 240
 QY 208 IFONISLRDVFVREMSKLNHNLVEVMSKLEKQHSNKVFWVKGSLSSSS---RRSLVISPP 264
 Db 241 TFQSIAGLEENFHKEMSKLNQNLNDVLVLSLEKQHSNTFTVKAQPSDSAPEKGNKSPSP 300
 QY 265 VRTATVSSLTPTSPSTLSKSESVSATDLAPDAQGEDNSEI----- 311
 Db 301 -----PDGSPAATPEIRVNHEPEPASGA---SPGATIPKSPQLKRGPPVPPPKHT 349
 QY 312 ---KELLEEE-----EIEKEG---SEASSSED-DPLPACNGPAQAQ 346
 Db 350 PSKEMKQKQILSLFDADFVPEISVTTQFPAEPFSEQAQLLDLDLDFELPPVAPVKA- 408
 QY 347 PSPTTERAKSQEVLV-----SSTTPSGGALSPSGQSSS---ATEVLRTRTASEGSPK 401
 Db 409 PTPSGQS-----IPWDLWEPTESQAGVL-PSGEPSSAEGSFVAVWPSQTAEPGPAQA 460
 QY 402 KRASIQTSAAPSPRPPPRATASPRSSGNIPSSPTASGG---GSPTSPRASLGTG----- 454
 Db 461 EASEVVGTOEPGTAASEATSSSLPAVVVETTSATVNGAVEGTTTGRDLDPGFMFKV 520
 QY 455 -----TASPRTSLEVPNPEPEKPVRTPEAKE-----NENIHQNPE-ELCTS--P 498
 Db 521 QAQHDYATDTDELQKAGDVVLVTFQNPPEQDEGLMGVKSQWQHKLEKCRGVFP 580

QY 499 TLMTSQV 505
Db 581 ENFTERV 587

RESULT 15

AD660842
ID ADE60842 standard; protein; 593 AA.

XX ADE60842;

XX 29-JAN-2004 (first entry)

XX Human Protein Q99688, SEQ ID NO 6755.

XX Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; Q99688.

PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 593 AA;

Query Match 29.8%; Score 851.5; DB 7; Length 593;
Best Local Similarity 36.6%; Pred No. 7e-44;
Matches 224; Conservative 82; Mismatches 179; Indels 127; Gaps 20;

QY 1 MAE-GKAGAGLFAKQVKKFSAQKVLQKLGKAVETKDRFQSFQASNFYQQQAEGHK 59
Db 1 MAEMGSKGVTAGKLASNVQKLTFAQKVLQKLGKADETKDEQFQCVQNFNKLTEGTR 60
QY 60 LYKDKNPLSAVKVMHSHSSKRVSETLQEIYSSSWDGEELKAIWNNDLILWEDYBEKLD 119
Db 61 LOKDLRTYLASVKAMHSAKSLNECQEVYEPDWRDEANKIAENNDLLWYDHOXKLV 120
QY 120 QAVRTMEIYVAQFSEIKERIAKGRKLVYDYSARHLEAVQNA-KDEAKTAK----- 171
Db 121 QALLTMDTYLQFPDIKSRIAKGRKLVYDYSARHVESLQAKKDEAKIAKPVSLLEK 180
QY 172 -----ABEEFNKAQTVEDLNQELLEELPILYNSRIGCYVT 207
Db 181 AAPQWCCQKLAHLVAQTNLRLNQABEELIAKQVFEEMNVDLQEEPLSLMNSRVGFVN 240
QY 208 IFQNISLRDVFYREMSKLNHLYEVMSKLEKQHSNKVFVVKGLSSSSRRSLVISPVRT 267
Db 241 TFQSTAGLEENFHKMSKLNQNLNDVLGLEKQSGNTFTVKAQPSDN-----APAKGN 294
QY 268 ATVSPLTSPSTSLKSESSEVSATEDLADPAQGEDNSEI-----K 312
Db 295 KSPSPDGGSPAATPEIRVNHEPEPAGGA---TPCATLPKSPSQLRGKGPVPPPPKHTPSK 351
QY 313 ELLREE-----EIEKEG---SEASSSEED-DLPACNGPAQAQPS 349
Db 352 EVKQEQILSLFEDTFVPEISVTTSPQFAEPGSEQASLLDLDFLPPVTSVKA-PTP 410
QY 350 TTERAKSQEVLV---SSTTSPGGLSPSGQSSS--ATEVVLRTRTASEGSEQPKKA 404
Db 411 SQQS-----IPWDLWEPTESAGSL-PSGEPSAAEGTFAVSWPQCTAEPGPAQPAEAS 462
QY 405 SIQRTSAPPSPRPPPRATASPRSSGNIPS-----SPTASGGSPSPRASLGTG 454
Db 463 EVAGTQPAQAQAPGEGTAASEAASSLPVAVVETPATVNGTVEGSG--AGRLDLPFG 520
QY 455 -----TASPTSTLEVPNPEPEKXPRTPEAKE-----NENIHNNPE-ELC 495
Db 521 FMEKVAQAHDYATDTDBELQKAGDVVLVTFQNPPEQDEGLMGVKESDWNQKLEKC 580
QY 496 TS--PTLMTSQV 505
Db 581 RGVPFENFTERV 592

Search completed: March 4, 2004, 17:26:42
Job time: 75.5656 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:23:55 ; Search time 25.865 Seconds
(without alignments)
2097.510 Million cell updates/sec

Title: US-10-069-540A-2
Perfect score: 2855
Sequence: 1 MAEGKAGGAGLFAKQVKK.....NNLTAPEQBEVSTENPOL 564

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	829	29.0	482	JC5593	amphiphysin II2 -
2	804.5	28.2	695	S2400	amphiphysin (clone
3	802.5	28.1	682	S22700	amphiphysin - chic
4	463	16.2	461	T22946	hypothetical prote
5	238	8.3	466	T11694	RVS167 protein hom
6	231	8.1	1200	A46194	neurofilament prot
7	230.5	8.1	916	A37864	neurofilament trip
8	228.5	8.0	858	S15762	neurofilament trip
9	214	7.5	763	T08929	hypothetical prote
10	213	7.5	1110	I31116	NF-180 - sea lamp
11	213	7.5	1560	T30282	calcium-binding pr
12	212	7.4	270	T43000	RVS161 protein hom
13	212	7.4	644	S55395	neurofilament prot
14	210	7.4	264	T40661	yeast reduced viab
15	206	7.2	971	T19431	hypothetical prote
16	204.5	7.2	1575	S68448	synaptotagmin, 170K
17	203	7.1	1367	S48478	glucan 1,4-alpha-g
18	202.5	7.1	3507	T34513	hypothetical prote
19	201	7.0	880	D89756	protein T23E7.2b l
20	200.5	7.0	845	D45669	neurofilament trip
21	200.5	7.0	2094	S33124	neurofilament trip
22	200.5	7.0	4377	A55575	tpx protein - huma
23	200	7.0	1020	1 QPHUH	ankyrin 3, long sp
24	200	7.0	1080	T43164	neurofilament trip
25	197.5	6.9	6642	T29757	lacta protein - li
26	195.5	6.8	2346	T13829	protein UNC-89 - C
27	194.5	6.8	706	A45990	tpx homolog - fru
28	194.5	6.8	2441	S39161	junctional sarcopl
29	194	6.8	699	T38073	CREB-binding prote
					nucleolar phosphop

30	194	6.8	836	2	S49940	cell division cont
31	193.5	6.8	816	2	S64439	hypothetical prote
32	192	6.7	1029	2	T30351	mucin-like protein
33	191.5	6.7	1849	2	C41859	IgA-specific metal
34	191	6.7	742	2	JC7595	scavenger receptor
35	191	6.7	1102	2	T39943	hypothetical prote
36	190	6.7	1664	2	T18262	S-layer protein -
37	189.5	6.6	849	2	S00030	neurofilament trip
38	189	6.6	292	2	S24169	mucin - rat
39	189	6.6	822	2	T51049	related to nucleol
40	189	6.6	870	2	T09137	extensin homolog
41	188	6.6	473	2	S50755	hypothetical prote
42	188	6.6	1121	2	T02764	myosin-I binding p
43	187.5	6.6	528	2	I47141	gastric mucin (C1c
44	187.5	6.6	744	2	F95013	pneumococcal surfa
45	187.5	6.6	2722	2	T20532	hypothetical prote

ALIGNMENTS

RESULT 1

JC5593
amphiphysin II2 - human
C:Species: Homo sapiens (man)
C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jun-2000
C:Accession: JC5593
R:Tautsui, K.; Maeda, Y.; Tautsui, K.; Seki, S.; Tokunaga, A.
Biochem. Biophys. Res. Commun. 236, 178-183, 1997
A>Title: cDNA cloning of a novel amphiphysin isoform and tissue-specific expression of i
A:Reference number: JC5593; MUID:97366618; PMID:9223448
A:Accession: JC5593
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-482 <TSU>
A:Cross-references: DDBJ:AF001383; NID:G2199534; PIDN:AA61363.1; PID:G2199535
A:Experimental source: fetal brain
C:Comment: This protein is involved in the synaptic vesicle recycling and in the regulat
C:Superfamily: amphiphysin; RVS161 protein homology
F16-275/Domain: RVS161 protein homology <RVS>
F1410-481/Domain: SH3 #status predicted <SH3>

Query Match 29.0%; Score 829; DB 2; Length 482;
Best Local Similarity 39.2%; Pred. No. 9.9e-29;

Matches 211; Conservative 70; Mismatches 167; Indels 90; Gaps 16;

QY	1	MAE-GKAGGAGLFAKQVKKFSRAQKVLQKLGKAVETKDRFQSASNFYQQQAEHGK	59
DB	1	MAENGSGVNTAGTASNVQKLTFAQKVLQKLGKADETKDRFQCVQNFNKLTEGTR	60
QY	60	LYKDLKNFLSAVKMHESKRVSETLQEIYSSWDGHEELKAVNNNDLLWEDYEKLAD	119
DB	61	LQKDLRTLASVAMEASKGLCEQLQEVTEPDWPGDRDKAENNDLLWEDYEKLVD	120
QY	120	QAVTMEIYVAQSEIKERIAKGRKLVYDYSARHLEAVQNA-KKDEAKTAKAEFEFNK	178
DB	121	QALLTMDTLQGPDIKRIAKGRKLVYDYSARHYESLQTKKKDEAKTAKAESELIK	180
QY	179	AQTFEDELNLEELPILYNSIGCTVTFQNIENLRDVFYREMSKLNHNIYFWSKLE	238
DB	181	AQVFEEENYVDLEELPILYNSIGCTVTFQNIENLRDVFYREMSKLNHNIYFWSKLE	240
QY	239	KQHSNKVFVVKGLSSSRSLVSPVTRATVYSSPTSPSTLSLSESESVSATEDL	298
DB	241	KQHSNTFTVYKQPSDN-----APAKGNKSPSPDGSPAATPEIRVNHPEPPAGA	291
QY	299	APDAAQEDNSETKEELLEETKEGSEASSEEDDPLPACNGPAQAQSPPTTERAKQ	358
DB	292	TPGATLPKSPSLRK-----GPPVPPPPKHTPSKEVQKE	325
QY	359	EVLP-----SSTTPSGGALSPSGQSSSATEVLRTRTASEGSEQPKKASTQR	408
DB	326	QILSLFEDTVPISVITPS-----QP-AAEASEVAGTQTPAA-GAQEPGETAA	371

QY 409 TSAPPSPPPRATASPPSSGNIPSSPTASGGSGPTSPRASLTG-----TAS 457
 Db 372 SEASSLFAVVVEVTFATVNTVSG-----GSGAG-----RLDLPFGVFKVQAOHQDYAT 423
 QY 458 PRTSLEVPNPPEPKPVRTPEAKE-----NENIHQNPE-ELCTS--PTLMTSQV 505
 Db 424 DTDELQKAGDVVLVFPQNPEEQDEGLMGVKSMDNQHKELEKCRGVFPENFTEV 481

RESULT 2
 S62400
 amphiphsin (clone 22-2) - human
 C:Species: Homo sapiens (man)
 C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C:Accession: S62400; 137166
 R:David, C.; Solimena, M.; de Camilli, P.
 FEBS Lett. 351, 73-79, 1994
 A:Title: Autoimmunity in Stiff-Man Syndrome with breast cancer is targeted to the C-term
 A:Reference number: S48686; MUID:94357284; PMID:8076697
 A:Accession: S62400
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-695 <DNA>
 A:Cross-references: EMBL:U07616; NID:G550449; PIDN:AAA21865.1; PID:G550450
 R:Yamamoto, R.; Li, X.; Winter, S.; Francke, U.; Kilimann, M.W.
 Hum. Mol. Genet. 4, 265-268, 1995
 A:Title: Primary structure of human amphiphsin, the dominant autoantigen of paraneoplasia
 A:Reference number: 137166; MUID:95276740; PMID:7757077
 A:Accession: 137166
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-695 <RES>
 A:Cross-references: EMBL:X81438; NID:G662991; PIDN:CAA57197.1; PID:G662992
 C:Genetics:
 A:Gene: GDB:AMPH
 A:Cross-references: GDB:386990
 A:Map position: 7p14-7p13
 C:Superfamily: amphiphsin; RVS161 protein homology
 F:11-270/Domain: RVS161 protein homology <RVS>

Query Match 28.2%; Score 804.5; DB 2; Length 695;
 Best Local Similarity 34.3%; Pred. No. 1.7e-27;
 Matches 206; Conservative 104; Mismatches 175; Indels 115; Gaps 18;

QY 11 GLFAQVQKFRAGAEKVLQKLGKAVETKDERPFSASNFYQQAEGHKLYKDLKNPLSA 70
 Db 7 GFAKNVQKRLNRAQAEKVLQKLGKADETKDEQFEYVQNFQKQAEGRQLQRELGLYLA 66
 QY 71 VKVMHSSKRVSETLQEIYSSEWDGHEELKAIWNNNDLLWEDYEKLDAQVETMELYA 130
 Db 67 IKMQEASMKLTESLHEVTEPDWYGREDVKMGVEKCDVWDFHQLVDGSLTLDLYLG 126
 QY 131 QFSEIKERIAKGRKLVYDYSARHLEAVQNAK-KDEAKTAKAEFEENKCAQTVFEDLNQE 189
 Db 127 QPFDIKNRIAKRSKLVYDYSARHLEALQSSKRKDESRISKAEEEFQKQKVFEEFNVD 186
 QY 190 LLEELPILYNSRIGCVTFIFQNLISLRDVFREMSKLNHLYEWSKLEKHQNKVFPVK 249
 Db 187 LOEELPILYNSRIGCVTFIFQNLISLRDVFREMSKLNHLYEWSKLEKHQNKVFPVK 246
 QY 250 GLSSSS---RRSLVSPVVRATVSPSLTS-----PTSPSTLSKSESVSATEDLAP 300
 Db 247 GAPSDGSLPIAKTSPPEEPLSPPTASPNHILAPASAPAPRPSQT-----297
 QY 301 DRAQGEDNSEIKELLEEEIEKEGSEASSEDPLP--ACNGPAQAPQSPPTERAKQOE 358
 Db 298 --RKGPVPPLPKVTFPTKELQOE--NIISFFEDNFVPEISVTPSQNE---VPEVKCE 349
 QY 359 EYL-----PSSTPSPGGLSPGSPSS-----SATEVILRTTASEGS-----EOP 400
 Db 350 TLILDLDLDFDFKFEVTPFASAGVTHSPMSQTLPWDLWTITSLDLV---QFASGGSGNFQTP 406

QY 401 KKRASI-----QRTSAPPSPPPRATASPPSSGNIPSSPTASGGSGPTSP 447
 Db 407 QDTSLFTWQTDQSMICNLAESQAPPTPEKAEPLAAVTEPAVG-----449
 QY 448 RASLTGTASTPRTSLEVPNPPEPKPVRTPEAKEENIHQNPEELCTSPTLMTSQVAS 507
 Db 450 -LDLGMOTRA-----EETVEAVIIPGADADAAGCT-----LVSAAGS 486
 QY 508 EPG---EAKM-----EDKDKONKLISADSSGQDQLQVSMVFPENNLLTAPBPQEVST 559
 Db 487 APGEAEAEKATVPAGEGVSLEAKIGTETTEGAESAQ-----PEAELEATVPQEKVIPS 542

RESULT 3
 S22700
 amphiphsin - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S22700
 R:Lichte, B.; Voh, R.W.; Meyer, H.E.; Kilimann, M.W.
 EMBO J. 11, 2521-2530, 1992
 A:Title: Amphiphsin, a novel protein associated with synaptic vesicles.
 A:Reference number: S22700; MUID:92331604; PMID:1628617
 A:Accession: S22700
 A:Molecule type: mRNA
 A:Residues: 1-682 <LIC>
 A:Cross-references: EMBL:X60422; NID:G62842; PIDN:CAA42953.1; PID:G62843
 C:Superfamily: amphiphsin; RVS161 protein homology
 F:11-270/Domain: RVS161 protein homology <RVS>

Query Match 28.1%; Score 802.5; DB 1; Length 682;
 Best Local Similarity 33.1%; Pred. No. 2e-27;
 Matches 206; Conservative 118; Mismatches 203; Indels 95; Gaps 19;

QY 1 MAEGKAGGAGLFAKQVQKFRAGAEKVLQKLGKAVETKDERPFSASNFYQQAEGHKL 60
 Db 1 MADNVK----TGIFAKNVQKRLNRAQAEKVLQKLGKADETKDEQFEYVQNFQKQAEGRSKL 56
 QY 61 YKDLNPLSAVKVNVHSSKRVSETLQEIYSSEWDGHEELKAIWNNNDLLWEDYEKLDAQ 120
 Db 57 QRELRAVLAAIKGMQDASKLTESLHEVTEPDWYGREDVKMGVEKCDVWDFHQLVDG 116
 QY 121 AVRTMELVYVQFSEIKERIAKGRKLVYDYSARHLEAVQNAK-KDEAKTAKAEFEFNKA 179
 Db 117 SLTLDLYLGQFPDIKRIAKRSKLVYDYSARHLEALQSSKRKDEGRITKAEFEFQKA 176
 QY 180 QTVFEDLNQELLEPLILYNSRIGCVTFIFQNLISLRDVFREMSKLNHLYEWSKLEK 239
 Db 177 QKVFEEFNLDQELPGLSLSRERGVYVNTFKNVSSLEAKFHEKLEIALCHLVYVMTKLD 236
 QY 240 QHSNKVYVVKGLSSSS---RRSLVSPVVRATVSPSLTS-----PTSPSTLSKSESE 290
 Db 237 QHADKAFTIQAPSDGSLPIAKTSPPEEPLSPPTASPNHILAPASAPAPRPSQT 296
 QY 291 SVSATEDLAPDAQGEDNSEIKELLEEEIEKEGSEASSEDPLPACNGPAQAPQSP-P 349
 Db 297 -----LRKGPVPPLPKVTFPTKELQOE--NIISFFEDNFVPEISVTPSQNEIP 343
 QY 350 TTERAKS-----QEEVLPSTTTPSGGLSPSG-----QPSSS-----382
 Db 344 ETKKVESLILLDFDFKFEVTPFASAGVTHSPMSQTLPWDLWTITSELVQPASSAFNGPAQD 403
 QY 383 ATEVVLK-----TETASEGSEQPKKASQRTS-----APPSPPPPPRA---TA 423
 Db 404 TPAFVQSNENVNTELTAEAEAPLGEKLVETPTAAVVEKEAILAEFPDFTQCAESIEA 463
 QY 424 SPRSSG--NIPSSPTASGGSGS---PTSPRASLTGTASPTSLSPVSPNPEPEKVPRT 478
 Db 464 GDKETTGAKESEVWSAAGAVAVEDSVVVAAGAGGAVRTEQEAAGGADKPGQEKDV 523
 QY 479 EAKENIHQNPEELCTSPTLMTSQVASPEPGAKWEDKEKNKLISAD--SSEGDQLQ 537
 Db 524 DVSQ-----EKVSSIPSVVIEPASNNEGEEHHVIMNESKDAAEAMGTQGTDS--E 573

QY 538 VSMVPENNLTAPEQREVST 559
 Db 574 TSQIGSEQKAT-----EIIQT 590

RESULT 4

T22946
 Hypothetical protein F58G6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T22946

R.Lloyd, C.

Submitted to the EMBL Data Library, December 1995

A:Reference number: Z19641

A:Accession: T22946

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-461 <WIL>

A:Cross-references: EMBL:Z68217; PIDN:CAA92465.1; GSPDB:GN00022; CESP:F58G6.1

A:Experimental source: clone F58G6

C:Genetics:

A:Gene: CESP:F58G6.1

A:Map position: 4

A:Introns: 19/3; 57/3; 96/3; 130/3; 157/3; 186/3; 219/3; 271/3; 302/3; 335/3; 357/3

C:Superfamily: amphiphysin; RVS161 protein homology

Query Match 16.2%; Score 463; DB 2; Length 461;
 Best Local Similarity 26.9%; Pred. No. 4.1e-13;
 Matches 144; Conservative 96; Mismatches 175; Indels 120; Gaps 18;

QY 10 AGLPAKOVKKFRAQKVLQKLGKAVETKDERFEQASNFYQQAEGHLYKDLKNFLS 69

Db 2 ADLFNKILKATNTKELLEGIGKATQDEVFDQAAINLKQSKCEKHLKQVKNYS 61

QY 70 AVKVMHSSKRVSTLQEIYSSWDGHEELKAIWVNDLLWEDYERKLDQAVRTWEIV 129

Db 62 ALRTLLSAEQRLRTIDAVEPEWPDREHLTAIFDNLIDITQLEKTVCDLPQIVTV 121

QY 130 AOFSEIKERAKRGLVDYDSARHLEAVQ-NAKQD-EAKTAKABEEFNKAQTFFEDLN 187

Db 122 NQFDLKKKIEKGRKLVYDSAKNSFNSVKASSKNDPFLAKATMELQAAEQMYTEM 181

QY 198 QELLEELPILNYSRIGCYVTIFONISNLRDVFVREMSKLNHLYEVMVSKLEKQHSNKVF 247

Db 182 NELLEILPAVFDSEITFTVDTLQTLFNANSVYQTDASKFHK---QIVMQLDK 230

QY 248 VKGLSSRSRLVTSPPVPTATV--SSPLTSPSTLSKSESVSATEDLAPDAAQ 305

Db 231 ---LGESNDYLRVARPEARALTPTDITSLASSDAPAT-----PDQNK- 269

QY 306 EDNSEIKELLEEEIEKEGSEASSSEDDPLPACNGPAQAQSPPTTERAKSQEEVLPSST 365

Db 270 SDNSSLRQ-----TPSPS-----VLPS- 286

QY 366 TPSPGALSPSGOPSSATEVILRTATSEGSQPKKRASIQRTSAPPSPPPPPTATASP 425

Db 287 -FVP-----APWAKPESVSWMANSTNPFDDDDAHDKEAT-----PTDVEKEFEAKYVP 335

QY 426 RPSSGNIPSSPTASGGSPSPASISGTGTASP-----RTSLVSP---NPEPEKPV 475

Db 336 KLNAAQTAQAQAIAAKREKKAAS-----NPFDDDEDESTEVEAPKCKDPEPTPKPL 389

QY 476 RTPEAKENINHNQPEEL--CTS-----PTLMTSQVASPGEAKQMKDKKNKL 524

Db 390 -----DGIETKRTKLTLYFTVSTNYKXAVDTDELSTFEQGVQIKVIEANEDQL 436

RESULT 5

T11684

RVS167 protein homolog - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000

C:Accession: T11684

R.Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z17313

A:Accession: T11684

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-466 <SEE>

A:Cross-references: EMBL:AL031536

A:Experimental source: strain 972h(-)

C:Genetics:

A:Map position: IIR

A:Introns: 444/3

A:Note: SPSC21D10.12

C:Superfamily: RVS167 protein; RVS161 protein homology; SH3 homology

F:4-270/Domain; RVS161 protein homology <RVS>

F:414-463/Domain; SH3 homology <SH3>

Query Match 8.3%; Score 238; DB 2; Length 466;
 Best Local Similarity 22.0%; Pred. No. 0.0017;
 Matches 110; Conservative 69; Mismatches 194; Indels 128; Gaps 16;

QY 15 KQVQKPSRAQKVLQKLGKAVETKDERFEQASNFYQQAEGHLYKDLKNFLSAVKVM 74

Db 4 KGFTKALARTPQTLRSKFNVEITKDPIYEDAGRRFKSLETEAKLAEDAKKYTDAINGL 63

QY 75 HESSKRVSTLQEIY-----SSEWDGH-----BELKAIWVNDLLWEDYEK 116

Db 64 LNHQIGFADACIIEYPIGRASDPSEYQEGNAEGIEAAEAYKEIVY-----DLQKN 116

QY 117 LAQAVRTMEIYVAQP-----SEIKERIAKRGKLVYDSARHLEAVQNAK-- 163

Db 117 LASE-----MDVINTRIVNPTGELLKIVKDVDKLLKRDHKQLDYDRHRSSEFKKLOEKDK 172

QY 164 --KDEAKTAKABEEFNKAQTFFEDLNQELLEELPILNYSRIGCYVTIFQNI-SNLRDVFVR 221

Db 173 SLQDEKGLYEATAPFQSSQEQVEYNEMLKEELPKLFAQAQFIAPLFGQ-----FY 225

QY 222 EMKLNHNLYEVMVSKLEKQHSNKVFVKGLSSRSRLVTSPPVPTATVSSPLTSPSPS 281

Db 226 MQLNVYVLYYERKMSHCIEIQYFD--FNWDILEYERRRGDKVRAEALITTKFTAKPTYK 283

QY 282 TLLKSESVSATEDLAPDAAQEDNSEIKELLEEEIEKEGSEASSSEDDPLPACNG 341

Db 284 RPNQGGCGKQDATAS-----SSSSFSFKREE----- 308

QY 342 PAQAQSPPTTERAKSQEEVLPSSTTPSPGALSPSGOPSSATEVILRTATSEGSQPK 401

Db 309 -AAAEPSST-----ATDIPPPYSTPSVAGASDYS--TPSAGYQTVQTTTTTTEAAAQY 360

QY 402 KRASIQRTSAPPSPPPPPTATSPSPSGNIPSSPTASGGSGSPSPASISGTGTASPT 461

Db 361 PQAAF-----PPPP--VMPQFAA-----AAVTPVAAPVAA 389

QY 462 LEVSNPEPEKPKVKTPEAK 481

Db 390 AAAAVFVPPPPAPAPAAAPAE 410

RESULT 6

A46194

neurofilament protein NF-220, high-molecular-weight splice form - longfin squid

C:Species: Loligo pealeii (longfin squid)

C>Date: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 17-Mar-2000

C:Accession: A46194

R;Way, J.; Hellmich, M.R.; Jaffe, H.; Szaro, B.; Pant, H.C.; Gainer, H.; Battey, J.

Proc. Natl. Acad. Sci. U.S.A. 89, 6963-6967, 1992

A:Title: A high-molecular-weight squid neurofilament protein contains a lamin-like rod d

A:Reference number: A46194; MUID:92357751; PMID:1379729

A:Accession: A46194

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1200 <WAY>

A;Cross-references: GB:M94389; NID:g161291; PID:g161292
 A;Experimental source: stellate ganglion
 A;Note: sequence extracted from NCBI backbone (NCBIP:113499)
 C;Superfamily: neurofilament triplet H protein
 C;Keywords: alternative splicing

Query Match 8.1%; Score 231; DB 2; Length 1200;
 Best Local Similarity 18.3%; Pred. No. 0.011;
 Matches 132; Conservative 129; Mismatches 240; Indels 222; Gaps 24;
 QY 18 QKFSRAQEKV-----LQKLGAVTVDKPEGASNFYQQAGHLYKDLNKLFSAV 71
 DB 196 QGCIARQONQADLEGEISMLRSIESLEKMKQSNILAKQNDMEKMDLNN-----E 251
 QY 72 KWHSSSKVSSTLQEIYSSSDGH-BELKAIV-----WNNDL-----LW 110
 DB 252 TINHLDAENRRGTLEEELEFQKVHQAELKELAAAYDITTAENRFRWELAQARDIQ 311
 QY 111 EYEEKLADQAVRTMEIY-----VAQF-----SEIKRIAKRGRKLVD 148
 DB 312 QEYDAK-CDQMRGDIETAYYNLKVQEFRTGATKQNNVTRNKEENTKLKSNNTBI RNRLAD 370
 QY 149 YDSARHLEAV-----QNAKQDAKTAKAEENFKATQVPEDLNQELLEELPILYN 199
 DB 371 LEARNAQLERTNQDLRLQEKDQNELESQYKEETIKLQGENESILKELQDLMIDIKUS 430
 QY 200 SRIGCVTIFQNISLNRDVFYREMSKLNHLYEYMSKLEKQHSNKVFFVVKGLSS----- 254
 DB 431 LEL-----EIAAYRKLLEGEESRIELVHPMTIGTREAYRPELITKNGKSASDDSS 482
 QY 255 ---SRSLVIGPPVPTATVSSPLTS-----PTSPSTLSKSESVSATDEL--- 298
 DB 483 KDGTVRAKSVSPDVVAETKLTITSYCGGDADDEGKDSDDTHTEAEABETRADSDADT 542
 QY 299 -----APDAAQEDNSEIKELLEEBEIEKEGSEASSEEDD 334
 DB 543 GTGLDEVKEESVLKSEKDKSVKRDDEBEEDNDQTESEVDEDEADIEKSQSESDKTE 602
 QY 335 PLPCNGAQAQAPPT-----TERAKQBEVLPSST-----PFGG----- 371
 DB 603 SDXAESERAEVKATTPESDKAESVKSSRSITSETAFIDKPKPGKRDTLFQSDKV 662
 QY 372 -----ALSP-----SQQSSSATEVLRTRA 393
 DB 663 TSPVLLERAMSLQAPTEKPLSDTIKSPVVSERPAISVSVRGATSTPAERTSPISGG 722
 QY 394 SEGSEQPKRASIORTSAPPR-----PPPRATASPPSSGNIPSSPTASGGSP 444
 DB 723 SEKSAKSPVRS--EATKSPVSEKSGSKSPVPSERALSPLVSMVSHSTAMSTSRSP 780
 QY 445 TSPRASLGTGTASPTSLVSPNPEPP--EKVPTPEAKENENIHQNPBELCTPTLMT 502
 DB 781 TASEKSVKSPHSTERT--SPTAKSPIIPEAPKPKDESEKLSPESESVMGSKSQIT 837
 QY 503 SQVASEPGEAKMEDKEKKNKLISADSSGQDQLQVSWPENNLTAPPEQBEV---STS 559
 DB 838 SSSAKSPVPSBK-----ADSEK-----SATSPTEKVDDESSA 871
 QY 560 ENP 562
 DB 872 RSP 874

RESULT 7
 A27864
 neurofilament triplet M protein - human
 N;Alternate names: NF-M (medium) protein
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C;Accession: A27864; A30157
 R;Myers, M.W.; Lazzarini, R.A.; Lee, V.M.Y.; Schlaepfer, W.W.; Nelson, D.L.
 EMBO J. 6, 1617-1626, 1987
 A;Title: The human mid-size neurofilament subunit: a repeated protein sequence and the

A;Reference number: A27864; MUID:87275853; PMID:3608989
 A;Accession: A27864
 A;Molecule type: DNA
 A;Residues: 1-916 <MYE>
 A;Cross-references: GB:Y00067; NID:g35045; PID:CAA6276.1; PID:g35046
 R;Lee, V.M.Y.; Otvos Jr., L.; Carden, M.J.; Hollosi, M.; Dietzschold, B.; Lazzarini, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 85, 1998-2002, 1988
 A;Title: Identification of the major multiphosphorylation site in mammalian neurofilament
 A;Reference number: A30157; MUID:88158120; PMID:2450354
 A;Contents: annotation; phosphorylation sites
 C;Genetics:
 A;Introns: 360/3; 402/2
 C;Superfamily: cytoskeletal keratin
 C;Keywords: coiled coil; phosphoprotein
 P;615,628,641,654,680/Binding site: phosphate (Ser) (covalent) #status predicted
 F;615,628,641,654,680/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 8.1%; Score 230.5; DB 2; Length 916;
 Best Local Similarity 22.4%; Pred. No. 0.0081;
 Matches 131; Conservative 96; Mismatches 264; Indels 93; Gaps 24;
 QY 41 ERPEQASNFYQQAGHLYKDLNKLFSNAVKMHSSKRVSETLQEIYSSSEWDGHEELK 100
 DB 187 ERFEERLRDDTEAIRAURKDIEE-ASLVK--ELDKKV-OSLQDEVAFLRSHEEV 242
 QY 101 AIVNNNDLWE-----DYEEKLADQAVRTMEIYVAQFS-----EIKRIAKRGR 144
 DB 243 A-----DLAQIQASHITVERKDYLTDTISTALKEIRSQLESHSDQNMHQAEEWFKCYA 297
 QY 145 KLVYDSARHLEAVQNAKQDAKTAKAE---EPNKAQTVFEDLNQELLEELPILYN 200
 DB 298 KLT--EAEQNKRAISAKKEEIAEYRQLOQSKSIELESVRGTKESLERQ-LSDIEERHNN 354
 QY 201 RIGCVTIFQNISLNRDVFYREMSKLNHLYEYMSKL-EKQHSNKVFFVVKGLSSSSRSRL 259
 DB 355 DLSSYQDTIQOLEN-----ELRGYKWEHARHREYQDLLNVKXALDIEIAAYRKL 404
 QY 260 VIPTVPTATVSSPLTSP--TSPSTLSKSESRSVA-----TEDLAPDAAQGE 306
 DB 405 LEGETRFSTFAGSIITGLYTHRPITITISSKIQTQKVEAPKLKVQKFEVEIIEETKVED 464
 QY 307 DNESEIKELL---EE-----EEIEKEGSEASSSE---EDDPLPACNGPAQA-QPSPTTER 353
 DB 465 EKSEMEALTAITEELAAASKKEKKAEEKEEPEAEHEEVAAKSPVKATAPVKEEE 524
 QY 354 AKSQEVLPSSTTPPGGALSPSGQSPSSATRVL-----RTRTASEGSE-OPKK 402
 DB 525 GEKEESEGQBEHEEDEGAKSDQABEGGSEKESKEGEQEGETEAEAEAGEEAEAKE 584
 QY 403 RASIQRTSAPPSPPPPRATA---SPRPSSGNIPSPSTASGGSP--SPRASLGTGTAS 457
 DB 585 EKKVEKSEEVATYKEELVADAKVPEKAKSPVKSPVVEEKGSVPVKSPVVEEKGSVPV- 643
 QY 458 PRTSLVSPNPEPPEKPVRTPEAKENENIHQNPBELCTSP-----LMTSOVASEPGEAK 513
 DB 644 PKSPVVEEKGSVPVKSPV--EKGKSPVKSPVVEEKAKSPVKSPVVEEKAKSFAVCKGE 700
 QY 514 KMEDKEDKNKLISADSSGQDQLQVSWPENNLTAPPEQBEVS 557
 DB 701 QKEEKEKVEAPKEKVEKSEKPKDQVPEKKAESPVKKEAVA 744

RESULT 8
 S15762
 neurofilament triplet M protein - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
 C;Accession: S15762; S08061; A27040
 R;Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E.D.
 Nucleic Acids Res. 18, 521-529, 1990
 A;Title: Isolation of the chicken middle-molecular weight neurofilament (NF-M) gene and
 A;Reference number: S15762; MUID:90174973; PMID:2106668
 A;Accession: S15762
 A;Status: preliminary

R;Jacobs, A.J.; Kamholz, J.; Selzer, M.E.
Brain Res. Mol. Brain Res. 29, 43-52, 1995
A;Title: The single lamprey neurofilament subunit (NF-180) lacks multiphosphorylation re
A;Reference number: I51116; MUID:95287814; PMID:777C000
A;Accession: I51116
A;Status: preliminary; translated from GE/EMBL/DBD
A;Molecule type: mRNA
A;Residues: 1-1110 <AC>
A;Cross-references: EMBL:U19361; NID:G632549; PIDD:AAA80106.1; PID:G632549
C;Superfamily: neurofilament triplet H protein

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Query Match      7.5%; Score 213; DB 2; Length 1110;
Best Local Similarity 20.9%; Pred. No. 0.057;
Matches 119; Conservative 89; Mismatches 223; Indels 138; Gaps 23;

QY 15 KQVKKFRAQEKVLQKLGKAVETKDRFFQSQSNFYQQAEGHKLKYLKDLNFLSAVKVM 74
Db 526 EBEVEKE--EAEAEVEE-ABAEETEAEAAEE-----EEEAEG-----559
QY 75 HESSKRVSETQEIYSSENDGHE-----ELKAIWNNDLLWEDYEKLADQAVTMIYV 129
Db 560 EEEAEEAEGBEEAEAEVEEEAEAEKAAAEAEVEEEAEAESEEEAESEEEAESE-----EVE- 614
QY 130 AOFSEIKRIARKGRKLVYDSARHLEAVQNAKDE-----AKTAKAEFEFNKAQTVEF 184
Db 615 ---AETKEVEAEAEVEEEGEAAEEAEAE-EEAESEVTSKKAQTOAEVEEEAEAAEA 670
QY 185 DLNQBLEELPILYNRIGCVVTTFQNISLRNVDFYREMSKLNHLNLYEVMSKLQKQSHNK 244
Db 671 EAEEEAEE-----AGEEV-----BAESESEEDSK 698
QY 245 VTFVKGLSRRSRSLVTSPPVTRTAVTSPTSTPSSTLSLKSESESVATSLADPAAQ 304
Db 699 -----EADAEDEAEVEEYKEEVE-----KSDAEAEAA--EAEEEAAK 735
QY 305 GEDNS--BIKELLBEERIEKEG-----SEASSSE-----EDDPLPACNGPAQAQSPPTT 353
Db 736 SEEEAAAEAKDEAESEEAEEAEVEETEAEAEAEKASDDEKP--EEEVKESAEPAVE 793
QY 354 AKSQEVLVPSSTTSPGNGNSPSCQPSSEATEVVLTRTASEGSGQPKKRASIORTSAPP 413
Db 794 AKKAPEPKAAPKKAPKAPKVPSTPEDEPKAEVVEKKGAEPKAPKAPAAAKKEAPV 853
QY 414 SRPPPPRATAPRFSNGNISPSPTASGGGSFTSPRASLGTGTASPTLSLEVPSPPEPEK 473
Db 854 EXEHEEPE--ESPTEEPEKKPAA--AKPAKAPAKP-----PAFKAAEEKPEPAKPAQ 902
QY 474 PVRTPEAKENENIHNQNPPELCTSPILTMTSQVASEPGEAKKMEDEKONKLISADSSEGO 533
Db 903 AKPAFAAEEDDEKEDDEEE-----EEVEEVKPED--AKPVKSKAPAKAE 948
QY 534 DQLQVSMVPENNNLTAPEQSEVSTSEN 562
Db 949 DEFEKAQPPKPKGKAPKAPKEEDPKAEP 977

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RESULT 11
T30282
calcium-binding protein - sea urchin (Strongylocentrotus purpuratus)
C/Species: Strongylocentrotus purpuratus (purple urchin)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C/Accession: T30282
R/SoItzyk-Espanola, M.; Klinzing, D.C.; Pfarr, K.; Burke, R.D.; Ernst, S.G.
Dev. Biol. 165, 73-85, 1994
A/Title: Endo16, a large multidomain protein found on the surface and ECM of endodermal
A/Reference number: Z20805, MUID:94374583, PMID:8088452
A/Accession: T30282
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1560 <SO>
A/Cross-references: EMBL:L34680; NID:G511893; PID:G511894; PIDN:AAA30047.1
C/Genetics:
A/Note: endo16

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Query Match          7.5%; Score 213; DB 2; Length 1560;
Best Local Similarity 20.5%; Pred.No.0.086;
Matches 142; Conservative 91; Mismatches 268; Indels 192; Gaps 28;

QY 25 QBKVLKGLKAVETKDERFQGS-ASNFYQOQAGHKLYKDLKNFTLSAVKMHSSKKVSE 83
DB 824 QVKPLVEFFKELPS-DTRFDANHQEDICQAVDPQSLYADLENGLD---VELNQPSRIQT 879
QY 84 TLQEIYSSWGHEHLLKAIYWNDDLWWEY--EKLADQAVRTMIYVAQSFETKERIAK 141
DB 880 ELQEL-----QDLA---BELTEEEFQELQAEQNEEQLELLAEQEFQEAELIAE 927
QY 142 RGRKLVDYDSARHLEAVQNAKDEAKTAKABEEFNKAQTFEDLNQELLEELPILNSR 201
DB 928 QBEERLEILEQAQLAEQNOQNEEEEEEEEEEEEEEDRRRKERKATRRFRRTANKVR 987
QY 202 ICYVTIIFQNTISNL-----RDVFRMSKLNHLY-----E 232
DB 988 AAGRSIYE-VDSLVHCCQCNFVAEENSCTWFWQLLDEACAALPYLPDSSSATSTGLE 1046
QY 233 VMKLEKHQSNKNFVWKLSSRRRLVISPVRVATVSSPLT-----275
DB 1047 YASEL-AQADNNVLAPLPIFGGGRDIRTSKAVKISBSTVVSNYDENFRSCCALPGEA 1105
QY 276 -----STPSSTLSLKSSESYSAT-----EDLPDAAQGDNS 309
DB 1106 QUKCFQMYSNPAPSS-QMESGASNPSTIGVSEGYVSESGQFESRSESGEGEGDSE 1164
QY 310 ELK-----ELLE-----BEETKEGSEASSSEEDDPLPACNGPAQAQPS 348
DB 1165 ETEGAEEPHQWSESGDQSESGAQPOQVQVSESGQPESEEDVDSGETDGSDDMMPG 1224
QY 349 P-----TTTRAKSQEVLPSSTTSPGGLSP-----SQPPSSSTAEVVLVR 389
DB 1225 PGSSDGVPLGLTEVDQTSQDGE-----PEPEPGQGPQHPQWESGEQNESEEEVEE 1281
QY 390 TRTA--SQ-----SEQPKRASIQRTSAPPSPPPPPRATAPRPSGG-----430
DB 1282 POEVIESGQGSSESDPEFFGEPEPSEGEQPPQMESIIVQESGADVDGSGVTDGSD 1341
QY 431 -NIPSPSTAG-GGSP-----TSPRASL-GTGTPASPRTSLEVSPN 467
DB 1342 MNMPQGSDDAGVPLGLVEVNTSNQGESVQGESQDPQEQMEGEGGGSSEGE-----1397
QY 468 PPPPKPVRTPEAKENENIHONPELCTSPILMTSQVASBPFGAKKMKDEKDNKLISA 527
DB 1398 PEPEPGQGPQVQVSESGEENSEEEVZEP-----QGVNESEGGQSSSEPEFEGE--EP 1451
QY 528 DSESGQDQLQVSWVPENNNLTAPEQOEYVSTSE 560
DB 1452 ESEGEQPPQWSESGQE---PESEEDVDSGE 1481

```

RESULT 12

T43000
 RVS161 protein homolog - fission yeast (Schizosaccharomyces pombe) (fragment)
 C:Species: Schizosaccharomyces pombe
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
 C:Accession: T43000
 R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
 DNA Res. 4, 363-369, 1997
 A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
 A:Reference number: Z17323; MUID:98162722; PMID:9501991
 A:Accession: T43000
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-270 <VS>
 A:Cross-references: EMBL:D89200; NID:gl1749607; PIDN:BAAL3861.1; PID:gl1749608
 A:Experimental source: strain PR745
 C:Superfamily: RVS161 protein; RVS161 protein homology
 F:10-261/Domain: RVS161 protein homology <VS>

```

Query Match          7.4%; Score 212; DB 2; Length 270;
Best Local Similarity 27.5%; Pred. No. 0.012;
Matches 65; Conservative 42; Mismatches 111; Indels 18; Gaps 6;

QY      18 QKKFSRAQEKVLQKLGKAVETKDERFEQSASFYQQQAEGHKLYKDLKNFTLSAVKWHES 77
DB      13 KKA VNRAGTSVMNKTGHVETIVDREFETEERYRTMESAAKKLQKEAKGYLDLARMTAS 72
QY      78 SKSVSETIQEIY--SSEWDGHEELKAIWNNDLLWEDYEKLDAQAVTMEI-----YVA 130
DB      73 QTRIANTIDAFYGDGAGSXDGVSAYRVL-VKDLDADTVKE--LDGPFFTTVLDPISRFCS 129
QY      131 QFSEIKERIAKRGLVDYDSARHLE-AVNNAKDKDEAKTAKABEEFNKAOTVFEDLNQOE 189
DB      130 YFPDINAAITKENHKLHDHWAERAKVKQLVKPSNDITKLPRTEKEAAMAEKVETLNQ 189
QY      190 LLEELPIILNSRIGCVTFIFQNISNLRDVPFRMSKLNHNLYEVMSKLEKQHSHKV 245
DB      190 LVSELFPQIALRVPYLDPSFEALVKIQIRFCREG-----YEKMAQVQQYFDNSV 238

RESULT 13
SS5395
neurofilament protein M - rabbit (fragment)
C Species: Oryctolagus cuniculus (domestic rabbit)
C Date: 15-Jul-1995 #sequence_revision 01-sep-1995 #text_change 13-Aug-1999
C Accession: SS5395
R Vitadillo, M.; Vettore, S.; Lamar, E.; Chien, K.R.; Gorza, L.
submitted to the EMBL Data Library, January 1995
A Description: Neurofilament mRNA and protein are expressed in precursors of heart conduction system
A Reference number: SS5395
A Accession: SS5395
A Status: Preliminary
A Molecule type: mRNA
A Residues: 1-644 <VIT>
A Cross-references: EMBL:Z47378; NID:g854352; PIDN:CAA87454.1; PID:g85453
C Superfamily: cytoskeletal keratin

```

```

Query Match      7.4%; Score 212; DB 2; Length 644;
Best Local Similarity 20.9%; Pred.No. 0.033;
Matches 121; Conservative 84; Mismatches 244; Indels 130; Gaps 22;

Qy      62 KDLKNFLSAVKVMHSESKR-----VSETLQETYS-----SEWDGHEELKAIWNNDLL 109
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      25 EEVADLLAQIQASHITVERDYLTDISLSALKETIRSQLECHSDNMHQ-----AEW----- 76

Qy      110 WEDYEELKADQAVRTMBIYYVAQFSIEKRIAKGRKLVYDYSARHHLLEAVQNAKQDEAKT 169
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      77 FKCRYAKLTAAEQNKAEIRSAKEETAEYRRLQSKSIELESVAWHKESLERHVSVD--- 132

Qy      170 AKAEFEENKQATVFEDLNQLELLBELPILYNSRIGCVYTI FQNI SLNRDLVYREMSKLNNH 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      133 --LEERHNHDLSSQDITIQLLENL-----RGTKWEMARHURE---YQOL--LN-- 174

Qy      230 LYEVMSKLEQHSKNKVPVFKGLSSSRSLVIGPVVRTATVSSPLTSP-----TSPS--TLS 284
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      175 -----VKALDIEIAAARKLLEGETRFTFTSGSITGPILYTHRQPSVTIS 219

Qy      285 LKSESESVSA-----TEDLAPAAQCEDNSSEIKELL-----ESEEIEK 322
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      220 SKIQKTVEAPKLKVQHKFVEEIIETKVEDEKSEMEDALTAAELAVSVKEEKEEBA 279

Qy      323 EGSEASSSEDDPLPACNGPAQA-QBSPTTERAKSGOEVLPSTTSPGGLSPSGQPS 381
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      280 EGKEEQEAEEVAAAKKSPVKATTPEIKEEGEKEEGQEEBEEBEDEGVKSDQAEEG 339

Qy      382 SATFVLRT-----RTASEG-----SQPKKRASIQTSPAPSRPPPPRATASPRPS 428
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      340 SEKEGGSKEGEQEEGETAEGVEEAAKKEKTEKSEVAAKEEPTVEAKVGPEKA 399

Qy      429 SGNIIPSPPTASGGSPSTSPRASLTGTASPRPTSL-----VSNPPE-----PPEK 473
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      400 KSVPSKSPV-----EVYKPAEATAGKEQEEKEEVEEKKAAKESKREEKVEKKSEK 454

```

```

474  PVRTPEAKENITHNQNPFLC--TSPTLMTSVASEPGEAKQKQEDKEKONKUISADS-S 530
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
455  PKDVPKKAASPVREARAAEAATITPTKVLGLEKTKEGEKPLQQEKEKAGEEGSSBE 514
Qy      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
531  EGQDQ-----LOVSMVPENNLTAPPEQEVSTSE 560
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
515  EGSDDGSKRAKEDIAVNGEGEKEREETPEKSGRE 553

```

RESULT 14
T40661
Yeast reduced viability upon starvation protein 161 homolog, implicated in cell growth a
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C/Accession: T40661
R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, November 1998
A/Reference number: Z21889
A/Accession: T40661
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-264 <LYN>
A/Cross-references: EMBL:AL034352; PIDN:CAA22181.1; GSPDB:GN00067; SPDB:SPBC725.09C
A/Experimental source: strain 972h-; cosmid c725
C/Genetics:
A/Gene: SPDB.SPBC725.09C
A/Map position: 2
A/Introns: 16/3
C/Superfamily: RVS161 protein; RVS161 protein homology
F:4-255/Domain: RVS161 protein homology <RVS>

[illegible]

RESULT 15
T19431
hypothetical protein C25A1.10 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C/Accession: T19431
R:Mortimore, B.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19124
A/Accession: T19431
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-971 <WIL>
A/Cross-references: EMBL:Z81038; PIDN:CA802755.1; GSPDB:GN00019; CESP:C25A1.10
A/Experimental source: clone C25A1
C:Genetics:

A:Gene: CESP:C25A1.10
A:Map position: 1
A:Introns: 38/3; 92/3; 201/3; 919/3
C:Superfamily: nucleolus-cytoplasm shuttle phosphoprotein

```

Query Match 3 7.2%; Score 206; DB 2; Length 971;
Best Local Similarity 22.7%; Pred. No. 0.097;
Matches 80; Conservative 56; Mismatches 147; Indels 70; Gaps 10;

QY 244 KVFVVKGLSSRRSLVISPPVVRTATVSSPLTSPSTLSLKSESESVSATEDLAPDAA 303
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
211 KWVAKKAASSSDSDDEKKPAKPTPAK-----TPKPVVVKAESSSDSDDEKKPVAK 265
QY 304 QGEDNSEIKELLEEEIEKEGSEASSEDDEPLPACNGPAOQSPPTTERAKSOEE----- 359
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
266 PAPAKATPPAAKK-----ADSSSDSDDEAPAKTTPAKAAPKPVAKKAESSSDSD 318
QY 360 -----VLPSSSTTPSGGALSPSQGPS-----SATEWVLRTRTASEGS 397
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
319 EKKPAKPTPAKATPKPVAKKAESSSDSDDEKKPVAKPAKATPKPVAKKAESSSDSS 378
QY 398 EQPKKASIQRTSAPSPRPPTPRATASPRPSGNIIPSS-----PTASGGGSPTS 448
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
379 DDEK-----PAKFTPAKAT--PKPVAKKAESSSDSDDEKKPVAKPTSATKATPK 427
QY 449 ASLGTGTASPRTSLEVSNNPEPPKPVRTPEAKENENIHNONPEELCTSTPLMTSQVASE 508
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
428 PAKKADSSSDSDDEAPAKTTPAKAAPKPAKAESSSDSDDE-----KPAKST 479
QY 509 PGEAKKMDKKNKLIADSEGGQDLQVSMVPENNNTAPEPQEBVSTSEN 561
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
480 PA---KITPKTAKKVASSSDSDDEKKPAKPTPANAT--PKPVAKKAESSS 528

```

Search completed: March 4, 2004, 17:31:42
Job time : 28.865 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:21:39 ; Search time 14.3694 Seconds
(without alignments)
2043.754 Million cell updates/sec

Title: US-10-069-540A-2

Perfect score: 2855

Sequence: 1 MARGKAGGAGLFAKQVQKK.....NNLTAPPEQEVSTSENQQL 564

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	858	30.1	588	1	BIN1_RAT
2	851.5	29.8	593	1	BIN1_HUMAN
3	847	29.7	588	1	BIN1_MOUSE
4	815.5	28.6	683	1	AMPH_RAT
5	804.5	28.2	695	1	AMPH_HUMAN
6	802.5	28.1	682	1	AMPH_CHICK
7	238	8.3	466	1	HOBA_SCHPO
8	232	8.1	810	1	NFM_BOVIN
9	230.5	8.1	915	1	NFM_HUMAN
10	228.5	8.0	857	1	NFM_CHICK
11	212.5	7.4	2517	1	NCR2_HUMAN
12	212	7.4	644	1	NFM_RABIT
13	210	7.4	264	1	HOB3_SCHPO
14	208.5	7.3	1090	1	ASPI_HUMAN
15	204.5	7.2	1324	1	TPM4_HUMAN
16	204.5	7.2	1574	1	SYJ1_BOVIN
17	203	7.1	1367	1	AMPH_YEAST
18	201.5	7.1	1087	1	ASPI_MOUSE
19	200.5	7.0	2349	1	TPR_HUMAN
20	200.5	7.0	4377	1	ANK3_HUMAN
21	200	7.0	845	1	NFM_EAT
22	199.5	7.0	518	1	TPM4_DROME
23	199.5	7.0	622	1	3BP1_HUMAN
24	199	7.0	1026	1	NFM_HUMAN
25	198	6.9	1338	1	ACIN_MOUSE
26	197.5	6.9	6632	1	UN89_CAREL
27	197	6.9	1360	1	TNIK_HUMAN
28	194.5	6.8	705	1	TRDN_RABIT
29	194.5	6.8	2441	1	CBP_MOUSE
30	194	6.8	699	1	NP14_HUMAN
31	194	6.8	836	1	NOT3_YEAST
32	194	6.8	1575	1	SVJ1_HUMAN
33	194	6.8	3644	1	MINT_MOUSE

34 193.5 6.8 816 1 YG3A_YEAST
35 193.5 6.8 5085 1 PCLO_RAT
36 193 6.8 758 1 K179_HUMAN
37 191.5 6.7 1849 1 IGA4_HAEIN
38 191 6.7 1102 1 YG49_SCHPO
39 190.5 6.7 3664 1 MINT_HUMAN
40 190 6.7 1864 1 SLPI_CLOTH
41 189.5 6.6 848 1 NFM_MOUSE
42 187 6.5 700 1 TRDN_CANFA
43 187 6.5 1087 1 NFM_MOUSE
44 187 6.5 1248 1 DIA1_HUMAN
45 186.5 6.5 1694 1 IGA0_HAEIN

ALIGNMENTS

RESULT 1
BIN1_RAT STANDARD; PRT; 588 AA.
AC O08839;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Myc box dependent interacting protein 1 (Bridging integrator 1)
DB (Amphiphysin-like protein) (Amphiphysin II).
GN BIN1 OR AMPHL OR AMPH2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., SUBUNIT. AND ALTERNATIVE SPLICING.
RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex, and Kidney;
RX MEDLINE=9809145; PubMed=9348539;
RA Wigge P., Kohler K., Hunt S., Doyle C., McMahon H.T.;
RT "Amphiphysin heterodimers: potential role in clathrin-mediated endocytosis."
RL Mol. Biol. Cell 8:2003-2015(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM AMPH2-1).
RC STRAIN-Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=97424383; PubMed=9280305;
RA McMahon H.T., Wigge P., Smith C.;
RT "Clathrin interacts specifically with amphiphysin and is displaced by dynamin."
RL PNAS Lett. 413:319-322(1997).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 506-588, FUNCTION, AND INTERACTION WITH DNMI.
RX MEDLINE=98409533; PubMed=9736607;
RA Owen D.J., Wigge P., Vallis Y., Moore J.D.A., Evans P.R., McMahon H.T.;
RT "Crystal structure of the amphiphysin-2 SH3 domain and its role in the prevention of dynamin ring formation."
RL EMBO J. 17:5273-5285(1998).
CC -!- FUNCTION: May be involved in regulation of synaptic vesicle endocytosis. May act as a tumor suppressor and inhibits malignant cell transformation.
CC -!- SUBUNIT: Heterodimer with AMPH. Binds SH3GLB1 (By similarity). Binds to SYN1 and DNMI through its SH3 domain, and to clathrin through a region outside of the SH3 domain. Also binds to alpha-adaptin. Interacts with the N-terminal transactivation domain of MYC in a manner requiring the integrity of the conserved MYC box regions 1 and 2.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Name=AMPH2-1;
CC IsoId=O08839-1; Sequence=Displayed;
CC Name=AMPH2-2;
CC IsoId=O08839-2; Sequence=VSP_000260;
CC Name=AMPH2-3;

CC IsoId=O08839-3; Sequence=VSP_000258;
 CC Name=AMP2-4;
 CC IsoId=O08839-4; Sequence=VSP_000256, VSP_000257;
 CC Name=AMP2-5;
 CC IsoId=O08839-5; Sequence=VSP_000259;
 CC Name=AMP2-6;
 CC IsoId=O08839-6; Sequence=VSP_000256, VSP_000259;
 CC -!- TISSUE SPECIFICITY: Isoform AMP2-1 is expressed in brain,
 CC concentrated at nerve terminals. Isoform AMP2-2 is widely
 CC expressed.
 CC -!- PTM: Phosphorylated by protein kinase C.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC -----
 CC EMBL; Y13380; CAA73807.1; -;
 CC FDS; 1BB9; 17-JUN-98.
 CC InterPro; IPR003005; Amphiphysin.
 CC InterPro; IPR006632; BAR.
 CC InterPro; IPR004148; BAR dom.
 CC InterPro; IPR001452; SH3.
 CC Pfam; PF03114; BAR; 1.
 CC Pfam; PF00018; SH3; 1.
 CC PRINTS; PR01251; AMPHIPHYSIN.
 CC PRINTS; PR00452; SH3DOMAIN.
 CC ProDom; PD000066; SH3; 1.
 CC SMART; SM00721; BAR; 1.
 CC SMART; SM00326; SH3; 1.
 CC PROSITE; PS50002; SH3; 1.
 CC KW Alternative splicing; SH3 domain; Coiled coil; Endocytosis;
 CC KW Anti-oncogene; Differentiation; Phosphorylation; 3D-structure.
 CC FT DOMAIN 15 42
 CC FT COILED COIL (POTENTIAL).
 CC FT DOMAIN 193 274
 CC FT COILED COIL (POTENTIAL).
 CC FT DOMAIN 379 422
 CC FT CLATHRIN-BINDING (BY SIMILARITY).
 CC FT DOMAIN 515 588
 CC FT SH3.
 CC FT VARSPLIC 173 205
 CC Missing (in isoform AMP2-4 and isoform
 CC AMP2-6).
 CC /FTId=VSP_000256.
 CC FT VARSPLIC 253 588
 CC Missing (in isoform AMP2-4).
 CC /FTId=VSP_000257.
 CC FT VARSPLIC 335 588
 CC Missing (in isoform AMP2-3).
 CC /FTId=VSP_000258.
 CC FT VARSPLIC 335 482
 CC Missing (in isoform AMP2-5 and isoform
 CC AMP2-6).
 CC /FTId=VSP_000259.
 CC FT VARSPLIC 423 460
 CC Missing (in isoform AMP2-2).
 CC /FTId=VSP_000260.
 CC SQ SEQUENCE 588 AA; 64533 MW; 164AC90E09547F1A CRC64;
 CC
 CC Query Match 30.1%; Score 958; DB 1; Length 588;
 CC Best Local Similarity 37.9%; Pred. No. 1.6e-26;
 CC Matches 230; Conservative 76; Mismatches 179; Indels 122; Gaps 20;
 CC
 CC QY 1 MAE-GKAGAGLFAKQVQKFSRAQEKVLQKAVETKDERPEQASNFYQQAEGHK 59
 CC |||||
 CC 1 MAEWSGKVTAGKIASNVQKQLTRAQKVLQKGADETKDEQEQCVQNFNQLTEGTR 60
 CC |||||
 CC QY 60 LYKDLNFKLSAVKWHESKRVSETLQBIYSSEWDGHEELKAIYWNDDLLWDEYKLD 119
 CC |||||
 CC 61 LQKDLRTYLASVKANHEASKKLSECLQBYEPFPGDEANKIAENNDDLLWMDYHOKLVD 120
 CC |||||
 CC QY 120 QAVRWETIYVAFSEIKRIARGRKLVYDSARHLEAVONA-KDEAKTAK----- 171
 CC |||||
 CC 121 QALLTWYLVGQFPDIKRIARGRKLVYDSARHYESLQTAKKDEAKIAPVSLLEK 180
 CC |||||
 CC QY 172 -----ABEEFNKAQTVFEDNLQELLEELPILYNSRIGCYVT 207

Db 181 AAPWCQCKLQAHVLAQTNLLRNQAEELIKAKVFEMVNDLQELPSLWNSRVGFYVN 240
 |||||
 QY 208 IFQINISLRDVFYREMSKLNHLYEYMSKLEKQHSNKVFVKGLSSSS---RRSLVISP 264
 |||||
 Db 241 TFQSIAGLEENFKEMSKLNQNLNDVLSLEKQHSNTFTVKAQPSDSAPEKGNKSPSP 300
 |||||
 QY 265 VRTATVSSPLTSPSTLSLSESVSATEDLADPAQAGDENSEI----- 311
 |||||
 Db 301 -----PDGSPAATFEIRVNHEPEPAGS---SPGATIPKSPQLRKGPVPPPPKHT 349
 |||||
 QY 312 --KELLEEE-----EIEKEG---SEASSEED-DPLPACNGPAQAQ 346
 |||||
 Db 350 PSKEMKQELSLFDADFVEISVTTSPQFEAPGPPSEQASLLDLEPLPPVASEVKA- 408
 |||||
 QY 347 PSPITERAKQEEVLP---SSITPPSGGALSQSGQPSSS--ATEVVLRTIRASEGSEOPK 401
 |||||
 Db 409 PTPSGQS-----IPMDWEPTESQAGVL-PSGEPSSAEGSFVAVPQTAEPGAPQA 460
 |||||
 QY 402 KRASIQTSTAPPSPRPPPRATASPRPSGNIPSSPTASGG--GSPTSPRASLTGC----- 454
 |||||
 Db 461 EASEVVGTOEPGETAASEATSSSLPAVVVFETFSATVNGAVEGTTTGRLLDLPFGFMFKV 520
 |||||
 QY 455 -----TASPTSTLEVPSPPEPEKPVRTPEAKE-----NENHNQNP-ELCTS--P 498
 |||||
 Db 521 QAQHDYATDTDELQKAGDWLVIPFQNPESQDEGLMGVKESDWNOHKELEKRCRVFP 580
 |||||
 QY 499 TLMTSQV 505
 |||||
 Db 581 ENFTERV 587
 |||||
 RESULT 2
 BIN1 HUMAN
 ID BIN1 HUMAN STANDARD; PRT; 593 AA.
 AC Q00459; Q00459; Q43867; Q60552; Q60553; Q60554; Q60555;
 AC Q75514; Q75515; Q75516; Q75517; Q75518; Q92944; Q93688;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Myc box dependent interacting protein 1 (Bridging integrator 1)
 DE (Amphiphysin-like protein) (Amphiphysin II) (Box-dependent myc-
 DE interacting protein-1).
 GN BIN1 OR AMPHL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM IIA).
 RC TISSUE=Brain;
 RX MEDLINE=97341217; PubMed=9195986;
 RA Ramjaun A.R., Micheva K.D., Bouchelet I., McPherson P.S.;
 RT "Identification and characterization of a nerve terminal-enriched
 RT amphiphysin isoform."
 RL J. Biol. Chem. 272:16700-16706(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM IIA AND BIN1).
 RC TISSUE=Brain, and Skeletal muscle;
 RX MEDLINE=97327761; PubMed=9182667;
 RA Butler M.H., David C., Ochoa G.-C., Freyberg Z., Daniell L., Grabs D.,
 RA Cremona O., De Camilli P.;
 RT "Amphiphysin II (SH3P9; BIN1), a member of the amphiphysin/Rvs family,
 RT is concentrated in the cortical cytomatrix of axon initial segments
 RT and nodes of Ranvier in brain and around T tubules in skeletal
 RT muscle."
 RL J. Cell Biol. 137:1355-1367(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM BIN1).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=96376973; PubMed=8782822;
 RA Sakamuro D., Elliott K.J., Wechsler-Reya R., Prendergast G.C.;
 RT "BIN1 is a novel Myc-interacting protein with features of a tumour

RT suppressor.";
RL Nat. Genet. 14:69-76(1996).
RN [4]
RP REVISIONS TO N-TERMINUS.
RA Sakamuro D., Elliott K.J., Wechsler-Reya R., Prendergast G.C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS IIB, IIC1, IIC2 AND IID).
RC TISSUE=Brain;
RX MEDLINE=98264340; PubMed=9603201;
RA Ramjaun A.R., McPherson P.S.;
RT "Multiple amphipysin II splice variants display differential clathrin
RT binding; identification of two distinct clathrin-binding sites.";
RL J. Neurochem. 70:2369-2376(1998).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS IIC2 AND IIC3).
RC TISSUE=Brain;
RX MEDLINE=97366618; PubMed=9223448;
RA Tautsui K., Maeda Y., Tautsui K., Seki S., Tokunaga A.;
RT "cDNA cloning of a novel amphipysin isoform and tissue-specific
RT expression of its multiple splice variants.";
RL Biochem. Biophys. Res. Commun. 236:178-183(1997).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS IIC3, IIC4, BIN1-10-13, BIN1-13 AND
RP BIN1-12A).
RC TISSUE=Fibroblast;
RX MEDLINE=98058932; PubMed=9395479;
RA Wechsler-Reya R.J., Sakamuro D., Zhang J., Duhadaway J.,
RA Prendergast G.C.;
RT "Structural analysis of the human BIN1 gene. Evidence for tissue-
RT specific transcriptional regulation and alternate RNA splicing.";
RL J. Biol. Chem. 272:31453-31458(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM IIC2).
RA Zhang J., Du W., Wechsler-Reya R.J., Duhadaway J., Sakamuro D.,
RA Prendergast G.C.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 133-593 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98078712; PubMed=9418903;
RA Wechsler-Reya R.J., Elliott K.J., Prendergast G.C.;
RT "A role for the putative tumor suppressor Bin1 in muscle cell
RT differentiation.";
RL Mol. Cell. Biol. 18:566-575(1998).
CC -!- FUNCTION: May be involved in regulation of synaptic vesicle
CC endocytosis. May act as a tumor suppressor and inhibits
CC malignant cell transformation.
CC -!- SUBUNIT: Heterodimer with AMPH. Binds SH3GLB1 (By similarity).
CC Binds to SYN1 and DNMI through its SH3 domain, and to clathrin
CC through a region outside of the SH3 domain. Also binds to alpha-
CC adaptin. Interacts with the N-terminal transactivation domain of
CC MYC in a manner requiring the integrity of the conserved MYC box
CC regions 1 and 2.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Isoform Iia is
CC found in the cytoplasm while isoform BIN1 is nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=11;
CC Comment=Additional isoforms seem to exist;
CC Name=IIA;
CC IsoId=000499-1; Sequence=Displayed;
CC Name=IIB;
CC IsoId=000499-2; Sequence=VSP_000246, VSP_000252;
CC Name=IIC1;
CC IsoId=000499-3; Sequence=VSP_000249;
CC Name=IIC2;
CC IsoId=000499-4; Sequence=VSP_000246, VSP_000249;
CC Name=IID;
CC IsoId=000499-5; Sequence=VSP_000248;
CC Name=IIE;
CC IsoId=000499-6; Sequence=VSP_000246, VSP_000253;
CC Name=IIF;
CC IsoId=000499-7; Sequence=VSP_000246, VSP_000250;
CC Name=BIN1;
CC IsoId=000499-8; Sequence=VSP_000246, VSP_000247, VSP_000250;
CC Name=BIN1-10-13;
CC IsoId=000499-9; Sequence=VSP_000246, VSP_000251;
CC Name=BIN1-13;
CC IsoId=000499-10; Sequence=VSP_000246, VSP_000247, VSP_000251;
CC Name=BIN1-12A;
CC IsoId=000499-11; Sequence=VSP_000246, VSP_000247, VSP_000253;
CC -!- TISSUE SPECIFICITY: ISOFORM IIA IS EXPRESSED ONLY IN THE BRAIN
CC WHERE IT IS CONCENTRATED IN AXON INITIAL SEGMENTS AND NODES OF
CC RANVIER. ISOFORM BIN1 IS WIDELY EXPRESSED WITH HIGHEST EXPRESSION
CC IN SKELETAL MUSCLE.
CC -!- PTM: Phosphorylated by protein kinase C (By similarity).
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF004015; AAC51345.1; -
CC DR EMBL; AF070576; AAC28646.1; -
CC DR EMBL; U68485; AAC17461.1; -
CC DR EMBL; AF001383; AAB51363.1; -
CC DR EMBL; AF043898; AAC39210.1; -
CC DR EMBL; AF043899; AAC39711.1; -
CC DR EMBL; AF043900; AAC39712.1; -
CC DR EMBL; AF043901; AAC39713.1; -
CC DR EMBL; U87558; AAB63263.1; -
CC DR EMBL; AF068914; AAC24126.1; -
CC DR EMBL; AF068915; AAC24127.1; -
CC DR EMBL; AF068916; AAC24128.1; -
CC DR EMBL; AF068917; AAC23750.1; -
CC DR EMBL; AF068918; AAC23751.1; -
CC DR EMBL; U84004; AAC23440.1; -
CC DR EMBL; U83999; AAC23440.1; JOINED.
CC DR EMBL; U84001; AAC23440.1; JOINED.
CC DR EMBL; U84002; AAC23440.1; JOINED.
CC DR EMBL; U84003; AAC23440.1; JOINED.
CC DR EMBL; U84004; AAC23441.1; ALT_INIT.
CC DR EMBL; U83999; AAC23441.1; JOINED.
CC DR EMBL; U84001; AAC23441.1; JOINED.
CC DR EMBL; U84002; AAC23441.1; JOINED.
CC DR EMBL; U84003; AAC23441.1; JOINED.
CC PIR; JC5593; JCS593.
CC TRANSFAC; T03490; -
CC Genew; HGNC:1052; BIN1.
CC MIN; 601248; -
CC GO; GO:0015629; C:actin cytoskeleton; TAS.
CC GO; GO:0008283; P:cell proliferation; TAS.
CC GO; GO:0006899; P:nonspecific vesicle transport; TAS.
CC GO; GO:0000074; P:regulation of cell cycle; TAS.
CC InterPro; IPR003005; Amphiphysin.
CC InterPro; IPR004148; BAR_dom.
CC InterPro; IPR001452; SH3.
CC Pfam; PF03114; BAR; 1.
CC Pfam; PF00018; SH3; 1.
CC PRINTS; PR01251; AMPHIPHYSIN.
CC PRINTS; PR00452; SH3DOMAIN.
CC PRODOM; PD000066; SH3; 1.
CC PROSITE; PSS0002; SH3; 1.
CC KW Alternative splicing; SH3 domain; Coiled coil; Endocytosis;
CC Anti-oncogene; Differentiation; Phosphorylation.
CC DOMAIN 15 42 COILED COIL (POTENTIAL).
FT

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FT DOMAIN 193 267 COILED COIL (POTENTIAL).
FT DOMAIN 378 421 CLATHRIN-BINDING.
FT DOMAIN 520 592 SH3.
FT VARSPLIC 174 204 Missing (in isoform IIB, isoform IIC2,
FT I12, isoform I13, isoform BIN1,
FT I14, isoform BIN1+12A, isoform BIN1-10-13 and
FT I15, isoform BIN1-13).
FT I16 VSP 000246.
FT I17 P -> PRKSLRLRKN (in isoform BIN1,
FT I18 isoform BIN1+12A and isoform BIN1-13).
FT I19 /FTID=VSP 000247.
FT I20 VARSPLIC 335 377 Missing (in isoform IID).
FT I21 /FTID=VSP 000248.
FT I22 VARSPLIC 335 421 Missing (in isoform IIC1 and isoform
FT I23 IIC2).

Query Match 29.8%; Score 851.5; DB 1; Length 593;
Best Local Similarity 36.6%; Pred. No. 2.9e-26;
Matches 224; Conservative 82; Mismatches 179; Indels 127; Gaps 20;

QY 1 MAE-GRAGGAAGLFAKQVOKFSAQKVLQKGLAVETKDEPQASNFYQQAEGHK 59
DB 1 MAEMSGKVTAGKIASNVQKLTQAEKVLQKGLADETQDEQEQCVQNFQKLTGTR 60
QY 60 LYKDLKFLSAVKVWHSESKRVSETLQEIYSEWDGHEELKAIYVNDLLWEDYEKLD 119
DB 61 LQKDLRTYLASVKAMHEASKLNECLQEVYEPDWPGRDEANKIAENNDLLWMDYHQKLD 120
QY 120 QAVRTWEIIVAOFSRIKARIGKGLVDYDSARHLEAVQNA-KDEAKTAK----- 171
DB 121 QALLTMDTGLQFPDKSRIARGRKLVYDSARHHESTAKKDEAKIAPVSLLEK 180
QY 172 -----AEEFNKAQTVFEDLNQELLEELPILYNSRIGCYVT 207
DB 181 AAPQWCGKLAHLVAQTLNLRNQAEELIKAQKVFEMVDLQELPSLWNSRVGFYN 240
QY 208 IFQNTSLNLDVYRMSKLNHLYVMSKLEKQHSNKVYVYKGLSSSRSLVISPVRT 267
DB 241 TFOSTAGLENFHKMSKLNQNLNDVLVGLKQKHSNTFTVKAQPSDN-----APAKGN 294
QY 268 ATVSSPLTSPSTLSLKSESVSATDLAPAAQGEDNSEI-----X 312
DB 295 KSPSPDGPSPATPEIRVNHPEPAGGA---TPGATLPKPSQLRKGPPVPPPKHTPSK 351
QY 313 ELLEER-----EIEKEG---SEASSSEED-DPLPACNGPAQAQPS 349
DB 352 EVKQEQILSLFEDTFVPEISVTPSQEAPGFSEQASLLDLPDPLPVTSPVKA-PTP 410
QY 350 TTERAKSQEVLVLP---SSTPSPGALSPSGOPSS--ATEVILRTTASEGSRPKRA 404
DB 411 SCGS-----IPWDLWEPTSPAGSL-PSGEPSAEGTFVSPWSTAGPQAQPAAS 462
QY 405 SIQRTSAPSPRPPTATASPRSPGNIPS-----SPTASGGSPSTSPRASLGTC 454
DB 463 EVAGGTQPAAGAQEPQETAAEASSSLPLAVVETFPATVNGTVEGSG--AGRLDLP 520
QY 455 -----TASRPTSLVSPNPEPEKVPVPRAKE-----NENTINQNP-ELC 495
DB 521 FFKVQAQHDYATDTDELQKAGVNLVLPQNPQEQDEGLWGVKESDNNQKLEK 580
QY 496 TS--PTLMTSQV 505
DB 581 RGVFPENFTEV 592

RESULT 3
BIN1 MOUSE
AC O08539; Q62434; STANDARD; PRT; 588 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Myc box dependent interacting protein 1 (Bridging integrator 1)

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DE (Amphiphysin-like protein) (Amphiphysin II) (SH3-domain containing
DE protein 9).
GN BIN1 OR AMPHL OR SH3P9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=97326078; PubMed=9182529;
RA Lepreince C., Romero F., Cussac D., Vayssiere B., Berger R.,
RA Tavitian A., Camonis J.H.;
RT "A new member of the amphiphysin family connecting endocytosis and
RT signal transduction pathways.";
RL J. Biol. Chem. 272:15101-15105(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Embryo;
RX MEDLINE=98294438; PubMed=9630982;
RA Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;
RT "Cloning of ligand targets: systematic isolation of SH3 domain-
RT containing proteins.";
RL Nat. Biotechnol. 14:741-744(1996).
RN [3]
RP INTERACTION WITH SH3GLE1.
RX MEDLINE=22450649; PubMed=12456676;
RA Modregger J., Schmidt A.A., Ritter B., Huttner W.B., Plomann M.;
RT "Characterization of endophilin B1b, a brain-specific
RT membrane-associated lysophosphatidic acid acyl transferase with
RT properties distinct from endophilin A1.";
RL J. Biol. Chem. 278:4160-4167(2003).
CC -!- FUNCTION: May be involved in regulation of synaptic vesicle
CC endocytosis. May act as a tumor suppressor and inhibits
CC malignant cell transformation.
CC -!- SUBUNIT: Heterodimer with AMPH (By similarity). Binds to SYN1 and
CC DNMI through its SH3 domain, and to clathrin through a region
CC outside of the SH3 domain. Also binds to alpha-adaptin. Interacts
CC with the N-terminal transactivation domain of MYC in a manner
CC requiring the integrity of the conserved MYC box regions 1 and 2.
CC Binds SH3GLE1.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=BRAMP2;
CC IsoId=O08539-1; Sequence=Displayed;
CC Name=2; Synonyms=SH3P9;
CC IsoId=O08539-2; Sequence=VSP_000254, VSP_000255;
CC -!- TISSUE SPECIFICITY: Isoform 1 is expressed mainly in the
CC brain. Isoform 2 is widely expressed.
CC -!- PTM: Phosphorylated by protein kinase C (By similarity).
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC -----
CC EMBL; U66405; AAC53318.1; --
CC EMBL; U60884; AAC52661.1; --
CC MGD; MGI:108092; Bini.
CC InterPro; IPR003005; Amphiphysin.
CC InterPro; IPR006632; BAR.
CC InterPro; IPR004148; BAR dom.
CC InterPro; IPR001452; SH3.
CC Pfam; PF03114; BAR; 1.
CC Pfam; PF00016; SH3; 1.
CC PRINTS; PR01251; AMPHIPHYSIN.
CC PRINTS; PR00452; SH3DOMAIN.

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GN  AMPH OR AMPH1.
OS  Rattus norvegicus (Rat).
OS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OS  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RX  MEDLINE=98009145; PubMed=9348539;
RA  Wigge P., Kohler K., Vallis Y., Owen D., Hunt S.P., McMahon H.T.;
RT  Amphipysin heterodimers: potential role in clathrin-mediated
RT  endocytosis";
RL  Mol. Biol. Cell 8:2003-2015(1997).
CC  -1- FUNCTION: May participate in mechanisms of regulated exocytosis in
CC  synapses and certain endocrine cell types. May control the
CC  properties of the membrane associated cytoskeleton (By
CC  similarity).
CC  -1- SUBUNIT: Heterodimer with BIN1. Binds SH3GLB1 (By similarity).
CC  -1- SUBCELLULAR LOCATION: Peripheral membrane protein associated with
CC  the cytoplasmic surface of synaptic vesicles (By similarity).
CC  -1- SIMILARITY: Contains 1 BAR domain.
CC  -1- SIMILARITY: Contains 1 SH3 domain.
CC  -----
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CC  -----
DR  ENBL; Y13381; CAA73808.1; --
DR  InterPro; IPR003005; Amphipysin.
DR  InterPro; IPR003017; Amphipysin_1.
DR  InterPro; IPR006632; BAR.
DR  InterPro; IPR004148; BAR_dom.
DR  InterPro; IPR001452; SH3.
DR  Pfam; PFO3114; BAR; 1.
DR  Pfam; PFO0018; SH3; 1.
DR  PRINTS; PR01251; AMPHIPHYSIN.
DR  PRINTS; PR00452; SH3DOMAIN.
DR  ProDom; PD003208; Amphipysin_1; 1.
DR  ProDom; PD000066; SH3; 1.
DR  SMART; SM00721; BAR; 1.
DR  SMART; SM00326; SH3; 1.
DR  PROSITE; PS50002; SH3; 1.
KW  Cytoskeleton; SH3 domain; Coiled coil.
FT  DOMAIN 10 83 COILED COIL (POTENTIAL).
FT  DOMAIN 144 191 COILED COIL (POTENTIAL).
FT  DOMAIN 610 683 SH3.
SQ  SEQUENCE 683 AA; 74877 MW; 7FEA4A9E5A1F6631 CRC64;
Query Match 28.6%; Score 815.5; DB 1; Length 683;
Best Local Similarity 33.9%; Pred.No.8e-25;
Matches 224; Conservative 101; Mismatches 182; Indels 153; Gaps 23;
QY 11 GLPAKQVQKFSRAQEKVLQKLGKAVETKDEDFEFSANFYQQQAEHGKLYKDLKNFLSA 70
DB 7 GIPKVVQKRLNRAQEKVLQKLGKADETKDEQFEYVQNFKQEAEGTRLOEELRGYLA 66
QY 71 VKVHSSRSRVSETLOEIIYSSSWDGHGHEELKAIVWNDLLWDEYSEKLADQAVRTMEIYVA 130
DB 67 IKMQASAKMLTESLHEVYEPDYGREDYKMGXGKCDVLWEDFHQKLVDSLLTLDYIG 126
QY 131 QFSEIKERIAKGRKLVYDSARHLEAVQNAK-KDEAKTAAKEEFNKAQVVFEDLNOE 189
DB 127 QPPDIKNRIAKSRKLVYDSARHLEALQSSKRDSEISIAKEEFQAKQVFEFNVD 186
QY 190 LLEELPILYNSIGCVTITFQNISLNRDVVFYEMSKLNHLNLYVMSKLEKQHSNKVFFVK 249
DB 187 LOBELPSLSRRVGFVYNTFKNVSSLEAKFHKEIAVLCHKLYEVMTKLDQHADKAFSIQ 246
QY 250 GLSSSS--RRSIVTSPPVETATVSDPLTSS-----ETSPSTVSIKSPSES----- 291

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Db 247 GAPSGLRKTAKTSPPEASPIPSPTASPNHTLAPASAPVRPSQTRKGPVPL 306
QY 292 --VSATEDLADAQ--EDN-----SEIKELLEEEIEKGSBASSEEDDL-----PA 338
Db 307 PKVPTKLEQENIINFEDFVPEINVTTPSQNEVLEVKETLLDLDFPFKPDVTPA 366
QY 339 CNGPAAQPSPTTERAKSQBEVLP-----SST---TPSPGALSPSQBSSSA----- 383
Db 367 --GSAATHSP-----MSOTLPDWLWTTSTDLVQPASGSGFNDFTQPDOTSLFTMQYD 417
QY 384 -----TEVLTTRTASE-----GSEQPKKRASIQRTSAPSRPP----- 417
Db 418 QNMAETEALPTEPQAEPPPTAAAPTAGLDLGLMEEPKEEAAI-----PPTDAGETV 472
QY 418 -----PPRATSPRSGNIPSSPTASGGSGFTSPRASLTGTAS----- 457
Db 473 GTEGSGTEAEAEKAAALPAGESGEPGAKIDVETELAS---SESQAAELEAGAPQEKV 529
QY 458 --PRTSLEVPNPEPEKEVPT--PEAKE-NENIHQNP-----BELCTSPMTLSQVAS-- 507
Db 530 IPSVVIENASNEGEHEQETTTGTETREATEDVAPQGPAGEKDELATEPTPLDSQAATPA 589
QY 508 -----EPGAKKME---DKEKDK-----LISADSSEGD 534
Db 590 PAGAVDASLSAGDAQAELPPGGLYKVELTHDFEAANSDELTLQRGDVVLVWPSSEADQD 649

RESULT 5
AMPH HUMAN
ID AMPH HUMAN STANDARD; PRT; 695 AA.
AC P49418; O43538;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amphiphysin.
GN AMPH OR AMPHL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Cerebellum;
RX MEDLINE=94357284; PubMed=8076697;
RA David C., Solimena X., de Camilli P.;
RT "Autoimmunity in stiff-man syndrome with breast cancer is targeted to
RT the C-terminal region of human amphiphysin, a protein similar to the
RT yeast proteins, Rvs167 and Rvs161."
RL FEBS Lett. 351:73-79(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=95276740; PubMed=7757077;
RA Yamamoto R., Li X., Winter S., Francke U., Kilian M.W.;
RT "Primary structure of human amphiphysin, the dominant autoantigen of
RT paraneoplastic stiff-man syndrome, and mapping of its gene (AMPH) to
RT chromosome 7p13-p14."
RL Hum. Mol. Genet. 4:265-268(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Breast;
RX MEDLINE=98174372; PubMed=9513187;
RA Floyd S.R., Butler M.H., Cremona O., David C., Freyberg Z., Zhang X.,
RA Solimena M., Tokunaga A., Ishizu K., Tsutsui K., De Camilli P.V.;
RT "Expression of amphiphysin I, an autoantigen of paraneoplastic
RT neurological syndromes, in breast cancer."
RL Mol. Med. 4:29-39(1998).
CC -!- FUNCTION: May participate in mechanisms of regulated exocytosis in
CC synapses and certain endocrine cell types. May control the
CC properties of the membrane associated cytoskeleton.
CC -!- SUBUNIT: Heterodimer of AMPH and AMPHL (By similarity).
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC SURFACE OF

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CC SYNAPTIC VESICLES.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=128 kDa;
CC IsoId=P49418-1; Sequence=Displayed;
CC Name=2; Synonyms=108 kDa;
CC IsoId=P49418-2; Sequence=VSP_000245;
CC TISSUE SPECIFICITY: Neurons, certain endocrine cell types and
CC spermatocytes.
CC -!- DISEASE: Patients with stiff-man syndrome, a rare disease of the
CC central nervous system characterized by progressive rigidity of
CC the body musculature with superimposed painful spasms, have
CC antibodies against AMPH.
CC -!- SIMILARITY: Contains 1 BAR domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
CC EMBL; U07616; AAA21865.1; -.
CC EMBL; X81438; CAA57197.1; -.
CC EMBL; AF034996; AAC02977.1; -.
CC PIR; S62400; S62400.
CC PDB; 1KV7; 12-JUN-02.
CC Genew; HGNC:471; AMPH.
CC MIM; 600418; -.
CC GO; GO:0015629; C:actin cytoskeleton; TAS.
CC GO; GO:0008021; C:synaptic vesicle; TAS.
CC GO; GO:0006897; P:endocytosis; TAS.
CC GO; GO:0007268; P:synaptic transmission; TAS.
CC InterPro; IPR003005; Amphiphysin.
CC InterPro; IPR003017; Amphiphysin_1.
CC InterPro; IPR006632; BAR.
CC InterPro; IPR004148; BAR_dom.
CC InterPro; IPR001452; SH3.
CC Pfam; PF01114; BAR; 1.
CC Pfam; PF00018; SH3; 1.
CC PRINTS; PR01251; AMPHIPHYSIN.
CC PRINTS; PR00452; SH3DOMAIN.
CC ProDom; PD003208; Amphiphysin_1; 1.
CC ProDom; PD000066; SH3; 1.
CC SMART; SM00721; BAR; 1.
CC SMART; SM00326; SH3; 1.
CC PROSITE; PS00002; SH3; 1.
CC Cytoskeleton; SH3 domain; Coiled coil; Alternative splicing;
CC 3D-structure.
FT DOMAIN 10 83 COILED COIL (POTENTIAL).
FT DOMAIN 144 191 COILED COIL (POTENTIAL).
FT DOMAIN 622 695 SH3.
FT VASPLIC 425 466 Missing (in isoform 2).
FT /FTId=VSP_000245.
FT SEQUENCE 695 AA; 76256 MW; 7884F75AB75BA357 CRC64;
QY 11 GLFAKQVQKFSRAQEKVLQKGLKAVETKDEPESASNFYQQAEGHKLKLNFLSA 70
Db 7 GIFAPNKKQLNKAQEKVLQKGLKAVETKDEPESASNFYQQAEGHKLKLNFLSA 66
QY 71 KVVMHSSKRVSETLQIYSSSEWDGHEELKALVWNNDLWEDYERKLADQAVRTMEIYVA 130
Db 67 IKGQEAEMKLTESLHEVTEPDWYGEDEVKVGKCDVLWEDFHQKLVDSLLTLDYLG 126
QY 131 QFSIKERIKAROKLVVDSDAPHHLEAVQNAK-KDEAKTAAEEFNKAQTVFEDLNQE 189
Db 127 QFPDKNIKRIKRLVDYDSAPHHLEALQSKKRKDESRISKABEEFQKACKVFEFNVD 186

Query Match 28.2%; Score 804.5; DB 1; Length 695;
Best Local Similarity 34.3%; Pred. No. 2.1e-24;
Matches 206; Conservative 104; Mismatches 175; Indels 115; Gaps 18;

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190 LLEELPILYNSRIGCVVTFIOMISNLRDVFYREMSKLNHNLYEVMKLEKOHNSKVFVWK 249
 187 LOELPSLSRRVGVVTFVKNVSSLEAKFHEIAVLCHKLYEVMKLGDDHAKATIIQ 246
 250 GLSSSS---RRSLVISPVRVTVTSPLTS-----PTSPSTLSLKSESVSATEDLAP 300
 247 GAPSDSGPLRIAKTSPSPPEPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 297
 301 DAAQGDSEIIEKELLEEEIEKEGSEASSEEDDPLP-ACNGPAQAQPSPTTERAKSQE 358
 298 ---RKGPVPVPLKAVYTKELQOE---NIISFFDNFVPEISVTTFSQNE---VPEVKKEE 349
 359 EVL-----PSSTPPSGGALSPSGOPSS-----SATEVLRTRTASEGS---EQP 400
 350 TLLDLDFDPKPEVTPAGSAGVTHSPMSQTLFWDLWTSTDLV---QPASGSGFNGFTQP 406
 401 KKRASI-----QRTSAPSPSPPPPRATASPRPSGNIPSPSPPTASGSGSPTSP 447
 407 QUTSLFTMTQDOSMICNLAEISQAPPTPEKAEELAAVTPAVG-----449
 448 RASLGTGTASPRTSLEVPSPPEKPVRTPEAKENENHNQNPPEELCTSPTLMTSQVAS 507
 450 -LDLGMDTTRA-----EPPVEEAVIIPGADADAAGV-----LVSAEG 486
 508 EPG---EAKOM-----EDKEKNKLISDSSEGGQDQLOVMSVPPNNNLTAPPEOEVST 559
 487 APGEAEAEKATVPAGEVSGVSEAKIGTETGAESAQ-----PEAELEATVPOEKVIPS 542

RESULT 6
 AMPH CHICK
 ID AMPH CHICK STANDARD; PRT; 682 AA.
 AC 250478;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amphiphysin.
 GN AMPH
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tetra-hybrid; TISSUE=Forebrain;
 RX MEDLINE=92331604; PubMed=1628617;
 RA Lichte B., Voh R.W., Meyer H.E., Killmann M.W.;
 RT "Amphiphysin, a novel protein associated with synaptic vesicles";
 RL EMBO J. 11:2521-2530(1992).
 CC -!- FUNCTION: May participate in mechanisms of regulated exocytosis in
 CC synapses and certain endocrine cell types. May control the
 CC properties of the membrane associated cytoskeleton.
 CC -!- SUBUNIT: Heterodimer with BIN1. Binds SH3GLB1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Peripheral membrane protein associated with
 CC the cytoplasmic surface of synaptic vesicles.
 CC -!- TISSUE SPECIFICITY: Is abundant in the forebrain and cerebellum.
 CC It is also found in the adrenal gland, anterior and posterior
 CC pituitary.
 CC -!- SIMILARITY: Contains 1 BAR domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
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 CC EMBL; X60422; CAA42953.1; -;
 DR PIR; S22700; S22700.

DR InterPro: IPR003005; Amphiphysin.
 DR InterPro: IPR003017; Amphiphysin_1.
 DR InterPro: IPR006832; BAR.
 DR InterPro: IPR004148; BAR_dom.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF03114; BAR; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR01251; AMPHIPHYSIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD003208; Amphiphysin_1; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART: SM00721; BAR; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS00002; SH3; 1.
 KW Cytoskeleton; SH3 domain; Coiled coil.
 FT DOMAIN 10 84 COILED COIL (POTENTIAL).
 FT DOMAIN 144 191 COILED COIL (POTENTIAL).
 FT DOMAIN 609 682 SH3.
 SQ SEQUENCE 682 AA; 75205 MW; 61617F494F39EB20 CRC64;
 Query Match 28.1%; Score 802.5; DB 1; Length 682;
 Best Local Similarity 33.1%; Pred. No. 2.5e-24;
 Matches 206; Conservative 118; Mismatches 203; Indels 95; Gaps 19;
 QY 1 MAEGAGGAGALFAKQVQKFSRAQEKVLQKLGKAVETKDERFEQASNFYQQAEGHKL 60
 DB 1 MADMK---TGIFAKYQKRLNRAQAEKVLQKLGKADETKDEQFEYVQNFKQAEAGSRL 56
 QY 61 YKDLNKLFLSAVKVMHSSKRVSETLQEIYSSWDGHEELKAIYNNNDLLWEDVEEKLAQ 120
 DB 57 QRELRLYLALIKGMQDASKKLTSLEHYVPDWDVGRVNGIKGKDELWEDPHQKLDVG 116
 QY 121 AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNAK-KDEAKTAKAESEEFNKA 179
 DB 117 SLLTLDYLGQFPDIKTRIAKRSKLVYDSARHLEALQSSKRGKDEGRITKAEEEFQKA 176
 QY 180 QTVFEDLNQELLELPILYNSRIGCVVTFIOMISNLRDVFYREMSKLNHNLYEVMKLEK 239
 DB 177 QKVFEENFDLQELPSLNSRVGFYNTFNKVSSEAKFPHKLEALLCHKLYEVMKLG 236
 QY 240 QHSNKFVFKGLSSSS---RRSLVISPVRVTVTSPLTS-----PTSPSTLSLKSESE 290
 DB 237 QHADKFTIQAPSDSGPLAIKATPSPPEVSPPLSPPTASPNHMLAPASAPARPKSP 296
 QY 291 SVSATEDLADAAQGDSEIIEKELLEEEIEKEGSEASSEEDDPLPACNGPAQAQPS-P 349
 DB 297 ---LRKGPVPVPLKAVYTKELQOE---NIISFFDNFVPEISVTTFSQNEIP 343
 QY 350 TTERAKS-----QEEVLPSTTPSPGALSPSG-----QPSSS-----382
 DB 344 ETKVSESLDLDPFPKPEVTVGTHSPMSQTLFWDLWTSTSELVQPAASSAFNGFAQ 403
 QY 383 ATEVLR-----TRTASEGSEQPKKRAIORIS-----APSPSPPPPPRA---TA 423
 DB 404 TTAFAVQSNENVTTLTAEAEALPGLKVEETPTAAVKEALAEFPDEPTQAAESIEA 463
 QY 424 SPRSSG--NIPSPPTASGSGS---PTSPRASLTGTASPRTSLEVPSPPEKPVRT 478
 DB 464 GDKETTGLAKESVSAAGGAVAVSDSVVAAGAGAVRTEQEAAGSGDPQGEEDV 523
 QY 479 EAKENENHNQNPPEELCTSPTLMTSQVASPGKAKEDKKNKLISAD--SSEGGDQIQ 537
 DB 524 DVSQ-----EKVSIPIVPIEASNNEGSEEHVIMNESKDAAEAMGTQGTDS-E 573
 QY 538 VSMVPENNNTAPEPQEVST 559
 DB 574 TSQIGSQKAT-----EEIQT 590

RESULT 7
 HOB1 SCHPO
 ID HOB1 SCHPO STANDARD; PRT; 466 AA.
 AC 074352;

DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein hbl (Homolog of Binl).
 GN HOB1 OR SPBC21D10.12.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=22457105; PubMed=12569356;
 RT "hob1", the fission yeast homolog of Binl, is dispensable for
 RT endocytosis or actin organization, but required for the response to
 RT starvation or genotoxic stress.;
 RL Oncogene 22:637-648(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Spouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Godle A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel K., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehmach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard J., Talla V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomycetes pombe".;
 CC -!- FUNCTION: Has a role in DNA damage signaling as a part of stress
 CC response processes.
 CC -!- SIMILARITY: Contains 1 BAR domain.
 CC -!- SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC -----
 DR EMBL; AF275637; AAF86458.1; -;
 DR EMBL; AL031536; CAA20768.1; -;
 DR PIR; T11684; T11684.
 DR HSSP; P08631; 1BU1.
 DR GeneDB; SPombe; SPBC21D10.12; -;
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.

DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW SH3 domain; Coiled coil.
 FT DOMAIN 7 230
 FT DOMAIN 294 409
 FT DOMAIN 407 466
 FT DOMAIN 31 67
 FT DOMAIN 177 204
 FT DOMAIN 466 AA; 51391 MW; 44179350D6C2C7E CRC64;
 SQ SEQUENCE 466 AA; 51391 MW; 44179350D6C2C7E CRC64;
 Query Match 8.3%; Score 238; DB 1; Length 466;
 Best Local Similarity 22.0%; Pred.No. 0.0061;
 Matches 110; Conservative 69; Mismatches 194; Indels 128; Gaps 16;
 QY 15 KQVOKKSRQAEKVLQKLGKAVETKDERPQSNFYQQQAEGHKLKDKNPLSAVKW 74
 DB 4 KGFTKALARTPQTLRSKFNVEITKPIYEDAGRFKSLTEAKLAEDAKKYTDAINGL 63
 QY 75 HESKRVSETLQRIY-----SSEWDGH-----EELKAIWNNDLLNEDYEK 116
 DB 64 LNHQIGFADACIETIKPISGRASDPSEYQEGNAEGIEAAEYKEIVY-----DLQKN 116
 QY 117 LADQAVRTMEIYVAF-----SEIKERIAKGRKLVYDYSARHHLBAVQNAK-- 163
 DB 117 LASE-----MDVINTRIVNPTGELLKIVKVDKLLRDHKQLDYDRHRSFFKLQEKDK 172
 QY 164 --KDEAKTAKAEENFNAQTVFEDLNQELLELPILYNSRIGCVYTFIQNINLRDVFYR 221
 DB 173 SLKDEKLYEAETAPEQSSQSEYETNMLKEELPKLFALAQAQSIAPLFQ-----FYY 225
 QY 222 EMSKLNHLNLEVMKLEKQHSNKFVVKVGLSSSRSLVISPVRTATVSSPLTSPSPS 281
 DB 286 MQLNVYVYVLEKMSHCIEIYFD--FNTDILESVERGDVKDRAEALTITTKFAKPTTK 283
 QY 282 TSLKSESESVSATADLAPDAAGDENSEIKELLEEEIEKEGSEASSEEDDPLPACNG 341
 DB 284 RFGMGPGGKDATS-----SSSSPSSKREE----- 308
 QY 342 PAQMGPSPTTTRAKSQEVLPSSTTSPGALSPSQSPSSATEVLRTRTASEGSEQPK 401
 DB 309 -AAAEPSST-----ATDIPPPYSTPSVAGASDYS--TPSAGYQTVQTTTTTEAAAAQY 360
 QY 402 KRASIQTSTAPSPPPPRATAGPRPSGNIPSSPTASGGSGSPSPRASLIGTGTSAPRPS 461
 DB 361 PQAPF-----PPPP--VMPQPA-----AAVTTFVAAPVAA 389
 QY 462 LEVS-PNPEPEKPVRTPEAK 481
 DB 390 AAAAVPVPPAPAPAPAPAAAE 410

RESULT 8

NFM_BOVIN
 ID NFM_BOVIN STANDARD; PRT; 810 AA.
 AC 077788;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neurofilament triplet M protein (160 kDa neurofilament protein)
 DE (Neurofilament medium polypeptide) (NF-M) (Fragment).
 GN NEF3 OR NEFM OR NFM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hill W.D., Zhang L., Balin B.J., Sprinkle T.J., Spicer K.,
 RA Gearhart D.A.;
 RT "The bovine neurofilament M subunit has a novel set of KSP repeats
 normally restricted to NF-H.";

Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Neurofilaments usually contain three intermediate
 CC filament proteins: L, M, and H which are involved in the
 CC maintenance of neuronal caliber.
 CC -!- PTM: There are a number of repeats of the tripeptide K-S-P, NFM is
 CC phosphorylated on a number of the serines in this motif. It is
 CC thought that phosphorylation of NFM results in the formation of
 CC intermediate cross bridges that are important in the maintenance
 CC of axonal caliber (By similarity).
 CC -!- PTM: Phosphorylation seems to play a major role in the functioning
 CC of the larger neurofilament polypeptides (NF-M and NF-H), the
 CC levels of phosphorylation being altered developmentally and
 CC coincident with a change in the neurofilament function (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC
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 CC
 CC EMBL; AF091342; AAC36357.1; -
 CC InterPro; IPR001664; IF.
 CC Pfam; PF00038; Keratin_1.
 CC PRINTS; PR01248; TYPE1KERATIN.
 CC PROSITE; PS00226; IF, 1.
 CC Intermediate filament; Coiled coil; Neurone; Phosphorylation.
 CC NON_TER 1
 CC FT DOMAIN <1 296 ROD.
 CC FT DOMAIN 297 810 TAIL.
 CC FT DOMAIN <1 20 COIL 1A.
 CC FT DOMAIN 21 33 LINKER 1.
 CC FT DOMAIN 34 132 COIL 1B.
 CC FT DOMAIN 133 149 LINKER 12.
 CC FT DOMAIN 150 171 COIL 2A.
 CC FT DOMAIN 172 175 LINKER 2.
 CC FT DOMAIN 176 296 COIL 2B.
 CC FT DOMAIN 503 582 8 X 13 AA TANDEM REPEATS.
 CC SEQUENCE 810 AA; 90759 MW; B8477D85560AC3F6 CRC64;
 CC
 CC Query Match 8.1%; Score 232; DB 1; Length 810;
 CC Best Local Similarity 21.5%; Pred. No. 0.018;
 CC Matches 138; Conservative 98; Mismatches 242; Indels 164; Gaps 25;
 CC
 CC 41 ERPEQASNFYQQQAGHKLKDLNFTLSAVKWHSESKVSTLQIYSSWDGHEELK 100
 CC 71 ERPEEARLRDTEAIPALRKDIEE-SSLVKV--ELDKV-QSLQDQVAFRLSNHEEV 126
 CC 101 A-----IWNNDLLWEDYEELAD-----QAVRTMEIYVAQFSE- 134
 CC 127 ADLLAQIQAHSITVERKDYLTDTISTALKEIRSQLSHSDQNMHQAEWPKRYAKLTEA 186
 CC 135 -----IKERIAKGRKLVYDSABHLEAVQAKD-EAKTAKAEFEFNKAQTFV 183
 CC 187 AEQNKAEIRAKBEIAEYRQL-----QSKSTELESVRGTESLERQLSDIEERHNDLSY 243
 CC 184 EDLNQELLEELPILYNSIGCVYTFIFONISNLRDVFVREMSKLNHLYEWSKLEKQHN 243
 CC 244 QDTIQLENELRGT-KWMAHSHLEYQDLLNVKALDIEIAAYR-----KLLEGEETRFST 298
 CC 244 KVVVKVQ-LSSSSRRSLVSPVTRATVSSP-----L 274
 CC 299 FAGSITGLYTHROPSIAISSKIQKTVKAPKLAVQHKVFVEIEETKVEDEKSEMEAL 358
 CC 275 TSPTSPTSLSKSE-----SESVATEDL-----APDAQGEDNSIKEL 314
 CC 359 TAITELAVSVKEEVEEAEKEKEEAEVEEVAAKKSPVKATAPELKEEKEEKEEG 418
 CC 315 LEEIEKEGSEASSEEDDPLPACNGPAQAPQSPFTTTRAKSQBEVLPSSTTPPGGALS 374

Db 419 QEEEEEAAKSDQAE-----GGSEKSSSEKEGEQEE-----GETAEGESE 466
 QY 375 PSQGP-----SSSATEVLTTRTASEGSPQPKGRASIQRTSAPPRPPPPRATASPRPS 428
 Db 467 AAABAKKEKMEKAEVAPKEELAAEKAEKPKAKSPVAKSPPTTKSPPTAKSPEAKSPE 526
 QY 429 SGNTPSPSTAGSGSP--SPRASLTGTGTASPTSLVSPNPPPEPKPVRTPEAKENENI 486
 Db 527 A-----KSPTAK-----SPTAKSPVAK-----SPTAKSPEAKSPTAKSPTAK----- 568
 QY 487 HNQNPBELCTSPTLMTSQV-----ASEPGRK-KWEDKEKDKNKLISADSSEGDQLOQVS 539
 Db 569 ---SPAASKPAKSPVEEVKAEAGKEQKEQKEVEEKEKESPKKEKAEKKEKPK 625
 QY 540 MYPENKLTAP-----EPQEVSTSENPO 563
 Db 626 DVPEKKKABSPVKAABSPKVEVPKPVKVSPEKAEKEEPKQ 667
 RESULT 9
 NFM_HUMAN
 ID NFM_HUMAN STANDARD; PRT; 915 AA.
 AC P07197;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neurofilament triplet M protein (160 kDa neurofilament protein)
 DE (Neurofilament medium polypeptide) (NF-M) (Neurofilament 3).
 GN NEF3 OR NEFM OR NFM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87275853; PubMed=3608989;
 RA Myers M.W., Lazzarini R.A., Lee V.M.-Y., Schlaepfer W.W., Nelson D.L.;
 RT "The human mid-size neurofilament subunit: a repeated protein
 RT sequence and the relationship of its gene to the intermediate
 RT filament gene family."
 RL EMBO J. 6:1617-1626(1987).
 RN [2]
 RP SEQUENCE OF ONE OF THE 13 RESIDUE REPEATS.
 RX MEDLINE=88158120; PubMed=2450354;
 RA Lee V.M.-Y., Otvos L. Jr., Carden M.J., Hollosi M., Dietzschold B.,
 RL Lazzarini R.A.;
 RT "Identification of the major multiphosphorylation site in mammalian
 RT neurofilaments."
 CC -!- FUNCTION: Neurofilaments usually contain three intermediate
 CC filament proteins: L, M, and H which are involved in the
 CC maintenance of neuronal caliber.
 CC -!- PTM: There are a number of repeats of the tripeptide K-S-P, NFM is
 CC phosphorylated on a number of the serines in this motif. It is
 CC thought that phosphorylation of NFM results in the formation of
 CC intermediate cross bridges that are important in the maintenance
 CC of axonal caliber.
 CC -!- PTM: Phosphorylation seems to play a major role in the functioning
 CC of the larger neurofilament polypeptides (NF-M and NF-H), the
 CC levels of phosphorylation being altered developmentally and
 CC coincident with a change in the neurofilament function.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC
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 CC
 CC EMBL; Y00067; CAA68276.1; -.


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DR PIR; A27864; A27864.
DR Genew; HGNC:7734; NEF3.
DR MIM; 162250; -.
DR GO; GO:0005883; C:neurofilament; TAS.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
DR InterPro; IPR006821; Filament_head.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_1.
DR Pfam; PF00038; filament; 1.
DR Pfam; PF04732; filament_head; 1.
DR PRINTS; PR01248; TYPEIKERATIN.
DR PROSITE; PS00226; IF; 1.
DR Intermediate filament; Coiled coil; Neurone; Phosphorylation;
KW Glycoprotein.
FT INIT MET 0 0
FT DOMAIN 1 103 HEAD.
FT DOMAIN 104 411 ROD.
FT DOMAIN 412 915 TAIL.
FT DOMAIN 104 135 COIL 1A.
FT DOMAIN 136 148 LINKER 1.
FT DOMAIN 149 247 COIL 1B.
FT DOMAIN 248 264 LINKER 12.
FT DOMAIN 265 286 COIL 2A.
FT DOMAIN 287 290 LINKER 2.
FT DOMAIN 291 411 COIL 2B.
FT DOMAIN 613 690 6 X 13 AA TANDEM REPEATS.
FT CARBOHYD 46 46 O-LINKED (GLCNAc) (BY SIMILARITY).
FT CARBOHYD 430 430 O-LINKED (GLCNAc) (BY SIMILARITY).
SQ SEQUENCE 915 AA; 102317 MW; 5F5D3DF34C9D9E50 CRC64;

Query Match
Best Local Similarity 8.1%; Score 230.5; DB 1; Length 915;
Matches 131; Conservative 96; Mismatches 264; Indels 93; Gaps 24;

QY 41 ERFQASNFYQQAGHKLKLDNPLSLAVKWHSESKRVSETLQIYSEWDGHEELK 100
DB 186 ERFEEARLRDDTEAIRALRKDIE-ASLVKV-ELDKV-QSLQDEVAFLASNHEEV 241
QY 101 ALVWNDLWE-----DYEEKLADQAVRTMEIYVAQFS-----EIKRIAKGR 144
DB 242 A-----DLAQIQASHITVERDYLKTDISTALKEIRSQLSHSDQNMHQAEWFKRYA 296
QY 145 KLVDYSARHLEAVONAKDEAKTAAE---EFNKAQTVFDLNOELLELPILYNS 200
DB 297 KLT--EAEQNKEARSAKEETAEVTRQIQSKS-ELESVRGTESLREQ-LSDIEERHNH 353
QY 201 RGCVYTFIPQINSLRDVYFREMKNLNHLYEVMKSL-EKQHSNKVFPVVKGLSSRRSL 259
DB 354 DLSSYQDTIQLEN-----ELRCKWMAHRLREYQDLLNVRKWLDBIAAYRKL 403
QY 260 VISPPVTVATVSSPLTSP-----TSPSTLSLXSESESYSA-----TEDLAPDAAQGE 306
DB 404 LGGEETRFSTPAGSITGPLYTHRPITTSKIQTKEAPLKVQHFKVBEIIEETKVED 463
QY 307 DNSEIKEL-----EEIEKEGSEASSE---EDDPLPACNGPAQA-QPSPTTER 353
DB 464 EKSEMEALTAITEELASMKKEEKEAEKEEPEAEKEEVAKKSVPKATPEVKEE 523
QY 354 AKSQREVLPSSVTPFGALSPGQPPSSATVVL-----RRTASEGSE-OPKK 402
DB 524 GKKEEEOGEEEBEEDGAKSDQAEQEGSEKEGSEKEGEGEGETEAEAEGEAEAKE 583
QY 403 RASIQRTSAPPPPPPPRATA---SPRPSGNIPSSPTASGGGSPT--SPRASLIGTGTA 457
DB 584 EKKVEKESEVATKEELVADAKVEKAKSPVKSPVKEGKSPVKSPVKEGKSPV- 642
QY 458 PRTSLVSNPPPEPKPVRTPEAKENINHNQNPPEELCTGPT----LMTSQVASEPCEAK 513
DB 643 PKSPVEEKGKSPVKSPV---EEKGSPVSKSPVKEAKSPVKSPVKEAKSKAEVKGGE 699
QY 514 KMEKEKKNKLISADSSEGDQLQVSMVYNNNTAPEPQEEVS 557
DB 700 QKEEKEKEVKEAPKEKVEKEKPKVPEKKKAEKSPVKEEAVA 743

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RESULT 10
NFM CHICK
ID NFM_CHICK STANDARD; PRT; 857 AA.
AC P16053;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Neurofilament triplet M protein (160 kDa neurofilament protein)
DE (Neurofilament medium polypeptide) (NF-M).
GN NEFM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174973; PubMed=2106668;
RA Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
RT "Isolation of the chicken middle-molecular weight neurofilament
RT (NF-M) gene and characterization of its promoter.";
RL Nucleic Acids Res. 18:521-529(1990).
RN [2]
RP SEQUENCE OF 259-857 FROM N.A.
RX MEDLINE=88112814; PubMed=3123320;
RA Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D.; Betz H.;
RT "Identification of gene products expressed in the developing chick
RT visual system: characterization of a middle-molecular-weight
RT neurofilament cDNA.";
RL Genes Dev. 1:699-708(1987).
CC -!- FUNCTION: Neurofilaments usually contain three intermediate
CC filament proteins: L, M, and H which are involved in the
CC maintenance of neuronal caliber.
CC -!- PTM: There are a number of repeats of the tripeptide K-S-P, NFM is
CC phosphorylated on a number of the serines in this motif. It is
CC thought that phosphorylation of NFM results in the formation of
CC interfilament cross bridges that are important in the maintenance
CC of axonal caliber.
CC -!- PTM: Phosphorylation seems to play a major role in the functioning
CC of the larger neurofilament polypeptides (NF-M and NF-H), the
CC levels of phosphorylation being altered developmentally and
CC coincident with a change in the neurofilament function.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X17102; CAA34958.1; -.
DR EMBL; X05558; CAA29073.1; -.
DR PIR; S15762; S15762.
DR InterPro; IPR006821; Filament_head.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin_1.
DR Pfam; PF00038; filament; 1.
DR Pfam; PF04732; filament_head; 1.
DR PRINTS; PR01248; TYPEIKERATIN.
DR PROSITE; PS00226; IF; 1.
DR Intermediate filament; Coiled coil; Neurone; Phosphorylation;
KW Glycoprotein.
FT INIT MET 0 0
FT DOMAIN 1 98 HEAD.
FT DOMAIN 99 406 ROD.
FT DOMAIN 407 857 TAIL.
FT DOMAIN 99 130 COIL 1A.
FT DOMAIN 131 143 LINKER 1.
FT DOMAIN 144 242 COIL 1B.

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FT DOMAIN 243 259 LINKER 12.
FT DOMAIN 260 281 COIL 2A.
FT DOMAIN 282 285 LINKER 2.
FT DOMAIN 286 406 COIL 2B.
FT CARBOHYD 46 46 O-LINKED (GLCNAC) (BY SIMILARITY).
FT CARBOHYD 426 426 O-LINKED (GLCNAC) (BY SIMILARITY).
FT CONFLICT 546 546 G -> R (IN REF. 2).
SQ SEQUENCE 857 AA; 95704 MW; 42E0FC6AC64778B CRC64;

Query Match 8.0%; Score 228.5; DB 1; Length 857;
Best Local Similarity 21.2%; Pred. No. 0.026;
Matches 149; Conservative 91; Mismatches 276; Indels 187; Gaps 27;

QY 18 QKFSRAQ-----EKVLQKLGAVETKD-----ERFQSA----- 47
DB 132 QKHAGRAQLGDAYQELFELGALAEQVSHKQAQIQDSEHIEDIOIRLERFERDEARLSD 191
QY 48 -----SNFYQQQAEGHLYKDLKNFLSAVKVNHSSKRVSEPLQIYSEWD 94
DB 132 ETEATIALRKEMEEASLMRAELDKVQSLQDEVAFLRGHE--EEVAELLAQLQASH-- 247
QY 95 GHEELKATVWNNLLMDEYEKLAD-----QAVRTMEIYVAQFSE----- 134
DB 248 -----ATVERKDYLTDTLTALKIRAQLEQSDHNMHQAEEWFKRYAKUTEAAEQNK 301
QY 135 -----IKERIAKGRKLVDSARHLEAVQNAKQD-EAKTAKAEFEFNAQTVPED----- 185
DB 302 EAIRSAKEEIAEYRQL-----QSKSIELESVRGKTESLESRLSDIEBRHNNDLTYQDTTH 358
QY 186 -LNOEL-----LEELFILNSR-----IGCVTIFONISNLROVF----- 219
DB 359 QLENELRTKWMARHLREYDOLLNVKMWALDIEIAVYKLLGEEETFPSPGSGITGPIF 418
QY 220 -YREMS-----KLNHNLVEW-----SKLEQKHSNK-----VFVVKGLSS 253
DB 419 THROPSVTIASTKIQTKEPPKLVQHKFVEEIEETKVEDEKSEMEDALSALAEEMAA 478
QY 254 SSRSLVISPVRTATVSSPLTSPSTSLSKSESVSATDLA--PDAAQ--CEDNS 309
DB 479 KAQEEQEEKAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 538
QY 310 EIKELLEEEETKSGSEASSEED-----DPLPACNGPAQAQFSPPTTERAKSQEVB 360
DB 539 EIEEKEGEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 597
QY 361 L-----PSTTTPSGALSPSQSPSSATEVVLTRPASESEQPKRASIQTSPAP- 412
DB 598 AAEVGVKQKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAE 653
QY 413 -----PSRPPPPPRATASP-RPSSGNIPSSPTASGGGSPSPRASLGVTGSPRTSLEVS 467
DB 654 KVRSPKPTTPEKVVSPKSPKPTPEKP--ASPEKPAPEKPTPEKPAPEKPS 711
QY 468 PEPEKPVPTPEAKENIHQNPEELCTSPMLTSQV-----ASEPGEAKKMD 517
DB 712 PEKESPLKDEKAVVEESI-----TVTKVTKVTAEEVSKAEKEDIANVEGEKKD 764
QY 518 KEKDKNLISADSSGDOLOVSMVPPNNNLTAPEPQEEVSTSE 560
DB 765 EAKEKEAEKEEGKVVTNGLVSPVDEKGEKVVTTKAEKIKTSE 807

RESULT 11
NCR2 HUMAN
ID NCR2 HUMAN STANDARD; PRT: 2517 AA.
AC Q9V618; Q00613; Q15416; Q13354; Q9V5U0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nuclear receptor co-repressor 2 (N-CoR2) (silencing mediator of
DE retinoic acid and thyroid hormone receptor) (SMRT) (Thyroid-,
DE retinoic-acid-receptor-associated co-repressor) (T3 receptor-
DE associating factor) (TRAC) (CTG repeat protein 26).

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GN NCR2 OR CTG26.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SMRT).
RC TISSUE=Pituitary;
RX MEDLINE=99178941; PubMed=10077563;
RA Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Evans R.M.;
RT "Unique forms of human and mouse nuclear receptor corepressor SMRT.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:2639-2644(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SMRT).
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=9919215; PubMed=10097068;
RA Park E.J., Schreen D.J., Yang M., Li H., Li L., Chen J.D.;
RT "SMRT, a silencing mediator for retinoid and thyroid hormone
RT receptor-extended isoform that is more related to the nuclear
RT receptor corepressor.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3519-3524(1999).
RN [3]
RP SEQUENCE OF 1023-2517 FROM N.A.
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=96008552; PubMed=7566127;
RA Chen J.D., Evans R.M.;
RT "A transcriptional co-repressor that interacts with nuclear hormone
RT receptors.";
RL Nature 377:454-457(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM TRAC-1).
RC TISSUE=Fetal liver;
RX MEDLINE=96408715; PubMed=8813722;
RA Sande S., Privalsky M.L.;
RT "Identification of TRACs (T3 receptor-associating cofactors), a family
RT of cofactors that associate with, and modulate the activity of,
RT nuclear hormone receptors.";
RL Mol. Endocrinol. 10:813-825(1996).
RN [5]
RP SEQUENCE OF 428-613 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=97369492; PubMed=9225980;
RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.-H., Kikwai A.S.,
RA Breachel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
RT "cDNAs with long 5' UTRs that encode repeats from human brain.";
RL Hum. Genet. 100:114-122(1997).
RN [6]
RP INTERACTION WITH MINT.
RX MEDLINE=21231190; PubMed=11331609;
RA Shi Y., Downes M., Xie W., Kao H.-Y., Ordentlich P., Tsai C.-C.,
RA Hon M., Evans R.M.;
RT "Sharp, an inducible cofactor that integrates nuclear receptor
RT repression and activation.";
RL Genes Dev. 15:1140-1151(2001).
RN [7]
RP INTERACTION WITH HDAC10.
RX MEDLINE=21839031; PubMed=11739383;
RA Fischer D.D., Cai R., Bhatia U., Asselbergs F.A.M., Song C., Terry R.,
RA Trogiani N., Widmer R., Atadja P., Cohen D.;
RT "Isolation and characterization of a novel class II histone
RT deacetylase, HDAC10.";
RL J. Biol. Chem. 277:6656-6666(2002).
CC -1- FUNCTION: Mediates the transcriptional repression activity of some
CC nuclear receptors by promoting chromatin condensation, thus
CC preventing access of the basal transcription.
CC -1- SUBUNIT: Interacts with HDAC7 (By similarity). Forms a large
CC corepressor complex that contains SIN3A/B and histone deacetylases
CC HDAC1 and HDAC2. This complex associates with the thyroid (TR) and
CC the retinoid acid receptors (RAR) in the absence of ligand, and
CC may stabilize their interaction with TRF1B. The SMRT isoform
CC interacts with HDAC10. Interacts with MINT.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:

```


GN NEF3 OR NEFM OR NFM.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]_TaxID=9986;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=97055255; PubMed=8999542;
 RT Vitadello M., Vettore S., Lamar E., Chien K.R., Gorza L.;
 RT "Neurofilament M mRNA is expressed in conduction system myocytes of
 RT the developing and adult rabbit heart.";
 RL J. Mol. Cell. Cardiol. 28:1833-1844(1996).
 CC -!- FUNCTION: Neurofilaments usually contain three intermediate
 CC filament proteins: L, M, and H which are involved in the
 CC maintenance of neuronal caliber.
 CC -!- PTM: There are a number of repeats of the tripeptide K-S-P. NFM is
 CC phosphorylated on a number of the serines in this motif. It is
 CC thought that phosphorylation of NFM results in the formation of
 CC interfilament cross bridges that are important in the maintenance
 CC of axonal caliber.
 CC -!- PTM: Phosphorylation seems to play a major role in the functioning
 CC of the larger neurofilament polypeptides (NF-M and NF-H). The
 CC levels of phosphorylation being altered developmentally and
 CC coincident with a change in the neurofilament function.
 CC -!- SIMILARITY: Belongs to the intermediate filament family.
 CC
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 CC
 CC EMBL; Z47378; CAA87454.1; --
 DR PIR; S55395; S55395.
 DR InterPro; IPR001664; IF.
 DR Pfam; PF00038; filament; 1.
 DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Coiled coil; Neurone; Phosphorylation;
 KW Glycoprotein.
 FT NON TER 1 1
 FT DOMAIN <1 197 ROD.
 FT DOMAIN 198 643 TAIL.
 FT DOMAIN <1 33 COIL 1B.
 FT DOMAIN 34 50 LINKER 12.
 FT DOMAIN 51 72 COIL 2A.
 FT DOMAIN 73 76 LINKER 2.
 FT DOMAIN 77 197 COIL 2B.
 FT CARBOHYD 217 217 O-LINKED (GLCNAC) (BY SIMILARITY).
 SQ SEQUENCE 644 AA; 72450 MW; 030FDA622898678 CRC64;
 Query Match 7.4%; Score 212; DB 1; Length 644;
 Best Local Similarity 20.9%; Pred. No. 0.083;
 Matches 121; Conservative 84; Mismatches 244; Indels 130; Gaps 22;
 QY 62 KDLKNFLSAVKVHESKR-----VSETLQRIYS-----SEWDGHEELKALVWNDLL 109
 DB 25 EVADLLAQIQASHITVERKDYLTDTISSALKRISQLECHSDQNWHQ-----AEW----- 76
 QY 110 WEDYEKLADQAVRTMEIYVAQFSEIKERIAKGRKLVYDVSARHLEAVQNAKDEAKT 169
 DB 77 FKCRYAKLTAEEQNKAEIRASKEEIAEYRQLQSKSIELESVAMHKSLEHRVSD----- 132
 QY 170 AKAEENFKATQVEDLNQELLEPLLYNSRIGCVYTFQINISNRDVFYREMSKLNHN 229
 DB 133 ---IEERHNDLSSYQDITQLENEL-----RGTKWMAHRLRE--YQDL--LN-- 174
 QY 230 LYEVMKLEKQHNKFNFWKGLSSSRSLVISPVPVTRATVSSPLTSP-----TSPS-TLS 284
 DB 175 -----VKMAUDIEIAVRKLEGEETRPFTFGSITGPLYTHRQPSVTIS 219

QY 285 LKSESESVSA-----TEDLPADAAQGDNDSEIKELL-----EBEIEIK 322
 DB 220 SKIQTKEAPKLVQKHKFVEEIIETKVEDEKSEMEDALTATAEELAVSVKEEKEEA 279
 QY 323 EGSEASSSEEDDPLPACNGPAQA-QPSPTTTERAKSQEEVLPSSTTPSPGALSPSQPSS 381
 DB 280 EGKEEQEAEAEVAAAKSPVKATTPEIKEEGEKEEKEEEDDEGKVDQAEGG 339
 QY 382 SATIWLRT-----RTASEG-----SEQPKRASIORTSAPSPRPPPPRATASPRPS 428
 DB 340 SEKEGSKNGEEOEGEETAEAGVEEAEAKKKEKTEEKSEVAAKEEPTVEATKVGKPEKA 399
 QY 429 SGNIFSSPTASGGGSPTPSPASLIGTIGTASPTSL-----VSPNPE-----PPEK 473
 DB 400 KSPVFKSPV-----EEVKPAEATAGKGEKEEVEEKKKAKEKSPKEKVKKEK 454
 QY 474 PVRTPEAKENHNQNPBELC--TSPTLMTSVAPEGAEAKMKDEKDKNLISADS-S 530
 DB 455 PDVPPKKAESPVKEEAAEAATITPTKVLGKETKEGKPLQOEKEKEKAGERGSGSE 514
 QY 531 EGQDQ-----LOVSMVPENNLTAPPEQEVSTSE 560
 DB 515 EGSQSGSKRAKEDIANGEGEKEEPEETKEGSGRE 553
 RESULT 13
 HOB3 SCHPO STANDARD; PRT; 264 AA.
 ID HOB3 SCHPO STANDARD; PRT; 264 AA.
 AC Q9TUM7; P78850;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein hcb3 (Homolog of Bin3).
 GN HOB3 OR SPBC725.09C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=21293007; PubMed=11274158;
 RA Routhier E.L., Burn T.C., Abbaszade I., Summers M., Albright C.F.,
 RA Prendergast G.C.;
 RT "Human Bin3 complements the F-actin localization defects caused by
 RT loss of Hob3p, the fission yeast homolog of Rvel6p.";
 RL J. Biol. Chem. 276:21670-21677(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hanlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Rucke E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolckardt G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RESULT 14	
ASPI_HUMAN	ASPI_MOUSE
ID	ASPI_MOUSE
AC	Q96KQ
DT	10-OCT-2005
DT	10-OCT-2005
DT	10-OCT-2005
DE	Apoptosis
DE	regulation
GN	PP1R1

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CC EMBL; AJ318887; CAC83011.2; -.
DR EMBL; AL049840; -. NOT_ANNOTATED_CDS.
DR EMBL; AB018314; BAA34431.1; -.
DR Genew; HGNC:14950; PPR1R13B.
DR MIM; 606455; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00248; ANK; 2.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50088; ANK_REPEAT; 2.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50002; SH3_1.
DR AP000001; Nuclear protein; Repeat; ANK repeat; SH3 domain.
KW REPEAT 920 952
FT REPEAT 953 985
FT DOMAIN 1019 1081
FT DOMAIN 132 292
FT DOMAIN 428 860
SQ SEQUENCE 1090 AA; 119585 MW; 92CF98EDDDDC89A4 CRC64;

Query Match 7.3%; Score 208.5; DB 1; Length 1090;
Best Local Similarity 22.5%; Pred. No. 0.19;
Matches 137; Conservative 85; Mismatches 224; Indels 163; Gaps 31;

12 LFAQGVKTSRADEKV--LQKLGKAVETKDEPEQSASNFVQQQAGHGLYKDLNFKLS 69
126 LTLSELQMARQQQLNQQQLNQQQLNQQQLNQQQLNQQQLNQQQLNQQQLNQQQLN 181
70 AVKMHSSKRVSETLQEI--YSSEWDGH-----EELKAIWNNDLLWEDYEKLDAQVR 123
182 RVZAEQNKLRAMRQVDYKIMGNLSAEIERFSAM-----FQEK--KQEVQ 229
124 TWEIYVAFSEIKERIAKGRKLVVDSDARHLEAVQNAKDEAKTAAKEEFNKAQTVF 183
230 TAILRVDQLSQLEDL-KKG-KLNGFQS-----YNGKLTPAAVELKRLYLQELQ-IR 278
184 EDLNOE---LLEELPILYNRIGCYVTIFQINLNRDVFYRMSKLNHLYEVMSKLEKQ 240
279 NQLNQEQNSKLQKQKELLNKRANVEVAMDKRISELRLRYGKIKLNR----- 326
241 HSNKVFVVKGLS-----SSRRSLVSPVPRVATVSS--PLTSPTSPETLSKSES--- 289
327 -----VNGTSSPQSPSLTSGRVAAGVPIQVPSAGSPVLGDPKPKQSLSIASNAAG 379
290 ESVSATEDLAPDAAQGDENSEIKEL---LEBEEIEKEGSEASSSEEDDPLP-ACNGPAQ 344
380 RSKSANDGNWPTLKQ--NSSSVKPVQVAGADWKDPSVEGSKQGVTSQVSPFPFSALGPT 438
345 AQPSPPTTERAKSQEV-----LPS--TTPSPGGLSPSGQPSGSSATEVVLRTASEG 396
439 ---KPGIEICKVPPPIPGVGKQLPPSYGVTPSP-----TLPGLGPTSSLE----- 480
397 SEQPKKRASTQRTSAP-PSRPPP---PRATASPRPSG-----NIPSSPTASGGSGPT 445
481 ---RRKEGSLPRPSAGLPSPQRPTLLPATGTPQPGSSQIQRISSVPPSPPTYPAGPPA 537
446 SPRASLGTGTASPTSLVSPNP-----EPPEKPVRTPEAKENENIENQNPEEL----- 494
538 FP-----AGDSKPELPTVAIRPFLADKGRSQSPKPGPTVNSSSIYMYLQQATPPKN 592
495 -----CTSP-----TLMTSQVASEFCEAKCKEDKEKQ 521
593 YQPAASHALNKSVAKVGVKPLPSGSGTSPSLPFLHGLSLSTGTPQPPSPSSTEKEPQD 652
522 NKLISADSS 530
653 GPAAPADGS 661

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RESULT 15
SYJL_BOVIN
ID SYJL_BOVIN STANDARD; PRT; 1324 AA.
AC O18964;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Synaptotagmin 1 (EC 3.1.3.36) (Synaptic inositol-1,4,5-trisphosphate 5-phosphatase 1) (p150) (Fragment).
GN SYNJ1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 321-339 AND 454-469.
RP TISSUE=Brain;
RC MEDLINE=97342621; PubMed=9199318;
RX Sakisaka T., Itoh T., Miura K., Takenawa T.;
RA "Phosphatidylinositol 4,5-bisphosphate phosphatase regulates the rearrangement of actin filaments.";
RT Mol. Cell. Biol. 17:3841-3849(1997).
RL CC -1- FUNCTION: Hydrolyzes PI(2) bound to actin regulatory proteins resulting in the rearrangement of actin filaments downstream of tyrosine kinase and ASH/GRB2.
CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-bisphosphate + H(2)O = 1-phosphatidyl-1D-myo-inositol 4-phosphate + phosphate.
CC -1- SUBUNIT: Binds to AMPH and ASH/GRB2.
CC -1- SUBCELLULAR LOCATION: Predominantly concentrated in the perinuclear areas.
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed with highest levels in brain.
CC -1- DOMAIN: The C-terminal proline-rich region mediates binding to a variety of SH3 domain-containing proteins including AMPH and ASH/GRB2.
CC -1- SIMILARITY: In the central section; belongs to the inositol-1,4,5-trisphosphate 5-phosphatase family.
CC -1- SIMILARITY: Contains 1 SAC domain.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -1- CAUTION: This is a conceptual translation; a number of potential framehifts were corrected starting in position 1213 so as to extend the similarity with the orthologs.
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EMBL; D85682; BAA21652.1; ALT_FRAME.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR000300; IPFC.
DR InterPro; IPR000504; RNA_rec_mot.
DR InterPro; IPR002013; SYJA_N.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF02383; SYJA_N; 1.
DR SMART; SM0128; IPFC; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
DR PROSITE; PS0275; SAC; 1.
KW Hydrolase; Endocytosis; RNA-binding; Multigene family.
FT DOMAIN 119 442
FT DOMAIN 475 859
FT DOMAIN 902 971
FT DOMAIN 860 1212
FT DOMAIN 1033 1036
FT DOMAIN 1108 1113
FT DOMAIN 1126 1129

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Search completed: March 4, 2004, 17:28:20
Job time : 17.3694 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:29:55 ; Search time 43.1083 Seconds
(without alignments)
2762.588 Million cell updates/sec

Title: US-10-069-540A-2

Perfect score: 2855

Sequence: 1 MAEGKAGGAGLFAKQVQKK.....NNLTAPPEQBEVSTSENPL 564

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	829	29.0	482	15	Sequence 238, App
2	816.5	28.6	434	9	Sequence 22, Appl
3	793.5	27.8	451	14	Sequence 4, Appl
4	675	23.6	404	9	Sequence 24, Appl
5	238	8.3	489	15	Sequence 2512, Ap
6	230	8.1	452	15	Sequence 3119, Ap
7	206.5	7.2	462	10	Sequence 5, Appl
8	203	7.1	1367	9	Sequence 108, App
9	202.5	7.1	3507	15	Sequence 5784, Ap
10	200.5	7.0	3913	15	Sequence 45, Appl
11	199.5	7.0	1297	15	Sequence 45, Appl
12	199	7.0	284	15	Sequence 14, Appl
13	199	7.0	818	15	Sequence 2410, Ap
14	197.5	6.9	6542	15	Sequence 2546, Ap
15	197	6.9	1360	9	Sequence 5013, Ap
					Sequence 2, Appl

16	197	6.9	1360	14	US-10-355-975-14	Sequence 14, Appl
17	195	6.8	600	15	US-10-357-587-16	Sequence 16, Appl
18	194.5	6.8	2441	13	US-10-109-886-8	Sequence 8, Appl
19	192	6.7	758	15	US-10-094-749-2451	Sequence 6, Appl
20	191.5	6.7	1848	10	US-09-839-996-6	Sequence 6, Appl
21	191.5	6.7	1848	14	US-10-080-505-6	Sequence 6, Appl
22	191	6.7	742	14	US-10-308-448-11	Sequence 11, Appl
23	190.5	6.7	2665	9	US-09-864-761-34248	Sequence 34248, A
24	190.5	6.7	3564	14	US-10-177-293-423	Sequence 423, App
25	190	6.7	742	14	US-10-203-860-2	Sequence 2, Appl
26	190	6.7	742	15	US-10-341-434-85	Sequence 85, Appl
27	189	6.6	1268	15	US-10-353-690-122	Sequence 122, App
28	188	6.6	474	14	US-10-032-585-7847	Sequence 7847, Ap
29	188	6.6	742	14	US-10-203-860-4	Sequence 4, Appl
30	187.5	6.6	528	10	US-09-840-746-20	Sequence 20, Appl
31	187.5	6.6	744	10	US-09-769-787-184	Sequence 184, App
32	187	6.5	258	15	US-10-104-047-3034	Sequence 3034, App
33	186.5	6.5	2440	15	US-10-341-434-236	Sequence 236, App
34	186	6.5	2478	9	US-09-815-242-5816	Sequence 5816, Ap
35	186	6.5	2478	9	US-09-815-242-12967	Sequence 12967, A
36	184.5	6.5	455	14	US-10-032-585-7399	Sequence 7399, Ap
37	184.5	6.5	511	9	US-09-864-761-34590	Sequence 34590, A
38	184.5	6.5	545	14	US-10-029-386-32280	Sequence 32280, A
39	184.5	6.5	551	9	US-09-864-761-34727	Sequence 34727, A
40	184.5	6.5	1702	10	US-09-839-996-5	Sequence 5, Appl
41	184.5	6.5	1702	14	US-10-080-505-5	Sequence 5, Appl
42	184	6.4	1125	14	US-10-100-957A-152	Sequence 152, App
43	184	6.4	1610	14	US-10-100-957A-22	Sequence 22, Appl
44	182	6.4	841	14	US-10-032-585-7122	Sequence 7122, Ap
45	181.5	6.4	1974	15	US-10-369-493-5455	Sequence 5455, Ap

ALIGNMENTS

RESULT 1

US-10-116-275-238
; Sequence 238, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-238

Query Match 29.0%; Score 829; DB 15; Length 482;

Best Local Similarity 39.2%; Pred. No. 1.2e-34;

Matches 211; Conservative 70; Mismatches 167; Indels 90; Gaps 16;

QY	1	MAE-GKAGAGLFAKQVQKKFSAQKVLQKLGKAVETKDERFESASNFYQQQAEHKK 59
DB	1	MAEMSGKGTAGKTASNVQKLTAKQKVLQKLGKADETKDEQFCVQVFNKLTGTR 60
QY	60	LYKDLKFLSAVKVMHSSKEVSTLQEIYSSWDGHEELKATVWNNLLWEDYEKKLAD 119
DB	61	LQDRTTTLASVKAMHESKKNLQECQVEYEPDPFGDEANKTAENNDLLWMDYHOKLVD 120
QY	120	QAVRTMEIYVQAFSEIKERIAKGRKLVVDYDSARHHLAVQNA-KKDEAKTAKAEFEFNK 178

Db 121 QALLTMDTYLQPPDIKSRKGRKLVYDSARHHYSLQAKKDEAKIAKEBELIK 180
 Qy 179 AQTVFELNQLLELPIYNSRIGCVTIFQINISLNDVYREMSKLNHLYVMKLE 238
 Db 181 AQVPEEMVLDQELPFLSNRVRGFFVNTFQSIAGLEENFKMSKLNQNLNDVLVGL 240
 Qy 239 KQHSNKVFFVVKGLSSRRSLVSPVRVATVSSSLTPTSPSTLSKSESESVATEDL 298
 Db 241 KQSGNTFTVKAQPSDN-----APAKNGKSPSPDGPATPEIRVNHPEPAGGA--- 291
 Qy 299 APDAAGDENSETKELLEEBIEKEGSEASSEEDDPLPACNGPAQAQSPSTTERAKSQE 358
 Db 292 TPGATLPKSPQLRK-----GPPVPPPPKPTSPSKVQKE 325
 Qy 359 EVLP-----SSTTSPGGLSPSPSSSATEVLRTRTASGSEOPKKRASIQR 408
 Db 326 CILSLFEDFVPEISVTTFS-----QP-AEASEVAGGTOPAA-GAQEPGTAA--- 371
 Qy 409 TSAPPRPPPPRATASPRSPSGNIPSPPTASGGGSPTPRASLGTG-----TAS 457
 Db 372 SEASSSLPAVVVETFPATVNGTVEG---GSGAG-----RLDLPDFMFKVQAQHDYAT 423
 Qy 458 PRTSLVSPNPEPEKPVETPEAKE-----NENIHQNP-ELECTS--PTLATSQV 505
 Db 424 DTDELQKAGVVVLVIFQNPPEQDEGWLGVKESDMNQHKELEKRCRVFPENFETRV 481

RESULT 2

US-09-879-957-22
 ; Sequence 22, Application US/09879957
 ; Patent No. US20020034755A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; HOFFMAN, No. US20020034755A1h
 ; KAY, Brian K.
 ; FOLKES, Dana M.
 ; MCCONNELL, Stephen J.
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
 ; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
 ; USING SAME

NUMBER OF SEQUENCES: 227
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/879,957
 FILING DATE: 13-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/630,915
 FILING DATE: 03-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Mirock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-174
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 434 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>

; TOPOLOGY: unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
 US-09-879-957-22
 Query Match 28.6%; Score 816.5; DB 9; Length 434;
 Best Local Similarity 45.1%; Pred. No. 4.4e-34;
 Matches 193; Conservative 47; Mismatches 105; Indels 83; Gaps 11;
 Qy 1 MAE-CKAGAGLFAKOVKKFSAQKVLQKLGKAVETKDERPEQASNFYQQQAEHGK 59
 Db 1 MAEMSGKGVTAGKASNVQKLTTRAQKVLQKLGKADETKDEQEQCVQNFNQLTEGTR 60
 Qy 60 LYKDLNLFSAVKVMHSSKRVSETLQEIYSSSEWDGHEELKAIWMNDLLMWDYFEKGLAD 119
 Db 61 LQKDLRTVLASVKAMHEASKCLSECLQEVYEPWPGRDEANKIAENNDLLMWDYHQLVD 120
 Qy 120 QAVRWELVYVQAFSEIKERIAKRGKLVYDSARHHLEAVQNA-KDEAKTAKAESEFNK 178
 Db 121 QALLTMDTYLQPPDIKSRKGRKLVYDSARHHYSLQAKKDEAKIAKEBELIK 180
 Qy 179 AQTVFELNQLLELPIYNSRIGCVTIFQINISLNDVYREMSKLNHLYVMKLE 238
 Db 181 AQVPEEMVLDQELPFLSNRVRGFFVNTFQSIAGLEENFKMSKLNQNLNDVLVSL 240
 Qy 239 KQHSNKVFFVVKGLSSRRSLVSPVRVATVSSSLTPTSPSTLSKSESESVATEDL 298
 Db 241 KQSGNTFTVKAQPSD-----NAPEKGNKSPSP----- 268
 Qy 299 APDAAGDENSETKELLEEBIEKEGSEASSE---EDDPLPACNGPAQAQSPSTTERAK 355
 Db 292 TPGATLPKSPQLRK-----GPPATPEIRVNHPEPA---SGASPGATIPKSP 302
 Qy 356 SQEEVLPSSTTSPGGLSPGQSPSSSATE-----VVLRTRTAS-----EGSQPKKGRAS 405
 Db 303 SQ-----PAEASEVVGGAQEPGTAASEATSSSLPAVVVETFSATVNGAVEGS-----AG 352
 Qy 406 IQTSAPP 413
 Db 353 TGLRLDLP 360

RESULT 3

US-10-123-807-4
 ; Sequence 4, Application US/10123807
 ; Publication No. US20030166021A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wistar Institute of Anatomy & Biology
 ; Prendergast, George C.
 ; Sakamuro, Daitoku
 ; TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
 ; Compositions and Uses Therefor
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, P O Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19477
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/123,807
 ; FILING DATE: 16-Apr-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/445,247
 ; FILING DATE: 03-Dec-1999
 ; APPLICATION NUMBER: US 08/870,126

FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WS*60DPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-123-807-4
Query Match 27.8%; Score 793.5; DB 14; Length 451;
Best Local Similarity 36.6%; Pred. No. 6.9e-33;
Matches 193; Conservative 66; Mismatches 152; Indels 117; Gaps 11;

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QY 10 AGLFAQVQKPSRAQEKVLQKLGKAVETWDRRFRPSASNFYQQAEGHKLYKDLKNFLS 69
DB 8 AKIASNVQKLTQRAQEKVLQKLGKAVETWDRRFRPSASNFYQQAEGHKLYKDLKNFLS 67
QY 70 AVKVMHESKRVSEITLQETYSSEWDGHELKAIKVNNDLLWEDYEKLADQAVRTMEIYV 129
DB 68 SVKAMHEASKKNECLQEVYEDFNDGRDEANKIAENNDLLWMDYHQKLVQALLTMDTYL 127
QY 130 AQPSEIKERIAKGRKLVYDYSARHLEAVQNA-KDEAKTAKAEENFNKAQTVFEDLNQ 188
DB 128 GQPPDIKRIAKGRKLVYDYSARHLEAVQNA-KDEAKTAKAEENFNKAQTVFEDLNQ 187
QY 189 ELLEELPILYNSRIGCVYTFQNIENLSDVYFVREMSKLNHLYVMSKLEKQHSNKVYV 248
DB 188 DLQELPILYNSRIGCVYTFQNIENLSDVYFVREMSKLNHLYVMSKLEKQHSNKVYV 247
QY 249 KGLSSSRSLVSPVPTATVSSPLTSPTSLKSESESVSATDLPADAAQEDN 308
DB 248 K-----AQPRKSKLSRLRRKNSDNAPAKGNKSP----- 278
QY 309 SEIKELLEEEIEKGESEASSEEDDPLPACNGPAQAQPSPTTERAKSQEVLSSPTPS 368
DB 279 -----SPPDGSPAATPEIRVNHE-----PE 298
QY 369 PGALSPSGQPSSSATEVVLRTKRTASEGSEQPKKRTASQRTSAPSPRPRATASPRPS 428
DB 299 PAGATPGA-----TLPKSPQAESAEEVAGGTQPAAGAQEFGETAASEAA 344
QY 429 SGNIPS-----SPTASGGSPSPRASLGTTG-----TASPRTSLEVSPN 467
DB 345 SSSLPAAVVTFTPATVNGTVEGGSG--AGRLDLPFGFMFKVQAQHDYATDTDELQKAL 402
QY 468 PEPEKPVRTPEAKE-----NENHNQNP-ELCTS--PTLMTSQV 505
DB 403 DVVLVTFQNPPEQDEGLWLVGKESDMNQHKLEKRCRGVFPENFTERV 450

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RESULT 4

US-09-879-957-24
Sequence 24, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWLES, Dana M.
MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-879-957-24
Query Match 23.6%; Score 675; DB 9; Length 404;
Best Local Similarity 34.1%; Pred. No. 6.5e-27;
Matches 169; Conservative 62; Mismatches 133; Indels 132; Gaps 12;

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QY 42 RFEQASAFYQQAEGHKLYKDLKNFLSAVKVMHESKRVSEITLQETYSSEWDGHELK 101
DB 8 RFEQVQNFNKLTEGTLQDLRTYLSAVKAMHEASKKNECLQEVYEDFNDGRDEANK 67
QY 102 IYVNDLLWEDYEKLADQAVRTMEIYVVAQFSEIKERIAKGRKLVYDYSARHLEAVQ 161
DB 68 IAENNDLLWMDYHQKLVQALLTMDTYLQPPDIKRIAKGRKLVYDYSARHLEAVQ 127
QY 162 A-KDEAKTAKAEENFNKAQTVFEDLNQELLELPILYNSRIGCVYTFQNIENLSDV 220
DB 128 AKKDEAKTAKAEELIKAKQVPEEMNVDLQELPILYNSRIGCVYTFQNIENLSDV 187
QY 221 REMSKLNHLYVMSKLEKQHSNKVYVVKGLSSSRSLVSPVPTATVSSPLTSPTSP 280
DB 188 KEMSKLNQNLNDVLVLEKQHSNTSTVK----- 216
QY 281 STLKSESESVSATDLPADAAQEDNSEIKELLEEEIEKGESEASSEEDDPLPACN 340
DB 217 -----AQPSDNAPAK-----GNKSPS----- 232
QY 341 GPAQAQPSPTTERAKSQEVLPSSTTPSPGALSPSGQPSSSATEVVLRTKRTASEGSE 400
DB 233 -PPDGSPAATPEIRVNHE-----PEPAGATPGA-----TLPKSPSQ 269
QY 401 KKRASQRTSAPSPRPRATASPRSPSGNIPS-----SPTASGGSPSPRAS 450
DB 270 ABASEVAGGTQPAAGAQEFGETAASEAASSLPAAVVTFTPATVNGTVEGGSG--AGRLD 327
QY 451 LGTG-----TASPRTSLEVSPNPEPEKPVRTPEAKE-----NENHNQNP 492
DB 328 LPPGFMFKVQAQHDYATDTDELQKALGVVLVTFQNPPEQDEGLWLVGKESDMNQHK 387
QY 493 -ELCTS--PTLMTSQV 505

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us-10-069-540a-2.rapb

Fri Mar 5 14:57:53 2004

RESULT 6
US-10-369-493-3119
; Sequence 3119, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3119
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3119
Query Match 8.1%; Score 230; DB 15; Length 452;
Best Local Similarity 21.5%; Pred. No. 0.00033;
Matches 96; Conservative 68; Mismatches 188; Indels 94; Gaps 14;
QY 23 RAQKVLQKLGKAVETKDERFEQASNFYQQAEGHLYKDLKFNLSAVKVMHESKRV 82
DB 1 QAPQKQKFNIGHTKOPVYIDSRERFQETETKRLHDSKKYFEALINGMLHQIEFS 60
QY 83 ETLQEIYS-----SEWDG-----HEELKAIWNNLLWEDYEKLADQ----- 120
DB 61 KAMTEIYKPIGRMSDDPSLVPHGNVEGIAACEYEAVV-----KDLQETLAPLEMI 113
QY 121 ---AVRTMEIYVAQFSEIKERIAKGRKLVYDSARHLEAVQNAK-----KDEAKTAAE 173
DB 114 EARVIRPANELLDVIVIRKTAVERHKKLDVDRHATLKLQDKKRSADKAMWKA 173
QY 174 EEFNKATQVFDLQELBELPILYNSRIGCVYTFQINSLNR-DVFYREMSKLNH---N 229
DB 174 NEVQATQYVYNDLLKDELPKLPALEKQFQIPLFQSFYFQNLNIFYLHEKMQHCDIG 233
QY 230 LYEVMSKLEKQHNKVFVVKGLSSSRSLVSPVVRTATVSSPLTSPSTLSKSES 289
DB 234 YFDLTLDIE-----EAFYAKRGDVQRAEALSIKVTGKMKRP----- 272
QY 290 ESVSATDLPDAAQGDENSEIKELLEEEIEKEGSEASSEDDPLPACNPAQAPSP 349
DB 273 -----PKYQRPAGLEGN-----KPAGLLTAGSSTTTS-----TGPPPEAPSV 309
QY 350 TTERAKSQEVLPSSTTSP-----GGALSPGQSPSSATEVVLRT--RTASEGSEOPKKR 403
DB 310 TAPREWEQQCAPAVTAPRFRWETOATVEAHAPPPYSVKPSTLHATPRLATPQASPKP 369
QY 404 ASIQTSAAPPSPRPPRATASPRSS 429
DB 370 SLSMAAAKAKPPPKP-----PKPKA 391

RESULT 7
US-09-819-104A-5
; Sequence 5, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138

US-10-069-540a-2.rapb
388 LEKRGVFPENFTERV 403
RESULT 5
US-10-369-493-2512
; Sequence 2512, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2512
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(489)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2512
Query Match 8.3%; Score 238; DB 15; Length 489;
Best Local Similarity 22.08%; Pred. No. 0.00014;
Matches 110; Conservative 69; Mismatches 194; Indels 128; Gaps 16;
QY 15 KQVKKFSRAQKVLQKLGKAVETKDERFEQASNFYQQAEGHLYKDLKFNLSAVKVM 74
DB 4 KGFTKALARTQTLRSKFNVEGIEITKDPIYEDAGRRFKSLTEAKGLAEADKTTDAINGL 63
QY 75 HESSKRVSETLQEIY-----SSEWDG-----EELKAIWNNLLWEDYEK 116
DB 64 LNHQGTGFADACIEIYKPIGRASDPESVEQEGNAEGTEAAEYKEIVY-----DLQKN 116
QY 117 LADQAVRTMEIYVAQF-----SEIKERIAKGRKLVYDSARHLEAVQNAK-- 163
DB 117 LASE-----MDVINTRIVNPTGELLKIVKVDKLLKRDHKQLDYDRHRSFKLQSKKOK 172
QY 164 --KDEAKTAAEENKACQTFEDLNQELBELPILYNSRIGCVYTFQINSLNRDVFYR 221
DB 173 SLKDEKLYEAETAPEQSQEYTYNEMLKDELPKLPALEKQFQIPLFQ-----FY 225
QY 222 ENSKLNHLYEVMSKLEKQHNKVFVVKGLSSSRSLVSPVVRTATVSSPLTSPSTPS 281
DB 226 MQLNVVYLYKMSHCEIQFD--FNTDILESYYERRRGVDKRAEALTIKFKTAKPTYK 283
QY 282 TSLKSESESVSATDLPDAAQGDENSEIKELLEEEIEKEGSEASSEDDPLPACNG 341
DB 284 RPKGPGGKGDATAS-----SSSFSSKREE----- 308
QY 342 PAQAPSPPTTERAKSQEVLPSSTTSPGGLSPGQSPSSATEVVLRTTRTASEGSEOPK 401
DB 309 -AAAEPSST-----ATDIPPPYSTPSVAGSDYS--TPSAGYQVQTITTTTTEAAAY 360
QY 402 KRASIORTSAPPSPRPPRATASPRSSGNIPSSPTASGGSGFTSPRASLGTGTASPRTS 461
DB 361 PQAAF-----PPPP-----VMPQFAA-----AAVTFVZAPVAA 389
QY 462 LEVS-PNPEPEKPVRTPEAK 481
DB 390 AAAAVPVPPPPAPAPAAPAAE 410

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Db 2066 VKSTPKBSSSEITVK-ISSKSPVETSVKSSPPTTQSQVTSIVPETSSTVLS 2124
Qy 286 KSESSEYATE-----DLAPDAQAQEDNSEIKELLEBEIEKEGSEASSSEDDPL 336
Db 2125 EAPVTSSTPTEVTSSTKPSLSASSTGDTNSTPSTSLASVSTSAPEGTSASVAP 2184
Qy 337 PACN-GPAQAQPSPTTERAKSQEVLPSSTPSPGALSPSGSSATEVVL----- 388
Db 2185 KLSLSFDVQSPSTKFDATESVQASET--SSGTSVASTSEPSHVKLSITSNPS 2242
Qy 389 -----RRTASEGSEQPKKASQRTASPPRPPPRATASPPRSGNTPSPSTAG 440
Db 2243 SVPTSPKSTPTPESTEQPTTTPSQSLTPMNSSEVLTTSEPHVLSL--SPDVS- 2299
Qy 441 GGSPTSFRASLGCTASPTSLVSPPNPP--EKPV-----RTPEA 480
Db 2300 QSSTTPNLSSTVETPKTSSEVSLNSEPSTTEPTLSPDLSTTNNLSQSTVST 2359
Qy 481 KENENIHQNPPEELCTSTLMTSQVASEPGEAKM--EDKXKONKLISADSS--EQDQL 536
Db 2360 EDRSEISSENSEKPTSAPELVTSVTHVASSPDVPTSESPDPLTGSSSTENIPEASSKQ 2419
Qy 537 QVSMVPPNNLTAPEQEEVSTSENQOL 564
Db 2420 TISSTPTPTTASE-EPTKSTGMSDPL 2446

RESULT 10
US-10-334-143-45
; Sequence 45, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 45
; LENGTH: 3913
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-334-143-45

Query Match 7.0%; Score 200.5; DB 15; Length 3913;
Best Local Similarity 20.7%; Pred. No. 0.14; Indels 211; Gaps 33;
Matches 144; Conservative 99; Mismatches 240; Indels 211; Gaps 33;
Qy 12 LFAQVQKK-FSRAQEV-LQKLGKAVETKDE-----RFEQSA-- 47
Db 2297 VFAREKQQAIDLPEBSVQKDFMWLTKTDEHAQSNIEVNDSGDNVVKQRTENSSKA 2356
Qy 48 --SNFYQQAQGHKLYKDKNFLSA-----VKYMH--ESS-----KRVSETL 85
Db 2357 MPDSFSEQQA-----KDLACHITSDDLATRGFWDKVFRTWSSGATNKSQKEKLSHVL 2410
Qy 86 QEIVSSEWDGHEELKAIWVNDLL--WEDYBEKLDAQVRTWETVYVAQFSIEKRIARGR 144
Db 2411 VHDVRENHIGPESKSVQDKNEFVSITERKLTN-----GSLSEIKEMTVKSPS 2461
Qy 145 KLVDYSARHLEAVQNAKDEAKTAKAEFEFNKAQTFEDLQELLEELPILYNSRIGC 204
Db 2462 KKVLY---REVY-----VKEGDHPGLLDQPSRES-----SAVSHIPV-----RVAD 2502
Qy 205 YVTIFQNLINLRDVFYRMSKLNENLYVMSK-----LEKQSNKVFVVKGLSS----- 253
Db 2503 ERMLS--SNIPDGFCEGASAPPKHLSOKLSQSSSKETVETQHFNSIEDEKVTYSEISK 2560

Qy 254 -SSRSLV-ISPVRTATVSSPLTSPT-SPSTLSLKSESES-----VSATEDLAP 300
Db 2561 VSKHQSIVGLCPLEETE-----ISPTKSPDLSFSPGKESPSDFDHPIDGLEKLAP 2615
Qy 301 DAAQGDENSEIKEL-----LEBEI-----E 321
Db 2616 -LAQTEGGKEIKTLFVYVSVQVQKYEKEIQOGGVKLIQOECKTVQETRGTYTTRQ 2674
Qy 322 KEGSEASSSEDDPLPACNCPAQAPSPPTTERAKSQEVLPSSTPSPGALS-PSQOPS 380
Db 2675 KQPPSPQSPEDTLEQVSEFLDSSGKSLTPTPSSSEVSYEFTSKTPDSLIAYIPGKPS 2734
Qy 381 SSATEVVLTRTASGSGOPK-----KRASIORTSAPPSPRPPPRATASPRSSGNI----- 432
Db 2735 P-----IPEVSESESEEEQAKSTLSKQTTVEETAVEREMPNDVSKDNQRPKNRVAYIE 2789
Qy 433 -PSSPTASGGSPTSFRASLGCTASPTSLV-----SPNPE 469
Db 2790 FPPPPPLDADQIESDKHY-----LPEKVDMEVNLQDEHDXVQLAEPVIRVQPPSPV 2844
Qy 470 PPEKPVRTPEAKENINHNQNPBELCTSTLMTSQVASEPGEAKMEDKONKLISADS 529
Db 2845 PPGADV--SDSSDESIIYQVPVKKYTF-----KLKEVDDQEKPKASAEK 2889
Qy 530 SEGQDOLQVSMVPENN--NLTAPEQEEVSTSEN 561
Db 2890 ASNQKESLENGSGKONFGLGDSFQNELAQGN 2923

RESULT 11
US-09-291-417-14
; Sequence 14, Application US/09291417A
; Publication No. US20030050230A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; CURRENT FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1297
; TYPE: PRT
; ORGANISM: Mammalian (Human) 2C2
US-09-291-417-14

Query Match 7.0%; Score 199.5; DB 10; Length 1297;
Best Local Similarity 18.6%; Pred. No. 0.042;
Matches 113; Conservative 113; Mismatches 258; Indels 123; Gaps 21;
Qy 15 KQVQKFSRAQEVKVLQKLGKAVETKDEPEREQSASFYQQAQGHK-----LYK 62
Db 262 ROVRIQLKDHIDRTKKRGEKDETE---YEYSGSEEEENDSGEPSSILNLPRESTLRR 318
Qy 63 DLKNFLSAVKVMHSSKRVSETLQETYSSEWDGHEELKAIWVNDLLWEDYEE---KLAD 119
Db 319 DFLQLQANKERSEALRR-----QQLQOQORENEHEKRLQLAERQKRIEEOKEQRRLEE 373
Qy 120 QAVRTMEIYVQFSEIKRIAKRGLVDYDSARHLEAVQNAKDEAKTAKAEFEFNKA 179
Db 374 QORREKLRQOQREQRHYEQMREERREARAEHQYKRLQLEQORQAERLQRLQKE 433
Qy 180 QTVFEDLNQELLELP-----LYNSRIGCVITFQNLINLRDVFYRMSKLN----- 227
Db 434 RDLVLSLQHQORQORPVKKPLHYKEG--MSSEKPAWAKEV--EERSLNRQSSPAMP 489
Qy 228 HNLVEMSKLEKQHSNKNFVVKGLSSSSRRSLVISPVRTATVSSPLTSPTSPSTLSLKS 287

Db 490 HKVNRISDPNLPRESFISGVQ-----PARTPMLRPV-DPQIPLHVAKS 537
Qy 288 ESESVSATEDLADAAQGDNSNBIKELLEIEKEGSEASSEEDDPLPA-----CN 340
Db 538 QGPALTASQSVHEQPTKGLSGFQBALNVISHRVEMPRQNSDPTSENPPPTRIEKFDRSS 597
Qy 341 GPAQAQ--PSPTTERAKSQEVLPSSTSPGALSP--SGOPSSSATEVLRTRTASEG 396
Db 598 WLREEDIPKVPORITISIPALARKNSPGNGALGRLGSDIRASNDLRT-----651
Qy 397 SEQPKKASIQRTASAPRPPPRATASPRSSGNIPSS-PTASGGGSPTSRASLTGTGT 455
Db 652 --EPILSPLORTSSGSS-----SSSTSPSQSPSSQSGSQSGS-----691
Qy 456 ASPTSLEVP---NPEPEKVPRTPEAKENIHNQPE-----492
Db 692 -SETRVRANKSGSVLPHEPAKVPKPEESDITRPSRPASYKKAIDEDLTALAKEURE 750
Qy 493 ---ELCTSPILMTSQVASEFGEAKKEDKEKKNKLISADSSEQD--QLQVSMVPPENNLT 548
Db 751 LRIETVRPMKKVTDYSSSEESSESEEDGE-----SETHDGTVAVSIDIPRLIPTG 804
Qy 549 APPEQBE 555
Db 805 APGSNEQ 811

RESULT 12
US-10-369-493-2410
; Sequence 2410, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2410
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(284)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2410

Query Match 7.0%; Score 199; DB 15; Length 284;
Best Local Similarity 26.4%; Pred. No. 0.0073;
Matches 60; Conservative 42; Mismatches 105; Indels 20; Gaps 6;
Qy 28 VLQKLGKAVETKDERFEQASNFYQQAGHGKLYKDLNLFSAVKVNHSSKRVSETLQ 87
Db 37 VMKGTGHVTRVDFEFETERYRTMESAAKLOKEAGYLDALRAMTASQTRIANTIDA 96
Qy 88 IYSEWDGHEELKALVWNNLLWEDYEE---KLADQAVRTWEI-----YVAQSEIKERI 139
Db 97 FYGDA--GSKDGVSAIYRQ--VWELDADTVKELDGFRTVLDPTSRFCYSFPDINA 152
Qy 140 AKRGKLVYDSARHLE-AVONAKQDEAKTAKAEFEFNKAQTVFEDLNQELLEELPILY 198
Db 153 TGENHLLDHDAMRAKVQKLVKESNTTKLPRTEKAAMAKVEYETLNNQLVSELPQLI 212
Qy 199 NSRICGYVTIFQNISLRADVREMSKLNHNLVYEMSKLEKQHSNKV 245

Db 213 ALRVPLDPSFEMLVKIQIRFCREG-----YKMAQVQQYFDSV 252
RESULT 13
US-10-104-047-2546
; Sequence 2546, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2546
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2546

Query Match 7.0%; Score 199; DB 15; Length 818;
Best Local Similarity 21.5%; Pred. No. 0.026;
Matches 128; Conservative 79; Mismatches 231; Indels 158; Gaps 24;
Qy 23 RAOEKVLQKLGKAVETKDERFEQASNFYQQAGHGKLY-----KDLNLFSAVKVM 74
Db 120 KMQRSAQLA--NAESRQKLEKLEKLOALQOEKLAARLEBERGKQVLMVKEC 178
Qy 75 HESSKRVSETLQBIYSEWDGHEELKALVWNNLLWEDYEEKLADQAVRTWEI---YVAQ 131
Db 179 KOLSGKVIIEAQKL-----EDVMKLEEEKKKTNEELSAE 216
Qy 132 FSEIKERIAKRGKLVYDYSARHLEAVONAKDKAKAEFEFNKAQTVFEDLNQELL 191
Db 217 KRSTMEAGKQLSEFTEIEQLAKLN--REAHNTDLKEEDKMKMIEQLKRG-S 273
Qy 192 EELPILYNSRIGCYVTIFQNISLRADVREMSKLNHNLVYEMSKLEKQHSNKV 251
Db 274 DSKPFLSLPR-----KTKDRRLVSI VGT 297
Qy 252 SSSRRSLVSPVTRATVSS-----PLTSPTSPSLSLKSESVSATEDLADAAQGED 307
Db 298 EGTVTRSVACQTLVTENADHMKKPLTMPVPESTGSLVSNAGSVCTSATMARPGID 357
Qy 308 -NSEIKELL-----EEBIEKEGSEASSSSEB-----DDPLPACMGPAQAQSPSTE 352
Db 358 RQASYGDLIGASVPAPPPPSANKIEENGFTGSTDPTSTSTPLPSNAAPPTAQ--TPGIA 416
Qy 353 RAKSQEVLPSSTTPPGGALSPSGOPSSSATEVLRTRTASEG--SEQPKKASIQRTSA 411
Db 417 PQNSQAPPMHSLHSPCANTSLHPLNPRIQA-----AERFRQGNANDPDQNGN--TTQS 468
Qy 412 PPSRPPPP-----RATASPRSSGNIPSPSTASGGGSPTSRASLTGTASPR 459
Db 469 PPSRDSPTSRDLNVAKQLARNTVQALSRFTSPQAGAPSRGVP--PTGDVGTTHPPVGR 526
Qy 460 TSLEV-----SNPBPPEKPP--VRTPEAKENIHNQPEELCTSPILMTSQVASE 508
Db 527 TSLKTHGVARVDRGNPPPIPKKPGILSQTSPSP-----HPQ-----LKVIDSSRSAN 574
Qy 509 PGEAKKVEDKKNKLISADSSEQDQLQVSMVPPENNLTAPPEPQEVSTSENPOL 564
Db 575 TG-----AKVDNKTVAFTPS-----LPQGNRVI-----NEENLPKSSPOL 611

RESULT 14
US-10-369-493-5013
; Sequence 5013, Application US/10369493
; Publication No. US20030233675A1


```

; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5013
; LENGTH: 6642
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5013

Query Match
Best Local Similarity 6.9%; Score 197.5; DB 15; Length 6642;
Matches 78; Conservative 48; Mismatches 185; Indels 29; Gaps 8;

QY 232 EVMSKLEKQHSNKFVVKVGLSSSSRRSLVISPVRTATVSSPLTSPSTSLKSESES 291
DB 1556 EIKSPVKEKSPKVEKPASPTKKEKSPKASPTKKESENVKSPKKEKSPKSWVEE 1615
QY 232 VSATEDLAPDAQGEDNSEIK-----ELLEEBEIEKEGSEASSEDDPLPACNGPAQAO 346
DB 1616 LKSPKESPEKADDPKSPKSPKSPKSPKSPKSPKSPKSPKSPKSPKSPKSPKSPK 1673
QY 347 PSPTTE-----RAKSQEVLPSTTPPGGALSPGQFSSSSATEVVLRT-----TASEG 396
DB 1674 SSPTKTDDEVKSPKKEKSPKKEKSPKKEKSPKKEKSPKKEKSPKKEKSPKKEK 1733
QY 397 SEQPKGRASIQTSAPPSPPPRATASPPSSGNIPSSSTASGGSPSPRASLTGTGA 456
DB 1734 KPSPTKKEKSPKSAAEVKSPTKKEKSPKSAEKPSPKSPK-----KESSPVKAADDEVK 1789
QY 457 SPRTSLEVPSP-----NPEPPEKPVRTPEAKENIHONPEELCTSPTLTMSQVASEPGE 511
DB 1790 SP-TKEKSPKVEKPASPTKKEKTPKSAEELKSPKKE--KSPSSPTKKTGTDESKE 1846
QY 512 AKKMDKEKONKLIADSEGGDQLQVSMVPPNNLTAPE 551
DB 1847 KSPKEPKSPKPTPKKPPGSPKPKKSPKPKKSPKPEAKPPAPK 1886

RESULT 15
US-09-871-916-2
; Sequence 2, Application US/09871916
; Patent No. US20020019519A1
; GENERAL INFORMATION:
; APPLICANT: BINGHAM, SHARON
; APPLICANT: CASE, PATRICK
; APPLICANT: LAWSON, SALLY NEALE
; APPLICANT: NEWTON, RICHARD ANTHONY
; APPLICANT: RAUSCH, OLIVER LARS
; APPLICANT: REITH, ALASTAIR DAVID
; APPLICANT: SANGER, GARETH JOHN
; TITLE OF INVENTION: NEW USE
; FILE REFERENCE: P32261-D1
; CURRENT APPLICATION NUMBER: US/09/871,916
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/393,569
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: GB 9907261.3
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: GB 9819779.1
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 2
; LENGTH: 1360
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-871-916-2

Query Match
Best Local Similarity 6.9%; Score 197; DB 9; Length 1360;
Matches 119; Conservative 110; Mismatches 248; Indels 166; Gaps 23;

QY 15 KQVKKFSQAQKVLQKKAIVETKDERFEQASNFYQQAEHGK-----LYK 62
DB 296 ROVRIQLKDHIDRTKKGKDETE---YBSGSEEESEENDSGEBSILNLPSESTLRR 352
QY 63 DLKNFLSAVKVWHSESKRVSETLQBIYSSEWPGHEELKAIYVNNDDLWEDYEKLDAQV 122
DB 353 DFLRLQLANKERSEALR-----QLEQQQORENEEHKQLL-----AEQKRIEQKE 400
QY 123 RTWEIVVAOFSEIKERIAKGRKLVYDSARHLEAVQNAKQDEAKTAKAEFP-----N 177
DB 401 QRRL-----EQQRREKELRKQEREQRRYEE--QVRREERERRAEHGEYIRROLE 452
QY 178 KACTVPEDLNQELLELPILYNSRIGCYVTIFQNTSNLRDV--FYREMSKLNHLIYVMS 235
DB 453 EGRQLEILQQLLHQAALLLYK-----RKQLEEQQAERLQRLKQERDYLVSQHQ 505
QY 236 KLEKQH-----SNKVVVYKGLSSSSRRSLVISP-----263
DB 506 QRQEQRPVEKKPLYHYKEGSPSEKPAWAKEVEERSRLNRQSSPAMPHKVANRISDPNLP 565
QY 264 -----PVRTATVSSPLTSPSTSLKSESESVSATEDLAPDAQGEDNSEI 311
DB 566 PRSESPISGVQPARPPMDLRPV-DQIPLHVAVKSQGPALTASQSVHEQPTKGLSGQEQ 624
QY 312 KELLEEBEIEKEGSEASSEDDPLPA-----CNGPAQAQ--PSPTTERAKSQEVLIP 362
DB 625 ALNVTSHRVEWMPQNSDPTSENPLTRIEKFDRSSWLRQEDIPPKVPQRTTSISPALA 684
QY 363 SSTTPSGGALSP--SQPSSSATEVVLRTTASGESEQPKKEASTORTSAPPSPPPPR 420
DB 685 KNSPFGNSALGPLGSGQPIRASNPDLRRT-----EPILSPLORTSSGSS-----730
QY 421 ATASPRSSGNIPSS-PTASGGSPSPRASLTGTGTASPTSLVSP-----NPEPPEKPV 475
DB 731 -----SSSTPSSQFSSQGGSPGSGAGS-----SERTVRANSKSEGSFVLPHPEA 777
QY 476 RTPKAXENENIHONPE-----ELCTSPILMTSQAASEPGEAK 513
DB 778 KVKPEESRDITRPSRPASYKKAIDEDLTALAKELRLRIETNRPMKVTDYSSSESE 837
QY 514 KMDKEKONKLIADSEGGD-OLQVSMVPPNNLTAPEPQEE 555
DB 838 SREHEEDGE-----SETHDGTAVSDIPRLIPTGAPGSGNEQ 874

```

Search completed: March 4, 2004, 17:41:16
Job time : 45.1083 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:39:06 ; Search time 11.3226 Seconds
(without alignments)
110.442 Million cell updates/sec

Title: US-10-069-540A-2_COPY_23_35
Perfect score: 61
Sequence: 1 RAQEKVLQKGLK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : PIR 78.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	61	100.0	482	2 JC5593	amphiphysin II2 -
2	61	100.0	682	1 S22700	amphiphysin - chic
3	61	100.0	695	2 S62400	amphiphysin (clone
4	41	67.2	570	1 C69985	probable DNA-depen
5	40	65.6	176	2 B75494	conserved hypotet
6	40	65.6	446	2 F83147	conserved hypotet
7	39	63.9	505	2 B92196	PTS system, IIBC c
8	39	63.9	510	2 G98062	phosphotransferase
9	39	63.9	516	2 T10000	cytochrome P450 (C
10	39	63.9	524	2 T09999	cytochrome P450 -
11	39	63.9	524	2 T09944	probable cytochrom
12	38	62.3	405	2 S68254	arrestin isoform 2
13	38	62.3	407	2 S68253	arrestin isoform 1
14	38	62.3	415	2 S68255	arrestin isoform 1
15	38	62.3	420	2 A47140	arrestin arr3L - b
16	38	62.3	427	2 A40735	TGF beta homolog d
17	38	62.3	439	2 C84981	hypothetical prote
18	38	62.3	461	2 T22946	hypothetical prote
19	38	62.3	474	1 D61410	conserved hypotet
20	38	62.3	474	1 C64801	ylea protein - Esc
21	38	62.3	474	2 E82261	conserved hypotet
22	38	62.3	474	2 F85566	hypothetical prote
23	38	62.3	474	2 C90716	ylea protein - Esc
24	38	62.3	488	2 AC0584	MiaB protein (prob
25	38	62.3	497	2 F82747	conserved hypotet
26	37	60.7	60	2 B61819	conserved hypotet
27	37	60.7	273	2 H70712	hypothetical prote
28	37	60.7	375	1 G64436	N-acetyl-gamma-glu
29	37	60.7	403	2 B69196	conserved hypotet

30	37	60.7	418	2 T23861	kynurenine-oxoglut
31	37	60.7	472	2 B90095	hypothetical prote
32	37	60.7	526	1 G71081	probable helicase
33	37	60.7	1208	2 T39068	coiled coil protei
34	37	60.7	1274	2 D84485	probable retroelem
35	37	60.7	1468	1 S30818	hypothetical prote
36	36	59.0	96	2 G69037	phosphoribosyl-ATP
37	36	59.0	285	2 I38248	steroidogenic acut
38	36	59.0	285	2 J64315	steroidogenic acut
39	36	59.0	296	2 F87411	hypothetical prote
40	36	59.0	381	2 B56607	arrestin homolog -
41	36	59.0	418	2 A34851	beta-arrestin, bra
42	36	59.0	418	2 B46682	beta-arrestin 1, s
43	36	59.0	418	2 B43404	beta-arrestin1 - r
44	36	59.0	442	2 C81978	hypothetical prote
45	36	59.0	442	2 C81034	conserved hypotet
46	36	59.0	462	2 C89770	hypothetical prote
47	36	59.0	500	2 T26078	hypothetical prote
48	36	59.0	856	2 A14110	Mg2+ transport ATP
49	36	59.0	933	2 T28995	hypothetical prote
50	36	59.0	1787	2 T20160	hypothetical prote
51	35	57.4	183	2 G70450	hypothetical prote
52	35	57.4	253	2 H31006	probable oxidoredu
53	35	57.4	253	2 A85851	probable oxidoredu
54	35	57.4	294	2 F87714	chromosome partiti
55	35	57.4	313	2 S61990	hypothetical prote
56	35	57.4	339	2 E86761	conserved hypotet
57	35	57.4	341	2 F82712	integral membrane
58	35	57.4	372	2 E81350	probable RNA nucle
59	35	57.4	375	2 A39777	41K blood stage an
60	35	57.4	406	2 E72366	conserved hypotet
61	35	57.4	409	2 S18984	arrestin - human (
62	35	57.4	410	2 A59279	beta-arrestin 2 -
63	35	57.4	413	2 G86181	hypothetical prote
64	35	57.4	433	2 A71912	glycerol-3-phospha
65	35	57.4	446	1 S57900	conserved hypotet
66	35	57.4	451	2 D82702	conserved hypotet
67	35	57.4	454	2 A81244	acetyl-CoA carboxy
68	35	57.4	454	2 A11606	acetyl-CoA carboxy
69	35	57.4	504	2 T35817	probable Glu-tRNA(
70	35	57.4	515	2 A81025	ATP synthase F1, a
71	35	57.4	515	2 A81970	H+-transporting tw
72	35	57.4	522	2 B71807	DNA repair protein
73	35	57.4	570	2 A75007	DNA mismatch recog
74	35	57.4	576	2 T22700	hypothetical prote
75	35	57.4	598	2 D95207	oligoendopeptidase
76	35	57.4	598	2 D98072	oligoendopeptidase
77	35	57.4	695	2 T40168	hypothetical prote
78	35	56.6	227	2 S05585	tropomyosin - huma
79	34	55.7	101	2 H97263	PTS system IIB com
80	34	55.7	145	2 A81935	hypothetical prote
81	34	55.7	164	2 T24200	hypothetical prote
82	34	55.7	173	2 D82771	hypothetical prote
83	34	55.7	239	2 T51686	probable transcrip
84	34	55.7	253	1 H64981	probable dehydroge
85	34	55.7	279	2 B87674	oxidoreductase, al
86	34	55.7	296	2 T06025	transcription fact
87	34	55.7	301	2 G71929	GTP-binding protei
88	34	55.7	302	2 E84584	GTP-binding protei
89	34	55.7	313	2 T00743	glutamyl tRNA synt
90	34	55.7	329	2 I64160	hypothetical prote
91	34	55.7	332	2 AC2282	group 2 sigma 70-t
92	34	55.7	341	2 H90267	arginine deiminase
93	34	55.7	361	2 A55081	arrestin 1 - blueb
94	34	55.7	363	2 T31460	probable magnesium
95	34	55.7	364	2 A34867	arrestin - fruit f
96	34	55.7	396	2 D82171	cystathionine beta
97	34	55.7	401	2 H72765	probable flap endo
98	34	55.7	401	2 A34856	49K photoreceptor
99	34	55.7	406	2 A50111	probable monooxyge
100	34	55.7	406	2 B81331	zinc proteinase-li
101	34	55.7	423	2 H86838	serine-tRNA ligase
102	34	55.7	455	2 G70136	heat shock protein

103 34 55.7 474 2 AH0319
 104 34 55.7 535 2 S40461
 105 34 55.7 535 2 S40462
 106 34 55.7 542 1 A70220
 107 34 55.7 545 2 T10662
 108 34 55.7 585 2 T10662
 109 34 55.7 609 1 G69843
 110 34 55.7 628 2 T44581
 111 34 55.7 657 2 G71377
 112 34 55.7 662 2 T04461
 113 34 55.7 666 2 F83340
 114 34 55.7 684 2 F85075
 115 34 55.7 775 2 E70320
 116 34 55.7 779 2 A86862
 117 34 55.7 818 2 T31464
 118 34 55.7 827 2 A90544
 119 34 55.7 855 2 E75191
 120 34 55.7 917 2 B81309
 121 34 55.7 1095 1 A31225
 122 34 55.7 1331 1 X0RTDH
 123 34 55.7 1335 1 X0MSDH
 124 34 55.7 1426 2 T00337
 125 33 54.1 77 2 B72271
 126 33 54.1 92 2 E64345
 127 33 54.1 94 2 D64446
 128 33 54.1 117 2 AB3298
 129 33 54.1 120 2 A81431
 130 33 54.1 141 2 AG2622
 131 33 54.1 141 2 G97404
 132 33 54.1 151 2 A75106
 133 33 54.1 165 2 AH1014
 134 33 54.1 172 2 JQ0391
 135 33 54.1 190 2 B72416
 136 33 54.1 256 2 G83953
 137 33 54.1 265 2 JC4509
 138 33 54.1 272 2 B71618
 139 33 54.1 277 2 C81231
 140 33 54.1 277 2 D82005
 141 33 54.1 280 2 A81746
 142 33 54.1 281 2 D71483
 143 33 54.1 284 2 A55455
 144 33 54.1 298 2 G90529
 145 33 54.1 318 1 D64417
 146 33 54.1 318 2 F84495
 147 33 54.1 318 2 T08695
 148 33 54.1 340 2 JC1357
 149 33 54.1 349 2 S03575
 150 33 54.1 380 2 C71698

ALIGNMENTS

RESULT 1
 JC5593
 amphiphysin II2 - human
 C:Species: Homo sapiens (man)
 C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jun-2000
 C:Accession: JC5593
 R:Tsutsui, K.; Maeda, Y.; Tsutsui, K.; Seki, S.; Tokunaga, A.
 Biochem. Biophys. Res. Commun. 236, 178-183, 1997
 A:Title: cDNA cloning of a novel amphiphysin isoform and tissue-specific expression of it
 A:Reference number: JC5593; MUID:97366618; PMID:9223448
 A:Accession: JC5593
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-482 <TSU>
 A:Cross-references: DBBJ:AF001383; NID:g2199534; PIDN:AA861363.1; PID:g2199535
 A:Experimental source: fetal brain
 C:Comment: This protein is involved in the synaptic vesicle recycling and in the regulation of autophagy
 C:Superfamily: amphiphysin; RVS161 protein homology
 F:16-275/Domain: RVS161 protein homology <RVS>
 F:410-481/Domain: SH3 #status predicted <SH3>

Query Match 100.0%; Score 61; DB 2; Length 482;
 Best Local Similarity 100.0%; Pred. No. 0.0074;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGKA 13
 |||||
 Db 24 RAQEKVLQKLGKA 36

RESULT 2

S22700
 amphiphysin - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S22700
 R:Lichte, B.; Veb, R.W.; Meyer, H.E.; Killmann, M.W.
 EMBO J. 11, 2521-2530, 1992
 A:Title: Amphiphysin, a novel protein associated with synaptic vesicles.
 A:Reference number: S22700; MUID:92331604; PMID:1628617
 A:Accession: S22700
 A:Molecule type: mRNA
 A:Residues: 1-682 <LIC>
 A:Cross-references: EMBL:X60422; NID:G62842; PIDN:CAA42953.1; PID:G62843
 C:Superfamily: amphiphysin; RVS161 protein homology
 F:11-270/Domain: RVS161 protein homology <RVS>

Query Match 100.0%; Score 61; DB 1; Length 682;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGKA 13
 |||||
 Db 19 RAQEKVLQKLGKA 31

RESULT 3

S62400
 amphiphysin (clone 22-2) - human
 C:Species: Homo sapiens (man)
 C>Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C:Accession: S62400; I37166
 R:David, C.; Solimena, M.; de Camilli, P.
 FEBS Lett. 351, 73-79, 1994
 A:Title: Autoimmunity in Sciff-Man Syndrome with breast cancer is targeted to the C-term
 A:Reference number: S48686; MUID:94357284; PMID:8076697
 A:Accession: S62400
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-695 <DAV>
 A:Cross-references: EMBL:U07616; NID:G550449; PIDN:AAA21865.1; PID:G550450
 R:Yamamoto, R.; Li, X.; Winter, S.; Francke, U.; Kilimann, M.W.
 Hum. Mol. Genet. 4, 265-268, 1995
 A:Title: Primary structure of human amphiphysin, the dominant autoantigen of paraneoplas
 A:Reference number: I37166; MUID:95276740; PMID:7757077
 A:Accession: I37166
 A:Status: preliminary; translated from GB/EMBL/DBBJ
 A:Molecule type: mRNA
 A:Residues: 1-695 <RES>
 A:Cross-references: EMBL:X81438; NID:G662991; PIDN:CAA57197.1; PID:G662992
 C:Genetics:
 A:Gene: GDB:AMPH
 A:Cross-references: GDB:386990
 A:Map position: 7p14-7p13
 C:Superfamily: amphiphysin; RVS161 protein homology
 F:11-270/Domain: RVS161 protein homology <RVS>

Query Match 100.0%; Score 61; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGKA 13
 |||||

Y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 193, 5709-5717, 2001
 A:Authors: tang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: G98062
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-510 <KUR>
 A:Cross-references: GB:A007317; PIDN:AAL00332.1; PID:G15459191; GSPDB:GN00174
 C:Genetics: PTS-EII
 A:Gene: PTS-EII
 C:Superfamily: phosphotransferase system glucose-specific enzyme II, factor II; phosphotransferase
 C:Keywords: phosphotransferase

Query Match 63.9%; Score 39; DB 2; Length 510;
 Best Local Similarity 88.9%; Pred. No. 54;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KYLQKLGKA 13
 |||:||||
 DB 8 KYLQKVGKA 16
 |||:||||

RESULT 9
 T10000
 cytochrome P450 (CYP72C) - Madagascar periwinkle (fragment)
 C:Species: Catharanthus roseus (Madagascar periwinkle)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
 C:Accession: T10000
 R:Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-
 Plant Sci. 96, 129-136, 1994
 A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth
 A:Reference number: Z16915
 A:Accession: T10000
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-516 <MAN>
 A:Cross-references: EMBL:L19075; NID:G404689; PID:G404690
 A:Experimental source: cv. cp3
 C:Genetics:
 A:Gene: CYP72C
 C:Superfamily: unassigned cytochrome P450; cytochrome P450 homolog
 C:Keywords: heme; iron; metalloprotein
 F:318-481/Domain: cytochrome P450 homolog <P45>
 F:459/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 63.9%; Score 39; DB 2; Length 516;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RACEKVLQKLGK 12
 |||:||||
 DB 346 RAREVLQAFGK 357
 |||:||||

RESULT 10
 T09999
 cytochrome P450 - Madagascar periwinkle
 C:Species: Catharanthus roseus (Madagascar periwinkle)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
 C:Accession: T09999
 R:Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-
 Plant Sci. 96, 129-136, 1994
 A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth
 A:Reference number: Z16915
 A:Accession: T09999
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-524 <MAN>
 A:Cross-references: EMBL:L19074; NID:G404687; PID:G404688
 A:Experimental source: cv. cp3
 C:Genetics:

A:Gene: CYP72B
 A:Introns: 96/1; 170/3; 252/2; 381/3
 C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homolog
 C:Keywords: heme; iron; metalloprotein
 F:329-492/Domain: cytochrome P450 homolog <P45>
 F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 63.9%; Score 39; DB 2; Length 524;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RACEKVLQKLGK 12
 |||:||||
 DB 357 RAREVLQAFGK 368
 |||:||||

RESULT 11
 T09944
 probable cytochrome P450 protein - Madagascar periwinkle
 N:Alternate names: CYP72 protein
 C:Species: Catharanthus roseus (Madagascar periwinkle)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
 C:Accession: T09944
 R:vetter, H.P.; Mangold, U.; Schroeder, G.; Warner, F.J.; Werck-Reichhart, D.; Schroeder
 Plant Physiol. 100, 998-1007, 1992
 A:Title: Molecular analysis and heterologous expression of an inducible cytochrome P-450
 A:Reference number: Z16902
 A:Accession: T09944
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-524 <VET>
 A:Cross-references: EMBL:L10081; NID:G167483; PID:G167484
 C:Genetics:
 A:Gene: CYP72
 C:Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homolog
 C:Keywords: heme; iron; metalloprotein
 F:329-492/Domain: cytochrome P450 homolog <P45>
 F:470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 63.9%; Score 39; DB 2; Length 524;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RACEKVLQKLGK 12
 |||:||||
 DB 357 RAREVLQAFGK 368
 |||:||||

RESULT 12
 S68254
 arrestin isoform 2S, erythrocyte - rainbow trout
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C:Accession: S68254
 R:Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.
 Biochem. J. 316, 497-506, 1996
 A:Title: Trout red blood cell arrestin (TRCarr), a novel member of the arrestin family:
 A:Reference number: S68253; MUID:96257743; PMID:8687393
 A:Accession: S68254
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-405 <JAH>
 A:Cross-references: GB:U48410
 C:Superfamily: arrestin

Query Match 62.3%; Score 38; DB 2; Length 405;
 Best Local Similarity 58.3%; Pred. No. 64;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RACEKVLQKLGK 12
 |||:||||
 DB 100 RQERLUKLGQ 111
 |||:||||

C:Comment: This protein plays a role in the regulation of G-protein-coupled receptors.

C:Superfamily: arrestin
F:1-420/Product: arrestin arr3L #status predicted <MAT>
F:1-362,374-420/Product: arrestin arr3S #status predicted <MA2>

Query Match 62.3%; Score 38; DB 2; Length 420;
Best Local Similarity 58.3%; Pred. No. 67;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
Db 100 RQERLLKLGQ 111

RESULT 16

A40735

TGP beta homolog dsl-1 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C:Accession: A40735

R:Basler, K.; Edlund, T.; Jessell, T.M.; Yamada, T.

Cell 73, 687-702, 1993

A:Title: Control of cell pattern in the neural tube: regulation of cell differentiation

A:Reference number: A40735; MUID:93272310; PMID:7916656

A:Accession: A40735

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-427 <BAS>

A:Cross-references: GB:112032; NID:G304379; PIDN:AAA48752.1; PID:G304380

A:Experimental source: spinal cord

A:Note: sequence extracted from NCBI backbone (NCBIN:132680, NCBI:P:132681)

C:Superfamily: inhibin

Query Match 62.3%; Score 38; DB 2; Length 427;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QEKVLQKLGK 12
Db 282 QESVLRKLGK 291

RESULT 17

C84981

Hypothetical protein [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: C84981

R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A

A:Reference number: A84930; MUID:20445173; PMID:10993077

A:Accession: C84981

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-439 <STO>

A:Cross-references: GB:AP000398; GSPDB:GN00144

A:Experimental source: strain APS

C:Genetics:

A:Gene: yLeA; BU441

C:Superfamily: conserved hypothetical protein b0835

Query Match 62.3%; Score 38; DB 2; Length 439;
Best Local Similarity 58.3%; Pred. No. 70;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
Db 53 KAQEKVFLQGR 64

RESULT 18

T22946

RESULT 13

S68253

arrestin isoform 1S, erythrocyte - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999

C:Accession: S68253

R:Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.

Biochem. J. 316, 497-506, 1996

A:Title: Trout red blood cell arrestin (TRCGarr), a novel member of the arrestin family:

A:Reference number: S68253; MUID:96257743; PMID:8687393

A:Accession: S68253

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-407 <JAH>

A:Cross-references: GB:U48410; NID:G1215723; PIDN:AAB16954.1; PID:G1215724

C:Superfamily: arrestin

Query Match 62.3%; Score 38; DB 2; Length 407;
Best Local Similarity 58.3%; Pred. No. 65;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
Db 100 RQERLLKLGQ 111

RESULT 14

S68255

arrestin isoform 1L, erythrocyte - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S68255

R:Jahns, R.; Borgese, F.; Lindenthal, S.; Straub, A.; Motaïs, R.; Fievet, B.

Biochem. J. 316, 497-506, 1996

A:Title: Trout red blood cell arrestin (TRCGarr), a novel member of the arrestin family:

A:Reference number: S68253; MUID:96257743; PMID:8687393

A:Accession: S68255

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-415 <JAH>

A:Cross-references: GB:U48410

C:Superfamily: arrestin

Query Match 62.3%; Score 38; DB 2; Length 415;
Best Local Similarity 58.3%; Pred. No. 66;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
Db 100 RQERLLKLGQ 111

RESULT 15

A47140

arrestin arr3L - bovine

N:Contains: arrestin arr3S

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Dec-1994 #sequence_revision 27-Jun-1994 #text_change 13-Sep-1998

C:Accession: A47140; B47140; JC2051

R:Stearns-Marr, R.; Gurevich, V.V.; Goldsmith, P.; Bodine, R.C.; Sanders, C.; Donoso, L.A.

J. Biol. Chem. 268, 15640-15648, 1993

A:Title: Polypeptide variants of beta-arrestin and arrestin3.

A:Reference number: A47140; MUID:93340166; PMID:8340398

A:Accession: A47140

A:Molecule type: mRNA

A:Residues: 1-420 <STE>

A:Cross-references: GB:LI4641

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBIN:136006, NCBI:P:136007)

A:Accession: B47140

A:Molecule type: mRNA

A:Residues: 1-362,374-420 <ST2>

hypothetical protein F58G6.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T22946
 R:Illyod, C.

submitted to the EMBL Data Library, December 1995

A:Reference number: Z19641

A:Accession: T22946

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-461 <WIL>

A:Cross-references: EMBL:Z68217; PIDN:CAA92465.1; GSPDB:GN00022; CESP:F58G6.1

A:Experimental source: clone F58G6

C:Genetics:

A:Gene: CESP:F58G6.1

A:Map position: 4

A:Introns: 19/3; 57/3; 96/3; 130/3; 157/3; 186/3; 219/3; 271/3; 302/3; 335/3; 357/3

C:Superfamily: amphiphysin; RVSL161 protein homology

Query Match 62.3%; Score 38; DB 2; Length 461;

Best Local Similarity 53.8%; Pred. No. 73;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 13

DB 15 RTKEKLEGGK 27

RESULT 19

D64140

conserved hypothetical protein HI0019 - Haemophilus influenzae

C:Species: Haemophilus influenzae

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000

C:Accession: D64140

R:Flaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: D64140

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-474 <TIGR>

A:Cross-references: GB:U32687; GB:U42023; NID:gl572955; PIDN:AAC21697.1; PID:gl572963; T

A:Experimental source: strain Rd KW20

C:Superfamily: conserved hypothetical protein b0835

Query Match 62.3%; Score 38; DB 1; Length 474;

Best Local Similarity 58.3%; Pred. No. 75;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12

DB 54 KAQEKVPHQLGR 65

RESULT 20

C64801

yleA protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002

C:Accession: C64801

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C64801

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-474 <BLAT>

A:Cross-references: GB:AE000170; GB:U00096; NID:gl786875; PIDN:AAC73762.1; PID:gl786882;

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: yleA

C:Superfamily: conserved hypothetical protein b0835

Query Match 62.3%; Score 38; DB 1; Length 474;

Best Local Similarity 58.3%; Pred. No. 75;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12

DB 54 KAQEKVPHQLGR 65

RESULT 21

E82251

conserved hypothetical protein VC0962 [imported] - Vibrio cholerae (strain N16961 serogr

C:Species: Vibrio cholerae

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: E82251

R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P

l., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: E82251

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-474 <HEI>

A:Cross-references: GB:AE004177; GB:AE003852; NID:g9655398; PIDN:AAF94124.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0962

A:Map position: 1

C:Superfamily: conserved hypothetical protein b0835

Query Match 62.3%; Score 38; DB 2; Length 474;

Best Local Similarity 58.3%; Pred. No. 75;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12

DB 54 KAQEKVPHQLGR 65

RESULT 22

F85566

hypothetical protein yleA [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: F85566

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F85566

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-474 <STO>

A:Cross-references: GB:AE005174; NID:gl2513570; PIDN:AAG54994.1; GSPDB:GN00145; UWGP:Z08

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: yleA

C:Superfamily: conserved hypothetical protein b0835

Query Match 62.3%; Score 38; DB 2; Length 474;

Best Local Similarity 58.3%; Pred. No. 75;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12


```

Db      54 KAQEKVFHQLGR 65
      :||||| :||:
      54 KAQEKVFHQLGR 65

RESULT 23
C90716
YleA protein - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
C:Accession: C90716
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
  Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
  DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:2115231; PMID:11258796
A:Accession: C90716
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-474 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA834122.1; PID:gl3360157; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC90699
C:Superfamily: conserved hypothetical protein b0835

Query Match      62.3%; Score 38; DB 2; Length 474;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 RAQEKVLOKLGK 12
      :||||| :||:
      54 KAQEKVFHQLGR 65

Db      54 KAQEKVFHQLGR 65

RESULT 24
AC0584
MiaB protein (probable tRNA-thiotransferase (or tRNA-methylthiotransferase)) miaB [impor
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0584
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
  th, T.; Conneron, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
  S.; Moule, S.; O'Garra, P.
  Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
  A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
  A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0584
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-488 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05141.1; PID:gl6501914; GSPDB:GN00176
C:Genetics:
A:Gene: miaB
C:Superfamily: conserved hypothetical protein b0835

Query Match      62.3%; Score 38; DB 2; Length 488;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 RAQEKVLOKLGK 12
      :||||| :||:
      68 KAQEKVFHQLGR 79

Db      68 KAQEKVFHQLGR 79

RESULT 25
F82747
conserved hypothetical protein XF0906 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: F82747
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
  Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82747
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <SIM>
A:Cross-references: GB:AE003930; GB:AE003849; NID:g9105819; PIDN:AAF83716.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; F
  Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, I
  as-Neto, E.; Docena, C.; El-Dorri, H.; Pacincani, A.P.; Ferreira, A.J.S.
  submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
  J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
  chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
  A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
  F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.;
  Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasal
  A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
  M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; V
  A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0906
C:Superfamily: conserved hypothetical protein b0835

Query Match      62.3%; Score 38; DB 2; Length 497;
Best Local Similarity 58.3%; Pred. No. 79;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 RAQEKVLOKLGK 12
      :||||| :||:
      99 KAQEKVFHQLGR 110

Db      99 KAQEKVFHQLGR 110

RESULT 26
B69189
conserved hypothetical protein MTH67 / MTH82 - Methanobacterium thermoautotrophicum (str
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C:Accession: B69189; E69209
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
  Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.
  ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
  J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: B69189
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-60 <MTH>
A:Cross-references: GB:AE000798; GB:AE000799; GB:AE000666; NID:g2621112; PIDN:AAB84588.1
A:Experimental source: strain Delta H
C:Genetics: CPY1
A:Accession: B69209
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-60 <MTH>
A:Cross-references: GB:AE000666; NID:g2621094; PIDN:AAB84581.1; PID:g2621111
A:Experimental source: strain Delta H
C:Genetics: CPY2
A:Gene: MTH67
C:Genetics: <CPY2>
A:Gene: MTH82

Query Match      60.7%; Score 37; DB 2; Length 60;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 QEKVLOKLGK 12

```

Db 2 QGKTLQKLGK 11
| | | | |
RESULT 27
H70712
hypothetical protein rv1501 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: H70712
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtrooyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: H70712
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-273 <COL>
A:Cross-references: GB:Z79701; GB:AL123456; NID:g3261635; PIDN:CAB02015.1; PID:e264130;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: rv1501
Query Match 60.7%; Score 37; DB 2; Length 273;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 RAQKVQLQKLGK 12
| | | | |
Db 45 RVQERILTEIGK 56
| | | | |
RESULT 28
G64436
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: G64436
R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: G64436
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-375 <BUL>
A:Cross-references: GB:U67552; GB:L77117; NID:g1591737; PIDN:AAB99099.1; PID:g1591740; T
C:Genetics:
A:Map position: REV1036979-1035852
A:Start codon: TTG
A:Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase
C:Keywords: oxidoreductase
Query Match 60.7%; Score 37; DB 1; Length 375;
Best Local Similarity 80.0%; Pred. No. 89;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 EKVLQKLGKA 13
| | | | |
Db 248 EXELKGLGKA 257
| | | | |
RESULT 29
B69196
conserved hypothetical protein MTH72 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jan-2000
C:Accession: B69196
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicair, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:93711463
A:Accession: B69196
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-403 <MTH>
A:Cross-references: GB:AE000798; GB:AE000666; NID:g2621094; PIDN:AAB84576.1; PID:g2621110
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH72
A:Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat h
F16-49/Domain: tetratricopeptide repeat homology <TT01>
F50-83/Domain: tetratricopeptide repeat homology <TT02>
F84-117/Domain: tetratricopeptide repeat homology <TT03>
F118-151/Domain: tetratricopeptide repeat homology <TT04>
F152-185/Domain: tetratricopeptide repeat homology <TT05>
F186-219/Domain: tetratricopeptide repeat homology <TT06>
F220-253/Domain: tetratricopeptide repeat homology <TT07>
F254-287/Domain: tetratricopeptide repeat homology <TT08>
F288-321/Domain: tetratricopeptide repeat homology <TT09>
F322-355/Domain: tetratricopeptide repeat homology <TT10>
F356-389/Domain: tetratricopeptide repeat homology <TT11>
Query Match 60.7%; Score 37; DB 2; Length 403;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 QEKVLQKLGK 12
| | | | |
Db 362 QGKTLQKLGK 371
| | | | |
RESULT 30
T23861
kynurenine-oxoglutarate transaminase (EC 2.6.1.7) / glutamine-phenylpyruvate transaminase
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jun-2002
C:Accession: T23861
R:Hembry, C.
Submitted to the EMBL Data Library, February 1996
A:Reference number: Z19809
A:Accession: T23861
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-418 <WIL>
A:Cross-references: EMBL:Z69793; PIDN:CAA93673.1; GSPDB:GN00028; CESP:R03A10.4
A:Experimental source: clone R03A10
C:Genetics:
A:Gene: CESP:R03A10.4
A:Map position: X
A:Introns: 38/2; 142/1; 248/1; 348/1
A:Superfamily: aspartate transaminase
C:Keywords: aminotransferase
Query Match 60.7%; Score 37; DB 2; Length 418;
Best Local Similarity 63.6%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 AOEKVLQKLGK 12
| | | | |
Db 407 AAEILKLGK 417
| | | | |
RESULT 31
B90095
hypothetical protein orf472 [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A>Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: B90095
 R:Doughlas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Ren
 Nature 410, 1091-1096, 2001
 A>Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference numbers: A99082; MUID:11323671; PMID:11323671
 A:Accession: B90095
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-472 <DOU>
 A:Cross-references: GB:AF165818; NID:913794515; PIDN:AAK39890.1; GSPDB:GN00150
 C:Genetics:
 A:Gene: orf472
 A:Map position: 1
 A:Genome: nucleomorph
 C:Keywords: nucleomorph

Query Match 60.7%; Score 37; DB 2; Length 472;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 QEKVLQKLG 11
 DB 461 EKKVLQKIG 469

RESULT 32
 G71081
 probable helicase protein PH0917 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001
 C:Accession: G71081
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: G71081
 A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-526 <KAW>
 A:Cross-references: GB:AP000004; NID:93236131; PIDN:BAA30013.1; PID:93257330
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0917
 C:Superfamily: Pyrococcus horikoshii probable helicase PH0917
 C:Keywords: ATP; nucleotide binding; P-loop
 P:54-61/Region: nucleotide-binding motif A (P-loop)
 P:165-170/Region: nucleotide-binding motif B
 P:165-172/Region: DEAH motif

Query Match 60.7%; Score 37; DB 1; Length 526;
 Best Local Similarity 69.2%; Pred. No. 1.2e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 DB 11 RAFEDALQKLAKA 23

RESULT 33
 T39068
 coiled coil protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T39068
 R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Connor, R.E.; Wood, V.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: 221825
 A:Accession: T39068
 A>Status: Preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA

A:Residues: 1-1208 <MUR>
 A:Cross-references: EMBL:Z81317; PIDN:CA03608.1; GSPDB:GN00066; SPDB:SPAC699.06c
 A:Experimental source: strain 972h-; cosmid c699
 C:Genetics:
 A:Gene: SPDB:SPAC699.06c
 A:Map position: 1

Query Match 60.7%; Score 37; DB 2; Length 1208;
 Best Local Similarity 58.3%; Pred. No. 2.8e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
 DB 152 REQKVLKVS 163

RESULT 34
 D84485
 probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: D84485
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: D84485
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1274 <STO>
 A:Cross-references: GB:AE002093; NID:94309763; PIDN:AAD15532.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: Atg07400
 A:Map position: 2

Query Match 60.7%; Score 37; DB 2; Length 1274;
 Best Local Similarity 70.0%; Pred. No. 2.9e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 EKVQLKLGKA 13
 DB 1233 EKVLQVQGA 1242

RESULT 35
 S30818
 hypothetical protein YER164w - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Dec-2002
 C:Accession: S30818; S50667
 R:Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor,
 submitted to the EMBL Data Library, February 1993
 A:Reference number: S30812
 A:Accession: S30818
 A:Molecule type: DNA
 A:Residues: 1-1468 <MUL>
 A:Cross-references: GB:U18917; EMBL:L10718; NID:9603377; PIDN:AA64691.1; PID:9603404
 R:Dietrich, F.S.
 submitted to the EMBL Data Library, December 1994
 A:Description: The sequence of S. cerevisiae cosmids 8229, 9115, 9132, 9981, and lambda
 A:Reference number: S50667
 A:Accession: S50667
 A:Molecule type: DNA
 A:Residues: 1-1468 <DIE>
 A:Cross-references: EMBL:U18917; NID:9603377; PIDN:AA64691.1; PID:9603404; GSPDB:GN0000
 C:Genetics:
 A:Gene: SGD:CHD1; MIPS:YER164w
 A:Cross-references: SGD:S0000966; MIPS:YER164w
 A:Map position: 5R
 C:Superfamily: chromodomain helicase CHD1; chromobox homology
 C:Keywords: DNA binding; nucleus

F:195-233/Domain: chromobox homology <CB1>
F:285-327/Domain: chromobox homology <CB2>

Query Match 60.7%; Score 37; DB 1; Length 1468;
Best Local Similarity 70.0%; Pred. NO. 3.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQEVLQKLG 11
|:|:|:|:|
DB 668 AEERVLQKFG 677

RESULT 36

GC9037
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 03-Jun-2002
C:Accession: G69037
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Ji, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional
A:Reference number: AG9000; MUID:98037514; PMID:9371463
A:Accession: G69037
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-96 <MTH>
A:Cross-references: GB:AB000893; GB:AB000666; NID:g2622375; PIDN:AA885765.1; PID:g262239
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH283
C:Superfamily: phosphoribosyl-ATP pyrophosphatase h1se
C:Keywords: hydrolase
F:8-80/Region: h1se protein similarity

Query Match 59.0%; Score 36; DB 2; Length 96;
Best Local Similarity 45.5%; Pred. NO. 35;
Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 AQEVLQKLG 12
|:|:|:|:|
DB 37 AEDKLEKIGE 47

RESULT 37

I38248
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I38248; I38896
R:Sugawara, T.; Lin, D.; Holt, J.A.; Martin, K.O.; Javitt, N.B.; Miller, W.L.; Strauss, B.
Biochemistry 34, 12506-12512, 1995
A:Title: Structure of the human steroidogenic acute regulatory protein (STAR) gene: STAR
A:Reference number: I38248; MUID:96038208; PMID:7547998
A:Accession: I38248
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-285 <RES>
A:Cross-references: EMBL:U29105; NID:gl041696; PIDN:AAC50234.1; PID:g1041698
R:Sugawara, T.; Holt, J.A.; Driscoll, D.; Strauss III, J.F.; Lin, D.; Miller, W.L.; Patb
Proc. Natl. Acad. Sci. U.S.A. 92, 4778-4782, 1995
A:Title: Human steroidogenic acute regulatory protein: functional activity in COS-1 cell
A:Reference number: I38896; MUID:95281540; PMID:7761400
A:Accession: I38896
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-285 <RE2>
A:Cross-references: EMBL:U17280; NID:g727252; PIDN:AAC50141.1; PID:g727253
C:Genetics:
A:Gene: STAR
A:Cross-references: GDB:STAR; GDB:635457; OMIM:600617
A:Map position: sp11.2-sp11.2

A:Introns: 22/1; 60/1; 102/3; 155/3; 217/2; 248/3

Query Match 59.0%; Score 36; DB 2; Length 285;
Best Local Similarity 87.5%; Pred. NO. 1e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGK 12
|:|:|:|:|
DB 155 KVLQKLGK 162

RESULT 38

JC4315
steroidogenic acute regulatory protein - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 18-Jul-1997
C:Accession: JC4315
R:Hartung, S.; Rust, W.; Balvers, M.; Iwell, R.
Biochem. Biophys. Res. Commun. 215, 646-653, 1995
A:Title: Molecular cloning and in vivo expression of the bovine steroidogenic acute reg
A:Reference number: JC4315; MUID:96011827; PMID:7488004
A:Accession: JC4315
A:Molecule type: mRNA
A:Residues: 1-285 <HAR>
C:Comment: This protein is an acute controller of the rate-limiting transfer of cholesterol
C:Genetics:
A:Gene: STAR
F:226-264/Region: metalloproteinase-1 tissue inhibitor similarity

Query Match 59.0%; Score 36; DB 2; Length 285;
Best Local Similarity 87.5%; Pred. NO. 1e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLQKLGK 12
|:|:|:|:|
DB 155 KVLQKLGK 162

RESULT 39

P87411
hypothetical protein CCI309 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: P87411
R:Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolos
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11255967
A:Accession: P87411
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-296 <STO>
A:Cross-references: GB:AE005673; NID:gl3422650; PIDN:AAK23290.1; GSPDB:GN00148
C:Genetics:
A:Gene: CCI309

Query Match 59.0%; Score 36; DB 2; Length 296;
Best Local Similarity 58.3%; Pred. NO. 1.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RAQKVLQKLGK 12
|:|:|:|:|
DB 255 RGHAKLEKLGK 266

RESULT 40

B56607
arrestin homolog - tobacco budworm
C:Species: Heliothis virescens (tobacco budworm)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Sep-1998
C:Accession: B56607

QY 1 RAQEKVLQKLG 11
DB 316 RVGEKLLQKMG 326

K55001 43
 T28995
 hypothetical protein ZC513.4 - Caenorhabditis elegans
 C.Species: Caenorhabditis elegans
 C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C.Accession: T28995
 R.Wu, X.; Le, T.T.
 submitted to the EMBL Data Library, April 1996
 A.Description: The sequence of C. elegans cosmid ZC513.
 A.Reference number: Z20551
 A.Accession: T28995

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-933 <WUK>
A:Cross-references: EMBL:U53155; PIDN:AAC48266.1; GSPDB:GN00023; CESP:ZC513.4
A:Experimental source: strain Bristol N2; clone ZC513
C:Genetics:
A:Gene: CESP:ZC513.4
A:Map position: 5
A:Introns: 384/3; 425/2; 645/3; 689/3
C:Superfamily: valine-tRNA ligase

Query Match 59.0%; Score 36; DB 2; Length 933;
Best Local Similarity 63.6%; Pred. No. 3.2e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AQEKVLQKLGK 12
DB 322 AREKVIQLSE 332

RESULT 50
T20160
hypothetical protein T14G8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20160; T24924
R:McMurray, A.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19231
A:Accession: T20160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1787 <WIL>
A:Cross-references: EMBL:Z67881; PIDN:CAA91798.1; GSPDB:GN00028; CESP:T14G8.1
A:Experimental source: clone C52G5
R:Matthews, P.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19955
A:Accession: T24924
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1787 <W12>
A:Cross-references: EMBL:Z67884; PIDN:CAA91810.1; GSPDB:GN00028; CESP:T14G8.1
A:Experimental source: clone T14G8
C:Genetics:
A:Gene: CESP:T14G8.1
A:Map position: x
A:Introns: 112/3; 453/3; 597/3; 815/2; 1258/3; 1682/2; 1709/3; 1764/1

Query Match 59.0%; Score 36; DB 2; Length 1787;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QEKVLQKLGK 12
DB 1226 QETELQKLGK 1235

Search completed: March 4, 2004, 17:46:55
Job time : 16.3226 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:32:31 ; Search time 8.80645 Seconds

(without alignments)
76.865 Million cell updates/sec

Title: US-10-069-540A-2_COPY_23_35

Perfect score: 61

Sequence: 1 RAQKVLQKLGKA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	588	1 BIN1_MOUSE	O08539 mus musculus
2	61	100.0	588	1 BIN1_MOUSE	O08839 rattus norv
3	61	100.0	593	1 BIN1_HUMAN	O00499 homo sapien
4	61	100.0	682	1 AMPH_CHICK	P50478 gallus gall
5	61	100.0	683	1 AMPH_RAT	O08838 rattus norv
6	61	100.0	695	1 AMPH_HUMAN	P49418 homo sapien
7	40	65.6	446	1 Y310_PSEAE	O51470 pseudomonas
8	39	63.9	524	1 CP72_CATRO	O05047 catharanthu
9	38	62.3	405	1 ARR2_ONCMY	P51457 oncorhynchu
10	38	62.3	407	1 ARR1_ONCMY	P51466 oncorhynchu
11	38	62.3	415	1 ARR3_ONCMY	P51468 oncorhynchu
12	38	62.3	420	1 ARR2_BOVIN	P32120 bos taurus
13	38	62.3	427	1 DSL1_CHICK	P34822 gallus gall
14	38	62.3	439	1 Y426_BUCAP	O8K9C2 buchnera ap
15	38	62.3	439	1 Y441_BUCAI	P57516 buchnera ap
16	38	62.3	474	1 Y401_PASWU	O21699 pasteurella
17	38	62.3	474	1 YLEA_ECOLI	P77645 escherichia
18	38	62.3	474	1 YLEA_HAEIN	P71782 haemophilus
19	37	60.7	273	1 YF01_METCU	Q58496 methanobacteri
20	37	60.7	341	1 ARGC_METUA	Q50367 mycoplasma
21	37	60.7	362	1 P35_MYCPE	O50351 schizosacch
22	37	60.7	1208	1 PCPI_SCPEO	P32657 saccharomyc
23	37	60.7	1468	1 CHD1_YEAST	O87344 methanobact
24	36	59.0	96	1 HRS2_METTH	Q59f13 ginkgo bilo
25	36	59.0	155	1 RR7_GINBI	P70114 mesocricetu
26	36	59.0	284	1 STAR_MESAU	Q28918 bos taurus
27	36	59.0	285	1 STAR_BOVIN	O46689 equus cabal
28	36	59.0	285	1 STAR_HORSE	P49675 homo sapien
29	36	59.0	285	1 STAR_HUMAN	P79245 ovis aries
30	36	59.0	285	1 STAR_SHEEP	Q8R50 thermoanaer
31	36	59.0	298	1 ARRH_THETN	P55274 heliothis v
32	36	59.0	381	1 ARRH_HELVI	Q95223 oryctolagus
33	36	59.0	410	1 ARR1_RABIT	

34	59.0	418	1	ARR1_BOVIN	P17870 bos taurus
35	59.0	418	1	ARR1_HUMAN	P49407 homo sapien
36	59.0	418	1	ARR1_RAT	P29066 rattus norv
37	59.0	777	1	HEXA_PORGI	P49008 porphyromon
38	59.0	1787	1	CHD3_CABEL	Q22516 caenorhabdi
39	59.0	285	1	STAR_PIG	Q28996 sus scrofa
40	59.0	285	1	STAR_XENLA	Q94908 xenopus lae
41	59.0	294	1	PARE_CAUCR	O05190 caulobacter
42	59.0	313	1	Y006_YEAST	Q12094 saccharomyc
43	59.0	409	1	ARR2_HUMAN	P32121 homo sapien
44	59.0	410	1	ARR2_MOUSE	Q91Y14 mus musculu
45	59.0	410	1	ARR2_RAT	P29067 rattus norv
46	59.0	459	1	ARLY_OCEIH	O8elt9 oceanobacte
47	59.0	504	1	GATB_STRCO	Q22578 streptomyce
48	59.0	522	1	RECN_HELPJ	Q92180 helicobacte
49	59.0	636	1	NAF1_HUMAN	Q15025 homo sapien
50	59.0	647	1	NAF1_MOUSE	Q9WU08 mus musculu
51	59.0	253	1	YOHF_ECOLI	P33368 escherichia
52	59.0	285	1	STAR_BRARE	Q9dg10 brachydanio
53	59.0	301	1	ERA_HELPJ	Q9zlw0 helicobacte
54	59.0	301	1	ERA_HELPY	P56059 helicobacte
55	59.0	329	1	ISP8_HAEIN	P44916 haemophilus
56	59.0	351	1	FEN_AERPE	Q9Yfys aeropyrum p
57	59.0	363	1	ARR1_CALVI	P51486 calliphora
58	59.0	364	1	ARRA_DROME	P15372 drosophila
59	59.0	401	1	ARRB_DROME	P19107 drosophila
60	59.0	423	1	SYS_LACIA	Q9cex2 lactococcus
61	59.0	448	1	HSLU_BORBU	Q44772 borrelia bu
62	59.0	468	1	TIG_STRCO	Q9f314 streptomyce
63	59.0	469	1	LEU2_RALSO	Q8xxx3 ralstonia s
64	59.0	514	1	ATPA_THIFE	P41167 thiobacillu
65	59.0	535	1	TCE1_AVEA	P40412 avena sativ
66	59.0	535	1	TCE2_AVEA	P54411 avena sativ
67	59.0	535	1	TCPE_ARATH	Q84450 arabidopsis
68	59.0	539	1	CH60_FUSNP	O8GJ00 fusbacteri
69	59.0	574	1	C306_DROME	P98VW5 drosophila
70	59.0	585	1	C08A_RABIT	P98136 oryctolagus
71	59.0	609	1	PEPF_BACSU	O31605 bacillus su
72	59.0	657	1	GRAD_TREPA	O38062 treponema p
73	59.0	917	1	SVI_CAMJE	P13257 campylobact
74	59.0	1095	1	PIP1_DROME	P13217 drosophila
75	59.0	1330	1	XDH_RAT	P22385 rattus norv
76	59.0	1335	1	XDH_MOUSE	Q00519 mus musculu
77	59.0	1756	1	PEPL_HUMAN	O60437 homo sapien
78	59.0	80	1	CLVA_STYCL	P80710 styela clav
79	59.0	92	1	Y366_METJA	O57812 methanococc
80	59.0	120	1	RBFA_CAMJE	Q9p1z0 campylobact
81	59.0	138	1	ATPE_THETN	Q8rc14 thermoanaer
82	59.0	151	1	REG6_PTRAB	Q9v0y9 pyrococcus
83	59.0	172	1	MBEB_ECOLI	P13659 escherichia
84	59.0	175	1	CYT2_STOHE	P07845 stoichactis
85	59.0	265	1	FLIR_TREPA	P74932 treponema p
86	59.0	280	1	PARB_CHLMU	Q9pln9 chlamydia m
87	59.0	281	1	PARB_CHLTR	O84694 chlamydia t
88	59.0	281	1	STAR_MOUSE	P51557 mus musculu
89	59.0	318	1	Y940_METJA	Q58350 methanococc
90	59.0	349	1	RPAI_HALMO	P15349 halococcus
91	59.0	364	1	RSPD_LACLC	P58290 lactococcus
92	59.0	380	1	LPXB_RICPR	Q9zdk7 rickettsia
93	59.0	386	1	RPSD_LACLA	O84506 lactococcus
94	59.0	389	1	CC37_DROME	Q24276 drosophila
95	59.0	396	1	ARRS_RANCA	P51478 rana gatesb
96	59.0	396	1	ARRS_RANPI	P51479 rana pipien
97	59.0	396	1	ARRS_XENLA	P51477 xenopus lae
98	59.0	397	1	ACK2_VIBPA	Q871j5 vibrio para
99	59.0	397	1	ACK2_VIBVU	Q8d7k4 vibrio vuln
100	59.0	400	1	ARRB_CALVI	P51487 calliphora
101	59.0	401	1	ARRB_DROMI	P19108 drosophila
102	59.0	404	1	ARRS_BOVIN	P08168 bos taurus
103	59.0	429	1	GDF2_HUMAN	Q9UK05 homo sapien
104	59.0	448	1	ZFG1_CHICK	Q92010 gallus gall
105	59.0	449	1	ZFG1_HUMAN	O43829 homo sapien
106	59.0	449	1	ZFG1_MOUSE	Q08376 mus musculu

```

107 33 54.1 459 1 ARLY_BUCAI
108 33 54.1 500 1 DDC_CATRO
109 33 54.1 515 1 YMOO_YEAST
110 33 54.1 612 1 Y640_SYNY3
111 33 54.1 814 1 FADE_ECOS7
112 33 54.1 814 1 FADE_ECOS7
113 33 54.1 814 1 FADE_ECOS7
114 33 54.1 822 1 YF1_YEAST
115 33 54.1 838 1 HIS2_CANAL
116 33 54.1 880 1 SYA_ANASP
117 33 54.1 971 1 RPA1_HALHA
118 33 54.1 1272 1 Y228_METJA
119 33 54.1 1302 1 UBPY_CABEL
120 33 54.1 1444 1 DPO3_LISIN
121 33 54.1 1444 1 DPO3_LISIN
122 33 54.1 1444 1 DPO3_LISIN
123 33 54.1 2179 1 POLG_HRV14
124 33 54.1 3023 1 POLG_HRV14
125 33 54.1 5430 1 MACF_HUMAN
126 33 54.1 5938 1 MACF_HUMAN
127 32 52.5 145 1 HBB2_TELPE
128 32 52.5 158 1 Y972_THETU
129 32 52.5 160 1 SSRP_MYCTU
130 32 52.5 164 1 UBI1_ECOLI
131 32 52.5 179 1 170K_TVPS
132 32 52.5 185 1 PORC_PYRFU
133 32 52.5 203 1 ARDE_DICDI
134 32 52.5 219 1 FLP_LACCA
135 32 52.5 223 1 GIBD_CORGL
136 32 52.5 229 1 UCK_CABEL
137 32 52.5 236 1 PYRF_BUCBP
138 32 52.5 238 1 PYRF_BRUME
139 32 52.5 238 1 PYRF_BRUSU
140 32 52.5 241 1 CYSH_XANAC
141 32 52.5 246 1 FASG_THEMA
142 32 52.5 247 1 F4828_SPIPL
143 32 52.5 270 1 Y980_THETN
144 32 52.5 284 1 STAR_RAT
145 32 52.5 284 1 SUHA_VACPA
146 32 52.5 289 1 PNPH_HUMAN
147 32 52.5 360 1 MTLG_MTCPU
148 32 52.5 368 1 RPSD_STPAAN
149 32 52.5 368 1 RPSD_STPAAN
150 32 52.5 371 1 RPSA_BACSU
151 32 52.5 372 1 RPSA_BACHD

P57159 buchnera ap
P17770 catharanthu
Q03264 synchococyt
P72958 synchococyt
Q8x7r2 escherichia
Q47146 escherichia
Q82x17 salmoneilla
P47046 saccharomyc
O74712 candida alb
Q8yud4 anabaena sp
P15350 halobacteri
Q60287 methanococ
Q09931 caenorhabdi
Q92c34 listeria in
Q8v7g1 listeria mo
P03303 h genome po
P09814 t genome po
Q9upb1 homo sapien
P96pk2 telmatobius
P83114 thermobacter
Q8rb52 thermobacter
P96294 mycobacteri
P26602 escherichia
P05079 tobaccu rat
Q51799 p pyruvate/
P36416 dictyosteli
P29284 lactobacilli
Q8nl53 corynebacte
Q17413 caenorhabdi
Q89a16 buchnera ap
Q8ye79 brucella me
Q8rfw9 brucella su
Q8phc7 xanthomonas
Q9x248 thermotoga
P34828 spirulina p
Q8rb44 thermococci
P97826 rattus norv
P52842 macaca fasc
P00491 homo sapien
Q98ph2 mycoplasma
P26766 staphylococ
Q99tt5 staphylococ
P06224 bacillus su
O66381 bacillus ha

SEQUENCE FROM N.A. (ISOFORM 1).
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=98294438; PubMed=9630982;
Sparks A.B., Hoffman N.G., McConnell S.J., Fowlkes D.M., Kay B.K.;
"Cloning of ligand targets: systematic isolation of SH3 domain-
containing proteins.";
Nat. Biotechnol. 14:741-744 (1996).
[3]
INTERACTION WITH SH3GLBL1.
MEDLINE=22456649; PubMed=12456676;
Modregger J., Schmidt A.A., Ritter B., Hutterer W.B., Plomann M.;
"Characterization of endophilin B1b, a brain-specific
membrane-associated lysophosphatidic acid acyl transferase with
properties distinct from endophilin A1.";
J. Biol. Chem. 278:4160-4167 (2003).
-!- FUNCTION: May be involved in regulation of synaptic vesicle
endocytosis. May act as a tumor suppressor and inhibits
malignant cell transformation.
-!- SUBUNIT: Heterodimer with AMPH (By similarity). Binds to SYNJ1 and
DNM1 through its SH3 domain, and to clathrin through a region
outside of the SH3 domain. Also binds to alpha-adaptin. Interacts
with the N-terminal transactivation domain of MYC in a manner
requiring the integrity of the conserved MYC box regions 1 and 2.
Binds SH3GLBL1.
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=BRAMP2;
IsoId=O08539-1; Sequence=Displayed;
Name=2; Synonyms=SH3P9;
IsoId=O08539-2; Sequence=VSP 000254; VSP 000255;
-!- TISSUE SPECIFICITY: Isoform 1 is expressed mainly in the
brain. Isoform 2 is widely expressed.
-!- PTM: Phosphorylated by protein kinase C (By similarity).
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 SH3 domain.
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
EMBL; U86405; AAC53318.1; -
EMBL; U60884; AAC52661.1; -
DR MGD; MGI:108092; Biol.
InterPro; IPR003005; Amphiphysin.
InterPro; IPR006632; BAR.
InterPro; IPR004148; BAR_dom.
InterPro; IPR001452; SH3.
Pfam; PF03114; BAR; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR01351; AMPHIPHYSIN.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
SMART; SM00721; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Alternative splicing; SH3 domain; Coiled coil; Endocytosis;
Anti-oncogene; Differentiation; Phosphorylation.
DOMAIN 15 42
DOMAIN 193 274
DOMAIN 379 422
DOMAIN 515 588
DOMAIN 174 204
Missing (in isoform 2).
FTID-VSP 000254.
VARSPLIC 335 457
Missing (in isoform 2).
FTID-VSP 000255.
SEQUENCE 588 AA; 64470 MW; 63CA362461500F38 CRC64;

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Query Match 100.0%; Score 61; DB 1; Length 588;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 DB 24 RAQEKVLQKLGKA 36

RESULT 2
 BIN1_RAT
 ID BIN1_RAT STANDARD; PRT; 588 AA.
 AC C08839;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Myc box dependent interacting protein 1 (Bridging integrator 1)
 DE (Amphiphysin-like protein) (Amphiphysin II).
 GN BIN1 OR AMPHL OR AMPH2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., SUBUNIT, AND ALTERNATIVE SPLICING.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex, and Kidney;
 RX MEDLINE=98069145; PubMed=9348539;
 RA Wigge P., Kohler K., Hunt S., Doyle C., McMahon H.T.;
 RT "Amphiphysin heterodimers: potential role in clathrin-mediated
 endocytosis."
 RL Mol. Biol. Cell 8:2003-2015(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM AMPH2-1).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=97424383; PubMed=9280305;
 RA McMahon H.T., Wigge P., Smith C.;
 RT "Clathrin interacts specifically with amphiphysin and is displaced by
 dynamin."
 RL FEBS Lett. 413:319-322(1997).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 506-588, FUNCTION, AND
 INTERACTION WITH DNMI.
 RX MEDLINE=98409533; PubMed=9736607;
 RA Owen D.J., Wigge P., Vallis Y., Moore J.D.A., Evans P.R.,
 RA McMahon H.T.;
 RT "Crystal structure of the amphiphysin-2 SH3 domain and its role in the
 prevention of dynamin ring formation."
 RL EMBO J. 17:5273-5285(1998).
 CC -!- FUNCTION: May be involved in regulation of synaptic vesicle
 endocytosis. May act as a tumor suppressor and inhibits
 malignant cell transformation.
 CC -!- SUBUNIT: Heterodimer with AMPH. Binds SH3GLB1 (By similarity).
 CC Binds to SYN1 and DNMI through its SH3 domain, and to clathrin
 through a region outside of the SH3 domain. Also binds to alpha-
 adaptin. Interacts with the N-terminal transactivation domain of
 MYC in a manner requiring the integrity of the conserved MYC box
 regions 1 and 2.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=AMPH2-1;
 CC IsoId=O08839-1; Sequence=Displayed;
 CC Name=AMPH2-2;
 CC IsoId=O08839-2; Sequence=VSP_000260;
 CC Name=AMPH2-3;
 CC IsoId=O08839-3; Sequence=VSP_000258;
 CC Name=AMPH2-4;
 CC IsoId=O08839-4; Sequence=VSP_000256, VSP_000257;
 CC Name=AMPH2-5;
 CC IsoId=O08839-5; Sequence=VSP_000259;
 CC Name=AMPH2-6;
 CC IsoId=O08839-6; Sequence=VSP_000256, VSP_000259;
 CC -!- TISSUE SPECIFICITY: Isoform AMPH2-1 is expressed in brain,

concentrated at nerve terminals. Isoform AMPH2-2 is widely
 expressed
 -!- PTM: Phosphorylated by protein kinase C.
 -!- SIMILARITY: Contains 1 BAR domain.
 -!- SIMILARITY: Contains 1 SH3 domain.

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 or send an email to license@sib-sib.ch)

 EMBL; Y13380; CAA73807.1; --
 PDB; 1BB9; 17-JUN-98.
 DR InterPro; IPR003005; Amphiphysin.
 DR InterPro; IPR006632; BAR.
 DR InterPro; IPR004148; BAR_dom.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF03114; BAR; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR01251; AMPHIPHYNSIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR ProDom; PD000066; SH3; 1.
 DR SMART; SM00721; BAR; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Alternative splicing; SH3 domain; Coiled coil; Endocytosis;
 KW Anti-oncogene; Differentiation; Phosphorylation; 3D-structure.
 FT DOMAIN 15 42
 FT DOMAIN 193 274
 FT DOMAIN 379 422
 FT DOMAIN 515 588
 FT VARSPLIC 173 205
 FT Missing (in isoform AMPH2-4 and isoform
 AMPH2-6).
 FT /FTId=VSP_000256.
 FT Missing (in isoform AMPH2-4).
 FT /FTId=VSP_000257.
 FT Missing (in isoform AMPH2-3).
 FT /FTId=VSP_000258.
 FT Missing (in isoform AMPH2-5 and isoform
 AMPH2-6).
 FT /FTId=VSP_000259.
 FT Missing (in isoform AMPH2-2).
 FT /FTId=VSP_000260.
 SQ SEQUENCE 588 AA; 64533 MW; 164AC90E09547F1A CRC64;
 Query Match 100.0%; Score 61; DB 1; Length 588;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
 DB 24 RAQEKVLQKLGKA 36

RESULT 3
 BIN1_HUMAN
 ID BIN1_HUMAN STANDARD; PRT; 593 AA.
 AC C00499; C00297; C00545; C04387; C06053; C06055; C060555;
 AC C075514; C075515; C075516; C075517; C075518; C092944; C099688;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Myc box dependent interacting protein 1 (Bridging integrator 1)
 DE (Amphiphysin-like protein) (Amphiphysin II) (Box-dependent myc-
 interacting protein-1).
 GN BIN1 OR AMPHL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A. (ISOFORM IIA).
 RP TISSUE=Brain;
 RX MEDLINE=97341217; PubMed=9195986;
 RA Ramjaun A.R., Micheva K.D., Bouchelet I., McPherson P.S.;
 RT "Identification and characterization of a nerve terminal-enriched
 RT amphiphsin isoform";
 RL J. Biol. Chem. 272:16700-16706(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS IIA AND BIN1).
 RC TISSUE=Brain, and Skeletal muscle;
 RX MEDLINE=97327761; PubMed=9182667;
 RA Butler M.H., David C., Ochoa G.-C., Freyberg Z., Daniell L., Grabs D.,
 RA Cremona O., De Camilli P.;
 RT "Amphiphysin II (SH3p9; BIN1), a member of the amphiphysin/Rvs family,
 RT is concentrated in the cortical cytomatrix of axon initial segments
 RT and nodes of ranvier in brain and around T tubules in skeletal
 RT muscle";
 RL J. Cell Biol. 137:1355-1367(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM BIN1).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=96376973; PubMed=8782922;
 RA Sakamuro D., Elliott K.J., Wechsler-Reya R., Prendergast G.C.;
 RT "Bkl1 is a novel Myc-interacting protein with features of a tumour
 RT suppressor";
 RL Nat. Genet. 14:69-76(1996).
 RN [4]
 RP REVISIONS TO N-TERMINUS.
 RA Sakamuro D., Elliott K.J., Wechsler-Reya R., Prendergast G.C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS IIB; IIC1; IIC2 AND IID).
 RC TISSUE=Brain;
 RX MEDLINE=98264340; PubMed=9603201;
 RA Ramjaun A.R., McPherson P.S.;
 RT "Multiple amphiphysin II splice variants display differential clathrin
 RT binding: identification of two distinct clathrin-binding sites";
 RL J. Neurochem. 70:2369-2376(1998).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORMS I12 AND I13).
 RC TISSUE=Brain;
 RX MEDLINE=97366618; PubMed=9223448;
 RA Tsutsui K., Maeda Y., Tsutsui K., Seki S., Tokunaga A.;
 RT "cDNA cloning of a novel amphiphysin isoform and tissue-specific
 RT expression of its multiple splice variants";
 RL Biochem. Biophys. Res. Commun. 236:178-183(1997).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS I13; I13; BIN1-10-13; BIN1-13 AND
 RP BIN1+12A).
 RC TISSUE=Fibroblast;
 RX MEDLINE=98058932; PubMed=9395479;
 RA Wechsler-Reya R.J., Sakamuro D., Zhang J., DuHadaway J.,
 RA Prendergast G.C.;
 RT "Structural analysis of the human BIN1 gene. Evidence for tissue-
 RT specific transcriptional regulation and alternate RNA splicing";
 RL J. Biol. Chem. 272:31453-31458(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM I12).
 RA Zhang J., Du W., Wechsler-Reya R.J., DuHadaway J., Sakamuro D.,
 RA Prendergast G.C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE OF 133-593 FROM N.A.
 RC TISSUE=Brain;
 RA Xu W., Gibbs R.A.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP CHARACTERIZATION.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98078712; PubMed=9418903;
 RA Wechsler-Reya R.J., Elliott K.J., Prendergast G.C.;
 RT "A role for the putative tumor suppressor Bin1 in muscle cell

RT differentiation";
 RL Mol. Cell. Biol. 18:566-575(1998).
 CC [-] FUNCTION: May be involved in regulation of synaptic vesicle
 CC endocytosis. May act as a tumor suppressor and inhibits
 CC malignant cell transformation.
 CC [-] SUBUNIT: Heterodimer with AMPH. Binds SH3GLB1 (By similarity).
 CC Binds to SYNJ1 and DNM1 through its SH3 domain, and to clathrin
 CC through a region outside of the SH3 domain. Also binds to alpha-
 CC adaptin. Interacts with the N-terminal transactivation domain of
 CC MYC in a manner requiring the integrity of the conserved MYC box
 CC regions 1 and 2.
 CC [-] SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Isoform IIA is
 CC found in the cytoplasm while isoform BIN1 is nuclear.
 CC [-] ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=11;
 CC Comment-Additional isoforms seem to exist;
 CC Name=IIA; IsoId=O00499-1; Sequence=Displayed;
 CC Name=IIB; IsoId=O00499-2; Sequence=VSP_000246, VSP_000252;
 CC Name=IIC1; IsoId=O00499-3; Sequence=VSP_000249;
 CC Name=IIC2; IsoId=O00499-4; Sequence=VSP_000246, VSP_000249;
 CC Name=IID; IsoId=O00499-5; Sequence=VSP_000248;
 CC Name=II2; IsoId=O00499-6; Sequence=VSP_000253;
 CC Name=I13; IsoId=O00499-7; Sequence=VSP_000250;
 CC Name=BIN1; IsoId=O00499-8; Sequence=VSP_000246, VSP_000247, VSP_000250;
 CC Name=BIN1-10-13; IsoId=O00499-9; Sequence=VSP_000251;
 CC Name=BIN1-13; IsoId=O00499-10; Sequence=VSP_000246, VSP_000251;
 CC Name=BIN1+12A; IsoId=O00499-11; Sequence=VSP_000246, VSP_000247, VSP_000253;
 CC [-] TISSUE SPECIFICITY: ISOFORM IIA IS EXPRESSED ONLY IN THE BRAIN
 CC WHERE IT IS CONCENTRATED IN AXON INITIAL SEGMENTS AND NODES OF
 CC RANVIER. ISOFORM BIN1 IS WIDELY EXPRESSED WITH HIGHEST EXPRESSION
 CC IN SKELETAL MUSCLE.
 CC [-] PTM: Phosphorylated by protein kinase C (By similarity).
 CC [-] SIMILARITY: Contains 1 BAR domain.
 CC [-] SIMILARITY: Contains 1 SH3 domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF004015; AAC51345.1; -
 CC EMBL; AF070576; AAC28646.1; -
 CC EMBL; U68485; AAC17461.1; -
 CC EMBL; AF001383; AAC61363.1; -
 CC EMBL; AF043898; AAC39710.1; -
 CC EMBL; AF043899; AAC39711.1; -
 CC EMBL; AF043900; AAC39712.1; -
 CC EMBL; AF043901; AAC39713.1; -
 CC EMBL; U87558; AAB63263.1; -
 CC EMBL; AF068914; AAC24126.1; -
 CC EMBL; AF068915; AAC24127.1; -
 CC EMBL; AF068916; AAC24128.1; -
 CC EMBL; AF068917; AAC23750.1; -
 CC EMBL; AF068918; AAC23751.1; -
 CC EMBL; U84004; AAC23440.1; -
 CC EMBL; U83999; AAC23440.1; JOINED.
 CC EMBL; U84001; AAC23440.1; JOINED.
 CC EMBL; U84002; AAC23440.1; JOINED.
 CC EMBL; U84003; AAC23440.1; JOINED.


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CC similarity).
CC -1- SUBUNIT: Heterodimer with BIN1. Binds SH3GLB1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Peripheral membrane protein associated with
CC the cytoplasmic surface of synaptic vesicles (By similarity).
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Y13381; CAA73808.1; -
CC InterPro: IPR003005; Amphiphysin.
CC InterPro: IPR003017; Amphiphysin_1.
CC InterPro: IPR006632; BAR.
CC InterPro: IPR004148; BAR_dom.
CC InterPro: IPR001452; SH3.
CC Pfam: PF03114; BAR; 1.
CC Pfam: PF00018; SH3; 1.
CC PRINTS: PR01251; AMPHIPHYSIN.
CC PRINTS: PR00452; SH3DOMAIN.
CC ProDom: PD003208; Amphiphysin_1; 1.
CC ProDom: PD000066; SH3; 1.
CC SMART: SM00721; BAR; 1.
CC SMART: SM00326; SH3; 1.
CC PROSITE: PS50002; SH3; 1.
CC Cytoskeleton; SH3 domain; Coiled coil.
CC FT DOMAIN 10 83 COILED COIL (POTENTIAL).
CC FT DOMAIN 144 191 COILED COIL (POTENTIAL).
CC FT DOMAIN 610 683 SH3.
CC SQ SEQUENCE 683 AA; 74877 MW; 7FBA4A9E5A1F6631 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 683;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RAQKVLQKLKGA 13
Db 19 RAQKVLQKLKGA 31

RESULT 6
AMPH_HUMAN STANDARD; PRT; 695 AA.
AC P49418; O43538;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amphiphysin.
GN AMPH OR AMPHI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Cerebellum;
RC MEDLINE=94357284; PubMed=8076697;
RA David C., Solimena M., de Camilli P.;
RT "Autoimmunity in stiff-man syndrome with breast cancer is targeted to
RT the C-terminal region of human amphiphysin, a protein similar to the
RT yeast proteins Rvs167 and Rvs161."
RL PNAS Lett. 351:73-79(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Brain;
RC MEDLINE=95276740; PubMed=7757077;
RA Yamamoto R., Li X., Winter S., Francke U., Killmann M.W.;
RT "Primary structure of human amphiphysin, the dominant autoantigen of

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RT paraneoplastic stiff-man syndrome, and mapping of its gene (AMPH) to
RT chromosome 7p13-p14."
RL Hum. Mol. Genet. 4:265-268(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Breast;
RX MEDLINE=98174372; PubMed=9513187;
RA Floyd S.R., Butler M.H., Cremona O., David C., Freyberg Z., Zhang X.,
RA Solimena M., Tokunaga A., Ishizu H., Teutsui K., De Camilli P.V.;
RT "Expression of amphiphysin I, an autoantigen of paraneoplastic
RT neurological syndromes, in breast cancer."
RL Mol. Med. 4:29-39(1998).
CC -1- FUNCTION: May participate in mechanisms of regulated exocytosis in
CC synapses and certain endocrine cell types. May control the
CC properties of the membrane associated cytoskeleton.
CC -1- SUBUNIT: Heterodimer of AMPH and AMPHL (By similarity).
CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC SURFACE OF
CC SYNAPTIC VESICLES.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=128 kDa;
CC IsoId=P49418-1; Sequence=Displayed;
CC Name=2; Synonyms=108 kDa;
CC IsoId=P49418-2; Sequence=VSP_000245;
CC -1- TISSUE SPECIFICITY: Neurons, certain endocrine cell types and
CC spermatocytes.
CC -1- DISEASE: Patients with stiff-man syndrome, a rare disease of the
CC central nervous system characterized by progressive rigidity of
CC the body musculature with superimposed painful spasms, have
CC antibodies against AMPH.
CC -1- SIMILARITY: Contains 1 BAR domain.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U07616; AAA21865.1; -
CC EMBL: X81438; CRA57197.1; -
CC EMBL: AF034996; AAC02977.1; -
CC PIR: S62400; S62400.
CC PDB: 1KY7; 12-JUN-02.
CC Genew; HGNC:471; AMPH.
CC MIM; 600418; -
CC GO; GO:0015629; C:actin cytoskeleton; TAS.
CC GO; GO:0008021; C:synaptic vesicle; TAS.
CC GO; GO:0006897; P:endocytosis; TAS.
CC GO; GO:0007268; P:synaptic transmission; TAS.
CC InterPro: IPR003005; Amphiphysin.
CC InterPro: IPR003017; Amphiphysin_1.
CC InterPro: IPR006632; BAR.
CC InterPro: IPR004148; BAR_dom.
CC InterPro: IPR001452; SH3.
CC Pfam: PF03114; BAR; 1.
CC Pfam: PF00018; SH3; 1.
CC PRINTS: PR01251; AMPHIPHYSIN.
CC PRINTS: PR00452; SH3DOMAIN.
CC ProDom: PD003208; Amphiphysin_1; 1.
CC ProDom: PD000066; SH3; 1.
CC SMART: SM00721; BAR; 1.
CC SMART: SM00326; SH3; 1.
CC PROSITE: PS50002; SH3; 1.
CC Cytoskeleton; SH3 domain; Coiled coil; Alternative splicing;
CC 3D-structure.
CC DOMAIN 10 83 COILED COIL (POTENTIAL).
CC FT DOMAIN 144 191 COILED COIL (POTENTIAL);
CC FT DOMAIN 622 695 SH3.
CC FT VARSPLIC 425 466 Missing (in isoform 2).
CC /FtId=VSP_000245.

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SQ SEQUENCE 695 AA; 76256 MW; 78B4F75AB75BA357 CRC64;
Query Match 100.0%; Score 61; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLG 13
    |||||
Db 19 RAQEKVLQKLG 31

RESULT 7
Y310_PSEAE
AC Q51470; STANDARD; PRT; 446 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein PA3980.
GN PA3980.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=96004705; PubMed=756500;
RA Hungerer C., Troup B., Romling U., Jahn D.;
RT "Cloning, mapping and characterization of the Pseudomonas aeruginosa
hemL gene.";
RL Mol. Gen. Genet. 248:375-380(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- SIMILARITY: Belongs to the UPF0004 family.
CC -!- SIMILARITY: Contains 1 TRAM domain.
-----
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-----
CC EMBL; X82072; CAA57577.1; --
CC EMBL; AE004816; AAG07367.1; --
CC PIR; F83147; F83147.
CC PIR; S57900; S57900.
CC InterPro; IPR006638; E1p3.
CC InterPro; IPR006463; MiaB_methylase.
CC InterPro; IPR007197; Radical_SAM.
CC InterPro; IPR002792; TRAM.
CC InterPro; IPR005839; UPF0004.
CC Pfam; PF04055; Radical_SAM; 1.
CC Pfam; PF01938; TRAM; 1.
CC Pfam; PF00919; UPF0004; 1.
CC SMART; SM00729; E1p3; 1.
CC TIGRFAMs; TIGR01574; miaB_methylase; 1.
CC TIGRFAMs; TIGR00089; TIGR00089; 1.
CC PROSITE; PS50926; TRAM; 1.
CC PROSITE; PS01278; UPF0004; 1.

KW Hypothetical protein; Complete proteome.
FT DOMAIN 378 442 TRAM.
FT CONFLICT 55 55 A -> V (IN REF. 1).
FT CONFLICT 60 60 F -> C (IN REF. 1).
FT CONFLICT 395 395 K -> E (IN REF. 1).
SQ SEQUENCE 446 AA; 49978 MW; 9F5EA90E62889850 CRC64;

Query Match 65.6%; Score 40; DB 1; Length 446;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLG 11
    :|||
Db 54 KAQEKVFSKLG 64

RESULT 8
CP72_CATRO
ID CP72_CATRO STANDARD; PRT; 524 AA.
AC Q05047;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome P450 72A1 (EC 1.3.3.9) (CYP72A1) (Secologanin synthase)
DE (SLS).
GN CYP72A1 OR CYP72 OR P450CR3.
OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
OC Catharanthus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. CP3A;
RA Vetter H.-P., Mangold U., Schroeder G., Marner F.-J.,
RA Werck-Reichhart D., Schroeder J.;
RT "Molecular analysis and heterologous expression of an inducible
cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).";
RL Plant Physiol. 100:998-1007(1992).
RN [2]
RP SEQUENCE OF 469-524 FROM N.A.
RC STRAIN=cv. G. Don;
RX MEDLINE=93283641; PubMed=8507839;
RA Meijer A.H., Souer E., Verpoorte R., Hoge J.H.C.;
RT "Isolation of cytochrome P-450 cDNA clones from the higher plant
Catharanthus roseus by a PCR strategy.";
RL Plant Mol. Biol. 22:379-383(1993).
RN [3]
RP FUNCTION.
RC STRAIN=cv. CP3A;
RX MEDLINE=20575722; PubMed=11135113;
RA Imler S., Schroeder G., St-Pierre B., Crouch N.P., Hotze M.,
RA Schmidt J., Strack D., Materin U., Schroeder J.;
RT "Indole alkaloid biosynthesis in Catharanthus roseus: new enzyme
activities and identification of cytochrome P450 CYP72A1 as
secologanin synthase";
RL Plant J. 24:797-804(2000).
CC -!- FUNCTION: Converts loganin into secologanin.
CC -!- CATALYTIC ACTIVITY: Loganin + NADPH + O(2) = secologanin + NADP(+)
CC + 2 H(2)O.
CC -!- PATHWAY: Indole alkaloids biosynthesis.
CC -!- SUBCELLULAR LOCATION: Vacuolar membrane (Probable).
CC -!- TISSUE SPECIFICITY: Upper and lower leaf epidermis.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
-----
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CC EMBL; L10081; AAA33106.1; -
DR EMBL; X69775; CAA49430.1; -
DR PIR; S35168; S35168.
DR PIR; T09944; T09944.
DR HSP; P14779; LUPZ.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Transmembrane;
KW NADP; Heme; Alkaloid metabolism.
FT TRANSMEM 12 32
FT METAL 470 470
FT VARIAT 190 190
FT VARIAT 194 194
FT VARIAT 223 223
FT VARIAT 312 312
FT VARIAT 318 318
FT VARIAT 403 403
FT VARIAT 405 405
FT VARIAT 411 411
SQ SEQUENCE 524 AA; 60557 MW; EFSD864E43C751E8 CRC64;
Query Match 63.9%; Score 39; DB 1; Length 524;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
DB 357 RAREEVLQAFGK 368
RESULT 9
ARR2_ONCMY STANDARD; PRT; 405 AA.
AC P51467;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Arrestin, red cell isoform 2 (CARR).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257743; PubMed=8687393;
RA Jahns R., Borgese F., Lindenthal S., Straub A., Motaïs R., Fievet B.;
RT "Trout red blood cell arrestin (TRCarr), a novel member of the
RT arrestin family: cloning, immunoprecipitation and expression of
RT recombinant TRCarr.";
RL Biochem. J. 316:497-506(1996).
CC -!- SIMILARITY: Belongs to the arrestin family.
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CC or send an email to license@isb-sib.ch).
CC EMBL; U48410; AAB16954.1; -
DR PIR; S68253; S68253.
DR HSP; P08168; 1CF1.
DR InterPro; IPR000698; Arrestin.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 1.
DR ProDom; PD002099; Arrestin; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Sensory transduction.
SQ SEQUENCE 405 AA; 45668 MW; B09B68171842F2E2 CRC64;
Query Match 62.3%; Score 38; DB 1; Length 405;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
DB 100 RLQERLLKLGQ 111
RESULT 10
ARR1_ONCMY STANDARD; PRT; 407 AA.
AC P51466;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Arrestin, red cell isoform 1 (CARR).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257743; PubMed=8687393;
RA Jahns R., Borgese F., Lindenthal S., Straub A., Motaïs R., Fievet B.;
RT "Trout red blood cell arrestin (TRCarr), a novel member of the
RT arrestin family: cloning, immunoprecipitation and expression of
RT recombinant TRCarr.";
RL Biochem. J. 316:497-506(1996).
CC -!- SIMILARITY: Belongs to the arrestin family.
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CC or send an email to license@isb-sib.ch).
CC EMBL; U48410; AAB16954.1; -
DR PIR; S68253; S68253.
DR HSP; P08168; 1CF1.
DR InterPro; IPR000698; Arrestin.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 1.
DR ProDom; PD002099; Arrestin; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Sensory transduction.
SQ SEQUENCE 407 AA; 45902 MW; 4986C2237E709F16 CRC64;
Query Match 62.3%; Score 38; DB 1; Length 407;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
DB 100 RLQERLLKLGQ 111
RESULT 11
ARR3_ONCMY STANDARD; PRT; 415 AA.
AC P51468;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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CC EMBL; L10081; AAA33106.1; -
DR EMBL; X69775; CAA49430.1; -
DR PIR; S35168; S35168.
DR PIR; T09944; T09944.
DR HSP; P14779; LUPZ.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Transmembrane;
KW NADP; Heme; Alkaloid metabolism.
FT TRANSMEM 12 32
FT METAL 470 470
FT VARIAT 190 190
FT VARIAT 194 194
FT VARIAT 223 223
FT VARIAT 312 312
FT VARIAT 318 318
FT VARIAT 403 403
FT VARIAT 405 405
FT VARIAT 411 411
SQ SEQUENCE 524 AA; 60557 MW; EFSD864E43C751E8 CRC64;
Query Match 63.9%; Score 39; DB 1; Length 524;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
DB 357 RAREEVLQAFGK 368
RESULT 9
ARR2_ONCMY STANDARD; PRT; 405 AA.
AC P51467;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Arrestin, red cell isoform 2 (CARR).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257743; PubMed=8687393;
RA Jahns R., Borgese F., Lindenthal S., Straub A., Motaïs R., Fievet B.;
RT "Trout red blood cell arrestin (TRCarr), a novel member of the
RT arrestin family: cloning, immunoprecipitation and expression of
RT recombinant TRCarr.";
RL Biochem. J. 316:497-506(1996).
CC -!- SIMILARITY: Belongs to the arrestin family.
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CC or send an email to license@isb-sib.ch).
CC EMBL; U48410; AAB16954.1; -
DR PIR; S68253; S68253.
DR HSP; P08168; 1CF1.
DR InterPro; IPR000698; Arrestin.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 1.
DR ProDom; PD002099; Arrestin; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Sensory transduction.
SQ SEQUENCE 405 AA; 45668 MW; B09B68171842F2E2 CRC64;
Query Match 62.3%; Score 38; DB 1; Length 405;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
DB 100 RLQERLLKLGQ 111
RESULT 10
ARR1_ONCMY STANDARD; PRT; 407 AA.
AC P51466;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Arrestin, red cell isoform 1 (CARR).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257743; PubMed=8687393;
RA Jahns R., Borgese F., Lindenthal S., Straub A., Motaïs R., Fievet B.;
RT "Trout red blood cell arrestin (TRCarr), a novel member of the
RT arrestin family: cloning, immunoprecipitation and expression of
RT recombinant TRCarr.";
RL Biochem. J. 316:497-506(1996).
CC -!- SIMILARITY: Belongs to the arrestin family.
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CC EMBL; U48410; AAB16954.1; -
DR PIR; S68253; S68253.
DR HSP; P08168; 1CF1.
DR InterPro; IPR000698; Arrestin.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002099; Arrestin; 1.
DR ProDom; PD002099; Arrestin; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Sensory transduction.
SQ SEQUENCE 407 AA; 45902 MW; 4986C2237E709F16 CRC64;
Query Match 62.3%; Score 38; DB 1; Length 407;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 RAQEKVLQKLGK 12
DB 100 RLQERLLKLGQ 111
RESULT 11
ARR3_ONCMY STANDARD; PRT; 415 AA.
AC P51468;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

DE Arrestin, red cell isoform 3 (CARR).

OS Oncorhynchus mykiss (Rainbow trout).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Telostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96257743; PubMed=8687393;

RX Johns R., Borgese F., Lindenthal S., Straub A., Motals R., Fievet B.,

RT "Trout red blood cell arrestin (TRCarr), a novel member of the

RT arrestin family: cloning, immunoprecipitation and expression of

RT recombinant rCarr."

RL Biochem. J. 316:497-506 (1996).

CC -|- SIMILARITY: Belongs to the arrestin family.

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CC -----

DR EMBL; U48412; AAB16956.1; -.

DR PIR; S68255; S68255.

DR HSP; P08168; ICF1.

DR InterPro; IPR000698; Arrestin.

DR InterPro; IPR007110; IG-like.

DR Pfam; PF00339; arrestin; 1.

DR Pfam; PF02752; arrestin; C; 1.

DR PRINTS; PR00309; ARRESTIN.

DR PRODOM; PD002099; Arrestin; 1.

DR PROSITE; PS00295; ARRESTINS; 1.

DR Sensory transduction.

KW Sensory transduction.

SQ SEQUENCE 415 AA; 46770 MW; 7797256F1A2FBC8 CRC64;

Query Match 62.3%; Score 38; DB 1; Length 415;

Best Local Similarity 58.3%; Pred. No. 36;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RAQEKVLQKLGK 12

Db 100 RLQERLLKLGQ 111

RESULT 12

ARR2 BOVIN

ID ARR2 BOVIN STANDARD; PRT; 420 AA.

AC P32120; O77565; O77566;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Beta-arrestin 2 (Arrestin, beta 2) (Arrestin 3).

GN ARRB2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=93340166; PubMed=8340388;

RX Sterne-Marx R., Gurevich V.V., Goldsmith P., Bodine R.C., Sanders C.,

RA Donoso L.A., Benovic J.L.;

RT "Polypeptide variants of beta-arrestin and arrestin3."

RL J. Biol. Chem. 268:15640-15648 (1993).

RN [2]

RP SEQUENCE OF 304-396 FROM N.A.

RP TISSUE=Retina;

RC MEDLINE=93145674; PubMed=9767391;

RX Komori N., Cain S.D., Roch J.-M., Miller K.E., Matsumoto H.;

RT "Differential expression of alternative splice variants of beta-

RT arrestin-1 and -2 in rat central nervous system and peripheral

RT tissues";

RL Eur. J. Neurosci. 10:2607-2616 (1998).

CC -|- FUNCTION: Regulates beta-adrenergic receptor function. Beta-

CC arrestins seem to bind phosphorylated beta-adrenergic receptors,

CC thereby causing a significant impairment of their capacity to

CC activate G(s) proteins.

CC -|- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).

CC -|- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=Long;

CC IsoId=P32120-1; Sequence=Displayed;

CC Name=Short;

CC IsoId=P32120-2; Sequence=VSP_000323;

CC -|- TISSUE SPECIFICITY: Found in a variety of tissues. The short

CC isoform is the most abundant form in all tissues.

CC -|- SIMILARITY: Belongs to the arrestin family.

CC -----

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CC -----

DR EMBL; L14641; -; NOT ANNOTATED CDS.

DR EMBL; AF051456; AAC28615.1; -.

DR EMBL; AF051456; AAC28616.1; -.

DR PIR; A47140; A47140.

DR HSP; P08168; ICF1.

DR InterPro; IPR000698; Arrestin.

DR InterPro; IPR007110; IG-like.

DR Pfam; PF00339; arrestin; 1.

DR Pfam; PF02752; arrestin; C; 1.

DR PRINTS; PR00309; ARRESTIN.

DR PRODOM; PD002099; Arrestin; 1.

DR PROSITE; PS00295; ARRESTINS; 1.

KW Sensory transduction; Nuclear protein; Alternative splicing.

FT DONAIN 400 410 NUCLEAR EXPORT SIGNAL (BY SIMILARITY).

FT VARSPLIT 363 373 Missing (in isoform Short).

FT CONFLICT 362 362 A -> P (IN REF. 2).

FT SEQUENCE 420 AA; 47224 MW; 590ECF2D2D29F4D1 CRC64;

Query Match 62.3%; Score 38; DB 1; Length 420;

Best Local Similarity 58.3%; Pred. No. 37;

Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RAQEKVLQKLGK 12

Db 100 RLQERLLKLGQ 111

RESULT 13

DSL1 CHICK

ID DSL1 CHICK STANDARD; PRT; 427 AA.

AC P34822;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Dorsalin-1 precursor (DSL-1).

GN DSL-1.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.; AND SEQUENCE OF 319-322.

RC TISSUE=Spinal cord;

RX MEDLINE=93272310; PubMed=7916656;

RA Basler K., Edlund T., Jessell T.M., Yamada T.;
 RT "Control of cell pattern in the neural tube: regulation of cell
 RT differentiation by dorsalin-1, a novel TGF beta family member.";
 RL Cell 73:689-702(1993).
 CC -!- FUNCTION: APPEARS TO REGULATE CELL DIFFERENTIATION WITHIN THE
 CC NEURAL TUBE. MAY REGULATE THE DIFFERENTIATION OF CELL TYPES ALONG
 CC THE DORSOVENTRAL AXIS OF THE NEURAL TUBE, ACTING IN CONJUNCTION
 CC WITH DISTINCT VENTRALIZING SIGNALS FROM THE NOTOCHORD AND FLOOR
 CC PLATE. CONTROLS THE CELL DIFFERENTIATION IN THE NEURAL TUBE IN
 CC SEVERAL WAYS: (1) PROMOTES THE DIFFERENTIATION OF CELL TYPES THAT
 CC DERIVE FROM THE DORSAL NEURAL TUBE. (2) ENSURES THAT THE DORSAL
 CC NEURAL TUBE IS REFRACTORY TO VENTRALIZING SPECIES FROM THE
 CC NOTOCHORD. (3) CAN DIFFUSE AND INFLUENCE THE FATE OF CELLS IN MORE
 CC VENTRAL REGIONS OF THE NEURAL TUBE.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EXPRESSED SELECTIVELY IN THE DORSAL NEURAL
 CC TUBE. LOWER LEVELS SEEN IN KIDNEY AND MYOTOMAL CELLS.
 CC -!- DEVELOPMENTAL STAGE: IS NOT EXPRESSED IN NEURAL CELLS AT STAGES
 CC BEFORE NEURAL TUBE CLOSURE. IS EXPRESSED AT HIGH LEVELS IN THE
 CC DORSAL THIRD OF THE NEURAL TUBE, BEGINNING AT THE TIME OF NEURAL
 CC TUBE CLOSURE, BUT NOT BY VENTRAL NEURAL CELLS OR BY NONNEURAL
 CC CELLS. DORSAL RESTRICTION PERSISTS IN THE SPINAL CORD AT STAGES
 CC AFTER THE ONSET OF NEURONAL DIFFERENTIATION. AT LATER STAGES OF
 CC SPINAL DEVELOPMENT, IS RESTRICTED TO THE DORSOMEDIAL REGION OF
 CC THE SPINAL CORD, INCLUDING BUT NOT CONFINED TO THE ROOF PLATE.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC
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 CC
 CC EMBL; L12032; AAA48752.1; -
 CC FIC; A40735; A40735.
 CC HSSP; P12643; 3BMP.
 CC InterPro; IPR002405; Inhibin_alpha.
 CC InterPro; IPR001839; TGFb.
 CC InterPro; IPR001111; TGFb_N.
 CC Pfam; PF00019; TGF-beta; 1.
 CC Pfam; PF00688; TGFb_propeptide; 1.
 CC PRINTS; PR00669; INHIBIN.
 CC ProDom; PD000357; TGFb; 1.
 CC SMART; SM00204; TGFb; 1.
 CC PROSITE; PS00250; TGF BETA 1; 1.
 CC Signal; Growth factor; Cytokine; Glycoprotein.
 CC SIGNAL 1 20 POTENTIAL.
 CC PROPEP 21 318
 CC CHAIN 319 427 DORSALIN-1.
 CC DISULFID 325 391 BY SIMILARITY.
 CC FT DISULFID 354 424 BY SIMILARITY.
 CC FT DISULFID 358 426 BY SIMILARITY.
 CC FT DISULFID 390 390 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 427 AA; 48626 MW; 23AA42DC7085FABC CRC64;
 SQ
 Query Match 62.3%; Score 38; DB 1; Length 427;
 Best Local Similarity 80.0%; Pred. No. 37;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 QEKVLQKLGK 12
 DB 282 QESVLNKLK 291
 RESULT 14
 Y426_BUCAP

ID Y426_BUCAP STANDARD; PRT; 439 AA.
 AC Q8X9C2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 GN BUGC426.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22084549; PubMed=12089438;
 RA Tanas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
 RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";
 RL Science 296:2376-2379(2002).
 CC -!- SIMILARITY: BELONGS TO THE UPF0004 FAMILY. STRONG, TO E. COLI YLEA.
 CC -!- SIMILARITY: Contains 1 TRAM domain.
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 CC
 CC EMBL; AE014118; AM67969.1; -
 CC InterPro; IPR006638; Elp3.
 CC InterPro; IPR006463; MiaB_methylase.
 CC InterPro; IPR007197; Radical_SAM.
 CC InterPro; IPR002792; TRAM.
 CC InterPro; IPR005839; UPF0004.
 CC Pfam; PF04055; Radical_SAM; 1.
 CC Pfam; PF01938; TRAM; 1.
 CC Pfam; PF00919; UPF0004; 1.
 CC SMART; SM00729; Elp3; 1.
 CC TIGRFAMs; TIGR01574; miaB-methylase; 1.
 CC TIGRFAMs; TIGR00089; TIGR00089; 1.
 CC PROSITE; PS00926; TRAM; 1.
 CC PROSITE; PS01278; UPF0004; 1.
 CC Hypothetical protein; Complete proteome.
 CC DOMAIN 377 439 TRAM.
 CC SEQUENCE 439 AA; 50787 MW; 2E83E7F58CD0E5B8 CRC64;
 SQ
 Query Match 62.3%; Score 38; DB 1; Length 439;
 Best Local Similarity 58.3%; Pred. No. 38;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RAQEKVLQKLGK 12
 DB 53 KAQEKVFLHGR 64
 RESULT 15
 Y441_BUCAI
 ID Y441_BUCAI STANDARD; PRT; 439 AA.
 AC P57516;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 GN BUGC426.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=Tokyo 1998;

```

RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -!- SIMILARITY: BELONGS TO THE UPF0004 FAMILY. STRONG, TO E.COLI YLEA.
CC -!- SIMILARITY: Contains 1 TRAM domain.
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CC -----
DR EMBL; AF001119; BAB13139.1; -.
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR006463; MiaB_methylolase.
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR SMART; SM00729; Elp3; 1.
DR TIGRFAMs; TIGR01574; miaB_methylolase; 1.
DR TIGRFAMs; TIGR00089; TIGR00089; 1.
DR PROSITE; PS0926; TRAM; 1.
DR PROSITE; PS01278; UPF0004; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 377 439 TRAM.
SQ SEQUENCE 439 AA; 50464 MW; 287361B42483D610 CRC64;

Query Match 62.3%; Score 38; DB 1; Length 439;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
Db 53 KAQEKVFLQLGR 64

RESULT 16
YA01_PASMU STANDARD; PRT; 474 AA.
AC Q9L699;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein PM1001.
GN PM1001.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RA Fuller T.E., Kennedy M.J., Lowery D.E.;
RT "Identification of Pasteurella multocida virulence genes in a
RT septicemic mouse model using signature-tagged mutagenesis.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.D., Faustian M.L., Whittam T.S., Kapur V.;
RT "Complete genome sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- SIMILARITY: BELONGS TO THE UPF0004 FAMILY. STRONG, TO E.COLI YLEA.
CC -!- SIMILARITY: Contains 1 TRAM domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF237940; AAP68426.1; -.
DR EMBL; AE006140; AK03085.1; -.
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR006463; MiaB_methylolase.
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR SMART; SM00729; Elp3; 1.
DR TIGRFAMs; TIGR01574; miaB_methylolase; 1.
DR TIGRFAMs; TIGR00089; TIGR00089; 1.
DR PROSITE; PS0926; TRAM; 1.
DR PROSITE; PS01278; UPF0004; 1.
KW Hypothetical protein; Complete proteome.
FT DOMAIN 378 441 TRAM.
SQ SEQUENCE 474 AA; 53553 MW; 610A390EBF6D6629 CRC64;

Query Match 62.3%; Score 38; DB 1; Length 474;
Best Local Similarity 58.3%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RAQEKVLQKLGK 12
Db 54 KAQEKVFLQLGR 65

RESULT 17
YLEA_ECOLI STANDARD; PRT; 474 AA.
ID YLEA_ECOLI
AC Y77645;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein ylea.
GN YLEA OR B0661 OR C0747 OR Z0810 OR ECS0699.
OS Escherichia coli,
OS Escherichia coli O6, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federespiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22398234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
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RESULT 18
YLEA_HABIN
ID YLEA_HABIN STANDARD; PRT; 474 AA.
AC Q57163;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein HI0019.
GN HI0019.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Rd / KW20 / ATCC 51907;
RC MEDLINE=59350630; PubMed=7542800;
RX Fliessmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shireley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd."
RL Science 269:496-512(1995).
RC -1- SIMILARITY: BELONGS TO THE UPF0004 FAMILY. STRONG, TO E.COLI YLEA.
CC -1- SIMILARITY: Contains 1 TRAM domain.
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CC
CC EMBL; U32687; AAC21697.1; -.
DR FIR; D64140; D64140.
DR TIGR; HI0019; -.
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR006463; MiaB_methylase.
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR002792; TRAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR SMART; SM00729; Elp3; 1.
DR TIGRFAMs; TIGR01574; miaB_methylase; 1.
DR TIGRFAMs; TIGR00089; TIGR00089; 1.
DR PROSITE; PS0926; TRAM; 1.
DR PROSITE; PS01278; UPF0004; 1.
DR Hypothetical protein; Complete proteome.
FT DOMAIN 378 441
FT TRAM.
SQ SEQUENCE 474 AA; 53640 MW; A6ECDFFBAE16923D CRC64;

Query Match 62.3%; Score 38; DB 1; Length 474;
Best Local Similarity 58.3%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
DB 54 KAAQEKVFLQGR 65
:|||||:|:|:
:|||||:|:|:

RESULT 19
YF01_MYCTU
ID YF01_MYCTU STANDARD; PRT; 273 AA.

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P71782;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein, RV1501/MT1550/Wh1539.
RV1501 OR MT1550 OR MT1539 OR MB1539.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeyer K., Gass S., Barry C.E. III, Tekala P.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=2206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayan L.A., Emdolaeva M., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeyer K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Deggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.V., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
CC -1- SIMILARITY: TO M.TUBERCULOSIS RV3633.

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CC EMBL; Z79701; CAB02015.1; -;
CC EMBL; AE007023; AAK45816.1; -;
CC EMBL; BX248339; CAD96206.1; -;
CC PIR; H70712; H70712.
CC TIGR; MT1550; -;
CC TubercuList; RV1501; -;
CC InterPro; IPR008775; PhYH.
CC Pfam; PF05721; PhYH; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 273 AA; 30906 MW; 1F4DEDD028A2AE84 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 273;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

P71782;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein, RV1501/MT1550/Wh1539.
RV1501 OR MT1550 OR MT1539 OR MB1539.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeyer K., Gass S., Barry C.E. III, Tekala P.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=2206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayan L.A., Emdolaeva M., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeyer K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Deggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.V., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
CC -1- SIMILARITY: TO M.TUBERCULOSIS RV3633.

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CC EMBL; Z79701; CAB02015.1; -;
CC EMBL; AE007023; AAK45816.1; -;
CC EMBL; BX248339; CAD96206.1; -;
CC PIR; H70712; H70712.
CC TIGR; MT1550; -;
CC TubercuList; RV1501; -;
CC InterPro; IPR008775; PhYH.
CC Pfam; PF05721; PhYH; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 273 AA; 30906 MW; 1F4DEDD028A2AE84 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 273;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
DB 45 RVQERILTEIGK 56

RESULT 20
ARGC METJA STANDARD; PRT; 341 AA.
AC Q58456;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-
GN acetyl-L-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.P., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).
CC -1- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+) +
CC phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
CC -1- PATHWAY: Arginine biosynthesis; third step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the NAGSA dehydrogenase family. Subfamily
CC 1.

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CC EMBL; U67552; AAB99039.1; ALT_INIT.
CC TIGR; M1036; -;
CC HAMAP; MF_00150; -; 1.
CC InterPro; IPR000706; AGPR_act_site.
CC InterPro; IPR000534; Semialdh_dh.
CC Pfam; PF01118; Semialdehyde_dh; 1.
CC Pfam; PF02774; Semialdehyde_dhC; 1.
CC ProDom; PD003765; AGPR_act_site; 1.
CC PROSITE; PS01224; ARGC; 1.
CC Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome.
KW Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome.
FT ACT_SITE 149 149 BY SIMILARITY.
SQ SEQUENCE 341 AA; 38172 MW; 72AE13AD35061D88 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 341;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 EKVLQKLGKA 13
DB 214 EKELKLGKA 223

RESULT 21
P35_MYCP

ID P35 MYCPE STANDARD; PRT; 362 AA.
AC Q50367;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lipoprotein p35 precursor.
GN MPE6810.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OC NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 211-225.
RC STRAIN=GTU-54-6A1;
RX MEDLINE=99377619; PubMed=7649455;
RA Ferris S., Watson H.L., Neyrolles O., Montagnier L., Blanchard A.;
RT "Characterization of a major Mycoplasma penetrans lipoprotein and of
its gene.";
RL FEMS Microbiol. Lett. 130:313-319(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
RN [3]
RP CHARACTERIZATION.
RC MEDLINE=GTU-54-6A1;
RX MEDLINE=99173739; PubMed=10075417;
RA Neyrolles O., Eliane J.-P., Ferris S., da Cunha R.A.F., Prevost M.-C.,
Bahraoui E., Blanchard A.;
RT "Antigenic characterization and cytolocalization of P35, the major
Mycoplasma penetrans antigen.";
RL Microbiology 145:343-355(1999).
CC -!- FUNCTION: Major P35 Penetrans antigen.
CC Distributed all over the plasma membrane.
CC -!- PTM: The N-terminus is blocked (Probable).
CC -!- MISCELLANEOUS: The dominant B-epitopes are found at the N- and C-
terminal regions.
CC -!- SIMILARITY: BELONGS TO THE LIPOPROTEIN P35 FAMILY.
CC
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CC
CC EMBL; L38250; AAC16392.1; -;
CC EMBL; AP004172; BAC44473.1; -;
CC InterPro; IPR000437; Prok_lipprot S.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Antigen; Lipoprotein; Membrane; Signal; Complete proteome; Palmitate.
FT SIGNAL 1 30 PROBABLE.
FT CHAIN 31 362 LIPOPROTEIN P35.
FT LIPID 31 31 N-palmitoyl cysteine (Probable).
FT LIPID 31 31 S-diacylglycerol cysteine (Probable).
FT CONFLICT 354 354 D -> E (IN REF. 1).
SQ SEQUENCE 362 AA; 38370 MW; 6260A719B76F8837 CRC64;
Query Match 60.7%; Score 37; DB 1; Length 362;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 EKVLQKGA 13
| | | | |
DB 281 EKVLKGYA 290

RESULT 22
PCP1 SCHPO STANDARD; PRT; 1308 AA.
AC Q92351;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Spindle pole body protein pcpl.
GN PCP1 OR SPAC6G9.06C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RC MEDLINE=21852775; PubMed=11864908;
RA Flory M.R., Morpew M., Joseph J.D., Means A.R., Davis T.N.;
RT "Pcp1p, a Spcl10p-related calmodulin target at the centrosome of the
fission yeast Schizosaccharomyces pombe.";
RL Cell Growth Differ. 13:47-58(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moulé S., Mungall K., Murphy I., Niblett D., Odell C.,
Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
Borzum K., Langer I., Beck A., Leirach H., Wambutt R., Purnelle B.,
Eger P., Zimmermann W., Wedler H., Wambutt R., Lelaue V., Mottier S.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaue V., Mottier S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Spindle pole body component that binds calmodulin.
CC Overexpression of pcpl causes the formation of supernumerary SPB-
like structures and disrupts both mitotic spindle assembly and
chromosome segregation.
CC -!- SUBCELLULAR LOCATION: Spindle pole body.
CC
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CC
CC EMBL; Z81317; CAB03608.1; -;
CC EMBL; AF348506; AAK31344.1; -;
CC PIR; T39068; T39068.
CC GeneDB Spombe; SPAC6G9.06c; -;
KW Calmodulin-binding; Coiled coil.
FT DOMAIN 151 375 COILED COIL (POTENTIAL).
FT DOMAIN 387 803 COILED COIL (POTENTIAL).
FT DOMAIN 874 1091 COILED COIL (POTENTIAL).

FT DOMAIN 1177 1204 COILED COIL (POTENTIAL).
 SQ SEQUENCE 1208 AA; 140763 MW; 70264159ADD42424 CRC64;
 Query Match 60.7%; Score 37; DB 1; Length 1208;
 Best Local Similarity 58.3%; Pred. No. 1.4e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RAQKVLOKLGK 12
 Db 152 REQKVLEKVR 163
 RESULT 23
 CHDI_YEAST STANDARD; PRT; 1468 AA.
 AC P32657;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE CHDI protein.
 GN CHDI OR YER164W OR SYGP-ORF4.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=97313264; PubMed=9169968;
 RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
 RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
 RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
 RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
 RA Lin D., Moseedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
 RA Oh C., Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
 RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
 RL Nature 387:78-81(1997).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
 CC -1- SIMILARITY: Contains 2 chromo domains.
 CC
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 CC
 CC EMBL; U18917; AAB64691.1; -;
 CC PIR; S30818; S30818.
 CC GenOnline; 139241; -;
 CC SGD; S0000966; CHDI.
 CC GO; GO:0008023; C:transcription elongation factor complex; IPI.
 CC GO; GO:0016887; F:ATPase activity; IDA.
 CC GO; GO:0016944; F:Pol II transcription elongation factor acti. .; IPI.
 CC GO; GO:0006338; P:chromatin modeling; IDA.
 CC GO; GO:0006368; P:RNA elongation from Pol II promoter; IPI.
 CC InterPro; IPR000953; Chromo.
 CC InterPro; IPR001410; DRAD.
 CC InterPro; IPR001650; Helicase_C.
 CC InterPro; IPR000330; SNF2_N.
 CC Pfam; PF00385; chromo; 2.
 CC Pfam; PF00271; helicase_C; 1.
 CC Pfam; PF00249; myb DNA-binding; 1.
 CC Pfam; PF00176; SNF2_N; 1.
 CC SMART; SM00258; CHROMO; 2.
 CC SMART; SM00487; DEXDC; 1.
 CC SMART; SM00490; HELIC_C; 1.
 CC PROSITE; PS00598; CHROMO_1; 2.
 CC PROSITE; PS0013; CHROMO_2; 2.
 CC PROSITE; PS00690; DEAH_ATP_HELICASE; FALSE_NEG.
 KW Hydrolase; Helicase; Nuclear protein; ATP-binding; DNA-binding;
 KW Repeat.
 FT DOMAIN 195 257 CHROMO 1.
 FT DOMAIN 285 350 CHROMO 2.
 FT NP_BIND 401 408 ATP (POTENTIAL).
 FT SITE 513 516 DEAH BOX.
 SQ SEQUENCE 1468 AA; 168240 MW; 788DB74C7FEC6BE5 CRC64;
 Query Match 60.7%; Score 37; DB 1; Length 1468;
 Best Local Similarity 70.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AQEKVLOKLG 11
 Db 668 AEEVLOKFG 677
 RESULT 24
 HIS2_METTH STANDARD; PRT; 96 AA.
 AC O27344;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH).
 GN HIS2 OR MTH283.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashitzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mac J.-I., Rice P., Noelling J., Reeve J.N.;
 RA "Complete genome sequence of Methanobacterium thermoautotrophicum
 RA RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- CATALYTIC ACTIVITY: 1-(5-phosphoribosyl)-ATP + H(2)O = 1-(5-
 CC phosphoribosyl)-AMP + diphosphate.
 CC -1- PATHWAY: Histidine biosynthesis; second step.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the PRA-PH family.
 CC
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 CC
 CC EMBL; AE000893; AAB85765.1; -;
 CC PIR; G69037; G69037.
 CC HAMAP; MF 01020; -; 1.
 CC InterPro; IPR008179; PRA-PH.
 CC InterPro; IPR008178; PRA-PH/CH.
 CC Pfam; PF01503; PRA-PH; 1.
 CC ProDom; PD002611; PRA-PH/CH; 1.
 CC Histidine biosynthesis; Hydrolyase; Complete proteome.
 SQ SEQUENCE 96 AA; 11122 MW; D95A7F8E0672CE8B CRC64;
 Query Match 59.0%; Score 36; DB 1; Length 96;
 Best Local Similarity 45.5%; Pred. No. 22;
 Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AQEKVLOKLGK 12


```

RX MEDLINE=96011827; PubMed=7488004;
RA Hartung S., Rust W., Balvers M., Ivell R.;
RT "Molecular cloning and in vivo expression of the bovine steroidogenic
RL acute regulatory protein."
RL Biochem. Biophys. Res. Commun. 215:646-653 (1995).
RN [2]
RP REVISIONS TO 85 AND 174.
RA Hartung S., Rust W., Balvers M., Ivell R.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE=95352521; PubMed=7626524;
RA Hartigan J.A., Green E.G., Mortensen R.M., Menachery A.,
RA Williams J.H., Orme-Johnson N.R.;
RT "Comparison of protein phosphorylation patterns produced in adrenal
RT cells by activation of cAMP-dependent protein kinase and Ca-dependent
RT protein kinase."
RL J. Steroid Biochem. Mol. Biol. 53:95-101 (1995).
RN [3]
CC -!- FUNCTION: Plays a key role in steroid hormone synthesis by
CC enhancing the metabolism of cholesterol into pregnenolone.
CC Mediates the transfer of cholesterol from the outer mitochondrial
CC membrane to the inner mitochondrial membrane where it is cleaved
CC to pregnenolone (By similarity).
CC -!- PATHWAY: Steroidogenesis; rate-limiting step.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- TISSUE SPECIFICITY: Corpus luteum and adrenal gland.
CC -!- SIMILARITY: Contains 1 START domain.
CC
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CC
CC EMBL; Y17259; CAA76717.1; -
CC DR EMBL; Y17260; CAA76718.1; -
CC DR PIR; J4315; JC4315.
CC DR HSP; Q14849; IEM2.
CC DR InterPro; IPR000799; STAR.
CC DR InterPro; IPR002913; START.
CC DR Pfam; PF01852; START; 1.
CC DR PRINTS; PR00978; STARPROTEIN.
CC DR SMART; SM00234; START; 1.
CC DR SMART; SM00234; START; 1.
CC DR PROSITE; PS50848; START; 1.
CC DR Lipid-binding; Lipid transport; Transport; Steroidogenesis;
CC Mitochondrion; Transit peptide; Phosphorylation.
CC TRANSIT ? MITOCHONDRION (POTENTIAL).
CC FT CHAIN ? 285 STEROIDOGENIC ACUTE REGULATORY PROTEIN.
CC FT DOMAIN 67 280 START.
CC FT MOD_RES 57 57 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
CC FT MOD_RES 195 195 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
CC FT CONFLICT 75 75 H -> Y (IN REF. 1; CAA76718).
CC FT CONFLICT 99 99 E -> K (IN REF. 1; CAA76718).
CC SQ SEQUENCE 285 AA; 31845 MW; EAFD5C14EE95E235 CRC64;
CC
CC Query Match 59.0%; Score 36; DB 1; Length 285;
CC Best Local Similarity 87.5%; Pred. No. 58;
CC Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 5 KVLQKLGK 12
CC DB 155 KVLQKLGK 162
CC
CC RESULT 28
CC STAR_HORSE
CC ID STAR HORSE STANDARD; PRT; 285 AA.
CC O46689;
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

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DE Steroidogenic acute regulatory protein, mitochondrial precursor
DE (STAR) (StARD1).
GN STAR.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=99124482; PubMed=9927292;
RA Kerban A., Boerboom D., Sirois J.;
RT "Human chorionic gonadotropin induces an inverse regulation of
RT steroidogenic acute regulatory protein messenger ribonucleic acid in
RT theca interna and granulosa cells of equine preovulatory follicles."
RL Endocrinology 140:667-674 (1999).
RN [1]
CC -!- FUNCTION: Plays a key role in steroid hormone synthesis by
CC enhancing the metabolism of cholesterol into pregnenolone.
CC Mediates the transfer of cholesterol from the outer mitochondrial
CC membrane to the inner mitochondrial membrane where it is cleaved
CC to pregnenolone (By similarity).
CC -!- PATHWAY: Steroidogenesis; rate-limiting step.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: Contains 1 START domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF031697; AAC04704.1; -
CC DR EMBL; AF031696; AAC04703.1; -
CC DR HSP; Q14849; IEM2.
CC DR InterPro; IPR000799; STAR.
CC DR InterPro; IPR002913; START.
CC DR Pfam; PF01852; START; 1.
CC DR PRINTS; PR00978; STARPROTEIN.
CC DR SMART; SM00234; START; 1.
CC DR SMART; SM00234; START; 1.
CC DR PROSITE; PS50848; START; 1.
CC DR Lipid-binding; Lipid transport; Transport; Steroidogenesis;
CC Mitochondrion; Transit peptide; Phosphorylation.
CC TRANSIT ? MITOCHONDRION (POTENTIAL).
CC FT CHAIN ? 285 STEROIDOGENIC ACUTE REGULATORY PROTEIN.
CC FT DOMAIN 67 280 START.
CC FT MOD_RES 57 57 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
CC FT MOD_RES 195 195 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
CC SQ SEQUENCE 285 AA; 31852 MW; B0360EF93299727D CRC64;
CC
CC Query Match 59.0%; Score 36; DB 1; Length 285;
CC Best Local Similarity 87.5%; Pred. No. 58;
CC Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 5 KVLQKLGK 12
CC DB 155 KVLQKLGK 162
CC
CC RESULT 29
CC STAR_HUMAN
CC ID STAR HUMAN STANDARD; PRT; 285 AA.
CC AC P49675; Q16396;
CC DT 01-FEB-1996 (Rel. 33, Created)
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Steroidogenic acute regulatory protein, mitochondrial precursor
CC (STAR) (StARD1).
CC GN STAR.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

NCBI_TaxID=9606;
 [1] SEQUENCE FROM N.A.
 RP TISSUE=Adrenal cortex;
 RC MEDLINE=95281540; PubMed=7761400;
 RA Sugawara T., Holt J.A., Driscoll D., Strauss J.F. III, Lin D.,
 RA Miller W.L., Patterson D., Clancy K.P., Hart I.M., Clark B.J.,
 RA Stocco D.M.;
 RT "Human steroidogenic acute regulatory protein: functional activity in
 RT COS-1 cells, tissue-specific expression, and mapping of the
 RT structural gene to 8p11.2 and a pseudogene to chromosome 13.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:4778-4782(1995).
 [2] SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RC MEDLINE=96038208; PubMed=7547998;
 RA Sugawara T., Lin D., Holt J.A., Martin K.O., Javitt N.B., Miller W.L.,
 RA Strauss J.F. III,
 RT "Structure of the human steroidogenic acute regulatory protein (STAR)
 RT gene: STAR stimulates mitochondrial cholesterol 27-hydroxylase
 RT activity.";
 RT Biochemistry 34:12506-12512(1995).
 [3] SEQUENCE FROM N.A.
 RP MEDLINE=96008588; PubMed=7548191;
 RA Gradi A., Tang-Wai R., McBride H.M., Chu L.L., Shore G.C.,
 RA Pelletier J.;
 RT "The human steroidogenic acute regulatory (STAR) gene is expressed in
 RT the urogenital system and encodes a mitochondrial polypeptide.";
 RT Biochim. Biophys. Acta 1258:228-233(1995).
 [4] SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC Yu W., Sarginson J., Gibbs R.A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 [5] SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6] PHOSPHORYLATION OF SER-57 AND SER-195.
 RP MEDLINE=20016600; PubMed=10548884;
 RA Strauss J.F. III, Kallen C.B., Christenson L.K., Watari H., Devoto L.,
 RA Arakane F., Kiriakidou M., Sugawara T.;
 RT "The steroidogenic acute regulatory protein (STAR): a window into the
 RT complexities of intracellular cholesterol trafficking.";
 RL Recent Prog. Horm. Res. 54:369-394(1999).
 [7] VARIANTS CLAH GLY-169; LYS-169; LEU-182; VAL-218; ARG-272 DEL AND
 RP PRO-275, AND CHARACTERIZATION OF VARIANTS.
 RX MEDLINE=97096837; PubMed=8948562;
 RA Bose H.S., Sugawara T., Strauss J.F. III, Miller W.L.;
 RT "The pathophysiology and genetics of congenital lipid adrenal
 hyperplasia.";
 RL New Engl. J. Med. 335:1870-1878(1996).
 [8] VARIANTS CLAH THR-225 AND VAL-218.
 RP MEDLINE=97252391; PubMed=9097960;
 RA Nakae J., Tajima T., Sugawara T., Arakane F., Hanaki K., Hotsubo T.,
 RA Igarashi N., Igarashi Y., Ishii T., Koda N., Kondo T., Kohno H.,
 RA Nakagawa Y., Tachibana K., Takeshima Y., Teibouchi K.,
 RA Strauss J.F. III, Fujieda K.;
 RT "Analysis of the steroidogenic acute regulatory protein (STAR) gene in
 RT Japanese patients with congenital lipid adrenal hyperplasia.";
 RL Hum. Mol. Genet. 6:571-576(1997).
 [9] VARIANT ALA-203.
 RP MEDLINE=98112495; PubMed=9452116;
 RA Katsumata N., Tanaka A., Shinagawa T., Nagashima-Miyokawa A.,
 RA Shimizu M., Yasunaga T., Tanaka T., Hibi I.;
 RT "A novel frameshift mutation 840delA and a novel polymorphism D203A in
 RT the steroidogenic acute regulatory protein gene in a Japanese patient
 RT with congenital lipid adrenal hyperplasia.";
 RL Hum. Mutat. Suppl. 1:S304-S307(1998).
 [10] VARIANTS CLAH THR-217 AND VAL-218.
 RP MEDLINE=20030913; PubMed=10566637;
 RA Katsumata N., Kawada Y., Yamamoto Y., Noda M., Nimura A., Horikawa R.,
 RA Tanaka T.;
 RT "A novel compound heterozygous mutation in the steroidogenic acute
 RT regulatory protein gene in a patient with congenital lipid adrenal
 RT hyperplasia.";
 RL J. Clin. Endocrinol. Metab. 84:3983-3987(1999).
 CC -1- FUNCTION: Plays a key role in steroid hormone synthesis by
 CC enhancing the metabolism of cholesterol into pregnenolone.
 CC Mediates the transfer of cholesterol from the outer mitochondrial
 CC membrane to the inner mitochondrial membrane where it is cleaved
 CC to pregnenolone.
 CC -1- PATHWAY: Steroidogenesis; rate-limiting step.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- TISSUE SPECIFICITY: Expressed in gonads, adrenal cortex and
 CC kidney.
 CC -1- DISEASE: Defects in STAR are a cause of congenital lipid
 CC adrenal hyperplasia (CLAH) [MIM:201710]; also called lipid CAH.
 CC CLAH is the most severe form of adrenal hyperplasia. This
 CC autosomal recessive and potentially lethal condition includes the
 CC onset of hyperpigmentation reflecting increased production of pro-
 CC opiomelanocortin, elevated plasma renin activity as a consequence
 CC of reduced aldosterone synthesis, and male pseudohermaphroditism
 CC resulting from deficient fetal testicular testosterone synthesis.
 CC CLAH is a rare disease, except in Japan and Korea where it
 CC accounts for a significant percentage of cases of congenital
 CC adrenal hyperplasia.
 CC -1- SIMILARITY: Contains 1 START domain.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; U17280; AAC50141.1; --
 CC EMBL; U29105; AAC50234.1; --
 CC EMBL; U29109; AAC50234.1; JOINED.
 CC EMBL; U29100; AAC50234.1; JOINED.
 CC EMBL; U29101; AAC50234.1; JOINED.
 CC EMBL; U29102; AAC50234.1; JOINED.
 CC EMBL; U29103; AAC50234.1; JOINED.
 CC EMBL; U29104; AAC50234.1; JOINED.
 CC EMBL; S79669; AAB35726.1; --
 CC EMBL; AF035277; AAB88174.1; --
 CC EMBL; BC010550; AAI10550.1; --
 CC PIR; I38248; I38248.

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DR HSSP; Q14849; 1EM2.
DR Genew; HGNC:11359; STAR.
DR MIN; 600617; -.
DR MIN; 201710; -.
DR GO; GO:0006934; P:steroid biosynthesis; TAS.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; STAR.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
KW Lipid-binding; Lipid transport; Transport; Steroidogenesis;
KW Mitochondrion; Transit peptide; Phosphorylation; Disease mutation;
KW Polymorphism.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 285 STEROIDGENIC ACUTE REGULATORY PROTEIN.
FT DOMAIN 67 280 START.
FT MOD_RES 57 57 PHOSPHORYLATION (BY PKA).
FT MOD_RES 195 195 PHOSPHORYLATION (BY PKA).
FT VARIANT 169 169 E -> G (in CLAH; partial loss of activity).
FT VARIANT 169 169 /FTID=VAR_014236.
FT VARIANT 169 169 E -> K (in CLAH; partial loss of activity).
FT VARIANT 182 182 /FTID=VAR_014237.
FT VARIANT 182 182 R -> L (in CLAH; partial loss of activity).
FT VARIANT 203 203 /FTID=VAR_005627.
FT VARIANT 203 203 D -> A.
FT VARIANT 217 217 /FTID=VAR_005628.
FT VARIANT 217 217 R -> T (in CLAH).
FT VARIANT 218 218 /FTID=VAR_014238.
FT VARIANT 218 218 A -> V (in CLAH; partial loss of activity).
FT VARIANT 225 225 /FTID=VAR_014239.
FT VARIANT 225 225 M -> T (in CLAH).
FT VARIANT 272 272 /FTID=VAR_014240.
FT VARIANT 272 272 Missing (in CLAH; partial loss of activity).
FT VARIANT 275 275 /FTID=VAR_014241.
FT VARIANT 275 275 L -> P (in CLAH; partial loss of activity).
FT VARIANT 275 275 /FTID=VAR_014242.

Query Match 59.0%; Score 36; DB 1; Length 285;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLQKLGK 12
Db 155 KVLQKICK 162

RESULT 30
STAR SHEEP
ID STAR SHEEP STANDARD; PRT; 285 AA.
AC P79245; O9GMD0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-FEB-2004 (Rel. 43, Last annotation update)
DE Steroidogenic acute regulatory protein, mitochondrial precursor
DE (STAR) (STAR1).
OS STAR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066334; PubMed=11145616;
RA West L.A., Horvat R.D., Roess D.A., Barisas B.G., Juengel J.L.,
RA Niswender G.D.;

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RT "Steroidogenic acute regulatory protein and peripheral-type
RL benzodiazepine receptor associate at the mitochondrial membrane.";
RL Endocrinology 142:502-505(2001).
RN [2]
RP SEQUENCE OF 97-217 FROM N.A.
RC TISSUE=Corpus luteum;
RX MEDLINE=96079887; PubMed=7588291;
RA Juengel J.L., Meberg B.M., Turzillo A.M., Nett T.M., Niswender G.D.;
RT "Hormonal regulation of messenger ribonucleic acid encoding
RT steroidogenic acute regulatory protein in ovine corpora lutea.";
RL Endocrinology 136:5423-5429(1995).
CC CC
CC -1- FUNCTION: Plays a key role in steroid hormone synthesis by
CC enhancing the metabolism of cholesterol into pregnenolone.
CC Mediates the transfer of cholesterol from the outer mitochondrial
CC membrane to the inner mitochondrial membrane where it is cleaved
CC to pregnenolone [By similarity].
CC -1- PATHWAY: Steroidogenesis; rate-limiting step.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: Contains 1 START domain.
CC
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CC
EMBL; AF290202; AAG02464.1; -.
DR EMBL; S80098; AAB47088.1; -.
DR HSSP; Q14849; 1EM2.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; START.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
KW Lipid-binding; Lipid transport; Transport; Steroidogenesis;
KW Mitochondrion; Transit peptide; Phosphorylation.
FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 285 STEROIDGENIC ACUTE REGULATORY PROTEIN.
FT DOMAIN 67 280 START.
FT MOD_RES 57 57 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT MOD_RES 195 195 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT CONFLICT 100 100 S -> N (IN REF. 2).
FT CONFLICT 103 103 V -> A (IN REF. 2).
FT CONFLICT 186 186 S -> R (IN REF. 2).
SQ SEQUENCE 285 AA; 31895 MW; AB130FD90A1DF295 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 285;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLQKLGK 12
Db 155 KVLQKICK 162

RESULT 31
ERA THETN
ID ERA THETN STANDARD; PRT; 298 AA.
AC Q9RB50;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GRP-binding protein era homolog.
DE NCBI_TaxID=119072;
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=WB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.,
RT "A complete sequence of the tengcongensis genome."
RL Genome Res. 12:689-700(2002).
CC -!- FUNCTION: Binds both GDP and GTP, has an intrinsic GTPase activity
CC and is essential for cell growth (By similarity).
CC -!- SIMILARITY: Belongs to the era/trme family of GTP-binding
CC proteins. Era subfamily.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC
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CC
CC EMBL; AE013062; AAC24229.1; -
CC HAMAP; MF_00367; -; 1.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR005662; Era.
CC InterPro; IPR005289; GTP-binding_dom.
CC InterPro; IPR006073; GTP1_OBG.
CC InterPro; IPR009019; KH_Prok.
CC InterPro; IPR004044; KH_Type_2.
CC InterPro; IPR002917; MMR_HSR1.
CC InterPro; IPR005225; Small_GTP.
CC Pfam; PF01926; MMR_HSR1; 1.
CC PRINTS; PR00326; GTP1_OBG.
CC SMART; SM00382; AAA; 1.
CC TIGRFAMS; TIGR00436; era; 1.
CC TIGRFAMS; TIGR00550; MG442; 1.
CC TIGRFAMS; TIGR00231; small_GTP; 1.
CC PROSITE; PS00823; KH_Type_2; 1.
CC GTP-binding; RNA-binding; Complete proteome.
KW NP_BIND 12 19 GTP (POTENTIAL).
FT NP_BIND 59 63 GTP (POTENTIAL).
FT NP_BIND 121 124 GTP (POTENTIAL).
FT DOMAIN 202 280 KH_Type-2.
SQ SEQUENCE 298 AA; 34113 MW; 902699D9202A8A1 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 298;
Best Local Similarity 61.5%; Pred. No. 60;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RAQKVLQKLGK 13
Db 283 RDNEKLRLKGYA 295

RESULT 32
ARRH_HELVI
ID ARRH_HELVI STANDARD; PRT; 381 AA.
AC P55274;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Arrestin homolog.
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Antenna;
RX MEDLINE=93199955; PubMed=8452755;
RA Raming K., Freitag J., Krieger J., Breer H.;
RT "Arrestin-subtypes in insect antennae."

RL Cell. Signal. 5:69-80(1993).
CC -!- SIMILARITY: Belongs to the arrestin family.
CC PIR; B56607; B56607.
DR HSP; P08168; ICF1.
DR InterPro; IPR006988; Arrestin.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin_C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PRODOM; PD002099; Arrestin; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Sensory transduction.
SQ SEQUENCE 381 AA; 42747 MW; 84BB92B1BB3DA573 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 381;
Best Local Similarity 54.5%; Pred. No. 74;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RAQKVLQKLG 11
Db 98 RTQERLIKLG 108

RESULT 33
ARR1_RABIT
ID ARR1_RABIT STANDARD; PRT; 410 AA.
AC Q95223;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-arrestin 1 (Arrestin, beta 1).
OS ARRB1.
GN Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RA Man X.L., Sears J.E., Sears M.L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Regulates beta-adrenergic receptor function. Beta-
CC arrestins seem to bind phosphorylated beta-adrenergic receptors,
CC thereby causing a significant impairment of their capacity to
CC activate G(s) proteins.
CC
CC -!- SIMILARITY: Belongs to the arrestin family.
CC
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CC
CC EMBL; U75838; AAC48753.1; -
DR HSP; P08168; ICF1.
DR InterPro; IPR006988; Arrestin.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin_C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PRODOM; PD002099; Arrestin; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Sensory transduction.
SQ SEQUENCE 410 AA; 46360 MW; A8AB781CF089B65A CRC64;

Query Match 59.0%; Score 36; DB 1; Length 410;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RAQKVLQKLGK 12
Db 98 RTQERLIKLG 108


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Db 99 RLQERLIKGLGE 110
PRT; 418 AA.

RESULT 34
ARBL_BOVIN STANDARD; PRT; 418 AA.
AC P17870;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-arrestin 1 (Arrestin, beta 1).
GN ARRB1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90296080; PubMed=2163110;
RA Lohse M.J., Benovic J.L., Codina J., Caron M.G., Lefkowitz R.J.;
RT "Beta-arrestin: a protein that regulates beta-adrenergic receptor
RT function."
RL Science 248:1547-1550 (1990).
RN [2]
RP ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=93340166; PubMed=8340388;
RA Sterne-Marr R., Gurevich V.V., Goldsmith P., Bodine R.C., Sanders C.,
RA Donoso L.A., Benovic J.L.;
RT "Polypeptide variants of beta-arrestin and arrestin3."
RL J. Biol. Chem. 268:15640-15648 (1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RT TISSUE=Brain;
RX MEDLINE=93352853; PubMed=8486559;
RA Fartuti G., Peracchia F., Salliese M., Ambrosini G., Masini M.,
RA Rotilio D., de Biasi A.;
RT "Molecular analysis of human beta-arrestin-1: cloning, tissue
RT distribution, and regulation of expression. Identification of two
RT isoforms generated by alternative splicing."
RL J. Biol. Chem. 268:9753-9761 (1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RT TISSUE=Brain;
RX MEDLINE=93352853; PubMed=8486559;
RA Fartuti G., Peracchia F., Salliese M., Ambrosini G., Masini M.,
RA Rotilio D., de Biasi A.;
RT "Molecular analysis of human beta-arrestin-1: cloning, tissue
RT distribution, and regulation of expression. Identification of two
RT isoforms generated by alternative splicing."
RL J. Biol. Chem. 268:9753-9761 (1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RT TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Regulates beta-adrenergic receptor function. Beta-
CC arrestins seem to bind phosphorylated beta-adrenergic receptors,
CC thereby causing a significant impairment of their capacity to
CC activate G(S) proteins.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1A;
CC ISOID=P17870-1; Sequence=Displayed;
CC Name=1B;
CC ISOID=P17870-2; Sequence=VSP_000321;
CC TISSUE SPECIFICITY: Beta-arrestin 1A is found in cortex,
CC cerebellum, striatum, pineal gland, retina and heart. Beta-
CC arrestin 1B is found in spleen, lung, pituitary and kidney.
CC -1- SIMILARITY: Belongs to the arrestin family.
CC
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CC EMBL; M33601; AAA30387.1; -
CC PIR; A34851; A34851.
CC PDB; 1G4M; 03-OCT-01.
CC PDB; 1G4R; 03-OCT-01.
CC PDB; 1J5Y; 27-MAR-02.
CC InterPro; IPR000699; Arrestin.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00339; arrestin; 1.
CC Pfam; PF02752; arrestin; 1.
CC PRINTS; PR00309; ARRESTIN.
CC PRODOM; PD002099; Arrestin; 1.
CC PROSITE; PS00295; ARRESTINS; 1.
CC Sensory transduction; Alternative splicing; 3D-structure.
CC VARSPLIC 334 341 Missing (in isoform 1B).
CC /FTID=VSP_000321.
SQ SEQUENCE 418 AA; 47131 MW; 345302C20FA3360 CRC64;
Query Match 59.0%; Score 36; DB 1; Length 418;

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Best Local Similarity 50.0%; Pred. NO. 81;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQKVQLKGLK 12
DB 99 RLQERLIKGLGE 110

RESULT 35
ARBL_HUMAN STANDARD; PRT; 418 AA.
AC P49407; O75625; O75630; Q9BTK8;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-arrestin 1 (Arrestin, beta 1).
GN ARRB1 OR ARRL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC TISSUE=Peripheral blood;
RX MEDLINE=93352853; PubMed=8486559;
RA Fartuti G., Peracchia F., Salliese M., Ambrosini G., Masini M.,
RA Rotilio D., de Biasi A.;
RT "Molecular analysis of human beta-arrestin-1: cloning, tissue
RT distribution, and regulation of expression. Identification of two
RT isoforms generated by alternative splicing."
RL J. Biol. Chem. 268:9753-9761 (1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RT TISSUE=Brain;
RX MEDLINE=93352853; PubMed=8486559;
RA Yu Q.M., Zhou T.H., Cheng Z.J., Ma L., Pei G.;
RT "Molecular cloning of two isoforms of human beta-arrestin 1."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RT TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Regulates beta-adrenergic receptor function. Beta-
CC arrestins seem to bind phosphorylated beta-adrenergic receptors,
CC thereby causing a significant impairment of their capacity to
CC activate G(S) proteins.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1A;
CC ISOID=P49407-1; Sequence=Displayed;
CC Name=1B;
CC ISOID=P49407-2; Sequence=VSP_000322;
CC -1- SIMILARITY: Belongs to the arrestin family.

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CC EMBL; L04685; AAA35558.1; --
 CC EMBL; L04685; AAA35558.1; --
 CC EMBL; AF084040; AAC33295.1; --
 CC EMBL; AF084940; AAC34123.1; --
 CC EMBL; BC003636; AAH03636.1; --
 CC PIR; B46682; B46682.
 CC HSSP; P08168; ICF1.
 CC Genew; HGNC:711; ARRB1.
 CC MIM; 107940; --
 CC GO; GO:0005737; C:cytoplasm; TAS.
 CC GO; GO:0005834; C:heterotrimeric G-protein complex; TAS.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0004857; F:enzyme inhibitor activity; TAS.
 CC GO; GO:0007155; P:signal transduction; TAS.
 CC InterPro; IPR000698; Arrestin.
 CC InterPro; IPR007110; Ig-like.
 CC Pfam; PF00339; arrestin; 1.
 CC Pfam; PF02752; arrestin; 1.
 CC PRINTS; PR00309; ARRESTIN.
 CC ProDom; PD02099; Arrestin; 1.
 CC PROSITE; PS00295; ARRESTINS; 1.
 CC Sensory transduction; Alternative splicing.
 CC VARSPLIC 334 341 Missing (in isoform 1B).
 CC FT CONFLICT 146 146 V -> A (IN REF. 1).
 CC FT CONFLICT 165 165 R -> G (IN REF. 1).
 CC FT CONFLICT 229 229 K -> E (IN REF. 1).
 CC FT CONFLICT 329 329 V -> E (IN REF. 2).
 CC FT CONFLICT 400 400 K -> E (IN REF. 1).
 CC FT CONFLICT 414 414 Q -> R (IN REF. 1).
 CC FT CONFLICT 417 417 N -> D (IN REF. 1).
 CC SQ SEQUENCE 418 AA; 47065 MW; 0A3C335092338D10 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 418;
 Best Local Similarity 50.0%; Pred. No. 81;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RAQKVQLKLGK 12
 Db 99 RLQERLIKLGK 110

RESULT 36
 ARRI RAT ID ARRI RAT STANDARD; PRT; 418 AA.
 AC P29066;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Beta-arrestin 1 (Arrestin, beta 1).
 GN ARRB1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RC STRAIN=FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=92388146; PubMed=1517224;
 RA Attamadal H., Arriza J.L., Aoki C., Dawson T.M., Codina J.,
 RA Kwatra M.M., Snyder S.H., Caron M.G., Lefkowitz R.J.;
 RA "Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene
 RT family."; Chem. 267:17892-17890 (1992).
 RT J. Biol. Chem. 267:17892-17890 (1992).

CC -!- FUNCTION: Regulates beta-adrenergic receptor function. Beta-
 CC arrestins seem to bind phosphorylated beta-adrenergic receptors,
 CC thereby causing a significant impairment of their capacity to
 CC activate G(S) proteins.
 CC -!- TISSUE SPECIFICITY: Predominantly localized in neuronal tissues
 CC and in the spleen.
 CC -!- SIMILARITY: Belongs to the arrestin family.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; M91589; AAA74459.1; --
 CC PIR; B43404; B43404.
 CC HSSP; P08168; ICF1.
 CC InterPro; IPR000698; Arrestin.
 CC InterPro; IPR007110; Ig-like.
 CC Pfam; PF00339; arrestin; 1.
 CC Pfam; PF02752; arrestin; 1.
 CC PRINTS; PR00309; ARRESTIN.
 CC ProDom; PD02099; Arrestin; 1.
 CC PROSITE; PS00295; ARRESTINS; 1.
 CC Sensory transduction.
 CC SQ SEQUENCE 418 AA; 47019 MW; 0A3C07D71B7ABC55 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 418;
 Best Local Similarity 50.0%; Pred. No. 81;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RAQKVQLKLGK 12
 Db 99 RLQERLIKLGK 110

RESULT 37

HEXA FORGI ID HEXA FORGI STANDARD; PRT; 777 AA.
 AC P49008;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Beta-hexosaminidase precursor (EC 3.2.1.52) (N-acetyl-beta-
 DE Glucosaminidase) (Beta-GlcNAcase) (Beta-N-acetylhexosaminidase)
 DE (Beta-NAHASE).
 GN NAHA OR PG0043.
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OC NCBI_TaxID=837;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=95187310; PubMed=7881557;
 RA Lovatt A., Roberts I.S.;
 RA "Cloning and expression in Escherichia coli of the nahA gene from
 RT Porphyromonas gingivalis indicates that beta-N-acetylhexosaminidase
 RT is an outer-membrane-associated lipoprotein."; Microbiology 140:3399-3406 (1994).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.,
 RA Hatt D.H., Kohn J.F., Nelson W.C., Mason T., Tallon L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RA "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83.";

RL J. Bacteriol. 185:5591-5601(2003).

CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides.

CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).

CC -!- SIMILARITY: Belongs to family 20 of glycosyl hydrolases.

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CC -----

DR EMBL; X78979; CAA55582.1; --

DR EMBL; AE017172; AAQ65295.1; --

DR TIGR; PG0043; --

DR InterPro; IPR001540; Glyco_hydro_20.

DR InterPro; IPR000437; Prok_Lipopr_t.s.

DR Pfam; PF00728; Glyco_hydro_20; 1.

DR Pfam; PF02838; Glyco_hydro_20b; 1.

DR PRINTS; PR00738; GLYDHLASE20.

DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

DR Hydrolase; Glycosidase; Signal; Outer membrane; Lipoprotein; Palmitate; Complete proteome.

KW SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 777 BETA-HEXOSAMINIDASE.

FT LIPID 19 19 N-palmitoyl cysteine (Probable).

FT LIPID 19 19 S-diacylglycerol cysteine (Probable).

FT CONFLICT 258 258 R -> H (IN REF. 1).

FT CONFLICT 265 265 E -> M (IN REF. 1).

FT CONFLICT 282 283 LA -> PR (IN REF. 1).

FT CONFLICT 575 575 T -> S (IN REF. 1).

FT CONFLICT 747 747 G -> A (IN REF. 1).

FT CONFLICT 777 777 AA; 87661 MW; DOA55D2C2FFAD864 CRC64;

SQ SEQUENCE 777 AA; 87661 MW; DOA55D2C2FFAD864 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 777;

Best Local Similarity 88.9%; Pred. No. 1.4e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 EKVLQKLGK 12

DB 371 EKVLQKLGK 379

RESULT 38

CHD3_CABEL STANDARD; PRT; 1787 AA.

ID -CHD3_CABEL STANDARD; PRT; 1787 AA.

AC Q22516; Q18794; (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chromodomain helicase-DNA-binding protein 3 homolog (CHD-3).

GN CHD-3 OR T14G8.1

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20530482; PubMed=11076750;

RA von Zelewsky T., Palladino F., Brunschwig K., Tobler H., Hajnal A., Mueller F.;

RA "The C. elegans Mi-2 chromatin-remodelling proteins function in vulval cell fate determination."

RT Development 127:5277-5284(2000).

RL [2]

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Matthews P., McMurray A.;

RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Chromatin-remodelling protein that function in vulval

cell fate determination.

CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.

CC -!- SIMILARITY: Contains 2 PHD-type zinc fingers.

CC -!- SIMILARITY: Contains 2 chromo domains.

CC -----

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CC -----

DR EMBL; AF308444; RAQ29837.1; --

DR EMBL; Z67884; CAA31810.1; --

DR EMBL; Z67881; CAA31810.1; JOINED.

DR EMBL; Z67881; CAA31798.1; --

DR EMBL; Z67884; CAA31798.1; JOINED.

DR PIR; T20160; T20160.

DR Wormpep; T14G8.1; CE03657.

DR InterPro; IPR000953; Chromo.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR002464; DEAH box.

DR InterPro; IPR001650; Helicase_C.

DR InterPro; IPR000330; SNF2 N.

DR InterPro; IPR001965; Znf_PHD.

DR InterPro; IPR001841; Znf_Ring.

DR Pfam; PF00385; Chromo; 1.

DR Pfam; PF00271; helicase_C; 1.

DR Pfam; PF00628; PHD; 2.

DR Pfam; PF00176; SNF2 N; 1.

DR SMART; SM00298; CHROMO; 2.

DR SMART; SM00487; DEXDC; 1.

DR SMART; SM00490; HELIC; 1.

DR SMART; SM00249; PHD; 2.

DR SMART; SM00184; RING; 2.

DR PROSITE; PS00598; CHROMO_1; FALSE_NEG.

DR PROSITE; PS00013; CHROMO_2; 1.

DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.

DR PROSITE; PS01359; ZF_PHD_1; 2.

DR PROSITE; PS00016; ZF_PHD_2; 2.

KW Chromatin regulator; Nuclear protein; Repeat; Helicase; DNA-binding; ATP-binding; Zinc-finger.

KW DOMAIN 59 62 POLY-LYS.

FT ZN_FING 265 312 PHD-TYPE 1.

FT ZN_FING 328 375 PHD-TYPE 2.

FT DOMAIN 373 476 CHROMO 1.

FT DOMAIN 501 583 CHROMO 2.

FT DOMAIN 1287 1291 POLY-ARG.

FT NP_BIND 641 648 ATP (POTENTIAL).

FT SITE 763 766 DEAH BOX.

SQ SEQUENCE 1787 AA; 205254 MW; 1EFCB1FPECB59740 CRC64;

Query Match 59.0%; Score 36; DB 1; Length 1787;

Best Local Similarity 80.0%; Pred. No. 2.9e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QEKVLQKLGK 12

DB 1226 QEKVLQKLGK 1235

RESULT 39

STAR_PIG STANDARD; PRT; 285 AA.

ID -STAR_PIG STANDARD; PRT; 285 AA.

AC Q28996; O95259;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Steroidogenic acute regulatory protein, mitochondrial precursor (STAR).

DE (STAR) (STARD1).

GN STAR.

CC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB15N / NA1000;
 RX MEDLINE=97207014; PubMed=9054507;
 RA Mohl D.A., Gober J.W.;
 RT "Cell cycle-dependent polar localization of chromosome partitioning
 proteins in *Caulobacter crescentus*.";
 RL Cell 88:675-684(1997).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Eisen J.A., Heideberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Petočka I., Nelson W.C., Newton A.S., Stephens C., Padke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 CC -!- FUNCTION: INVOLVED IN CHROMOSOME PARTITION. LOCALIZE TO BOTH POLES
 OF THE PREDIVISIONAL CELL FOLLOWING COMPLETION OF DNA REPLICATION.
 CC BINDS TO THE DNA ORIGIN OF REPLICATION.
 CC -!- SIMILARITY: Belongs to the parB family.
 CC
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 CC
 CC
 DR EMBL; U87804; AAB51268.1; -;
 DR EMBL; AE006032; AAK25714.1; -;
 DR PIR; F87714; F87714.
 DR TIGR; CC3752; -;
 DR InterPro; IPR004437; ParB_part.
 DR InterPro; IPR003115; ParBC.
 DR Pfam; PF02195; ParBc; 1.
 DR SMART; SM00470; ParB; 1.
 DR TIGRFAMS; TIGR00180; parB_part; 1.
 DR Chromosome partition; DNA-binding; Complete proteome.
 FT CONFLICT 15 26 LLGEVDAAPAAQ -> CWASRRRAGSG (IN REF. 1).
 FT CONFLICT 31 31 L -> F (IN REF. 1).
 FT CONFLICT 294 AA; 31824 MW; FAYD3DCPFA81AE639 CRC64;
 SQ SEQUENCE 294 AA; 31824 MW; 35686 MW; 6DF4703EA7252910 CRC64;
 Query Match 57.4%; Score 35; DB 1; Length 294;
 Best Local Similarity 46.2%; Pred. No. 88;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 RAEKVLQKLGKA 13
 DB 150 RTQENIAQTIGKS 162
 RESULT 42
 Y006 YEAST
 ID Y006 YEAST STANDARD; PRT; 313 AA.
 AC Q12094;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Hypothetical UPF0293 protein YOR006C.
 GN YOR006C OR UNL313.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97051599; PubMed=8896276;
 RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
 RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
 from *Saccharomyces cerevisiae* reveals 15 open reading frames, five of
 which correspond to previously identified genes.";
 RL Yeast 12:1091-1095(1996).
 CC -!- SIMILARITY: Belongs to the UPF0293 family.
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 CC
 CC
 DR EMBL; U43491; AAC49486.1; -;
 DR EMBL; Z74914; CAA99194.1; -;
 DR PIR; S61990; S61990.
 DR GerMOnline; 143594; -;
 DR SGD; S0005532; YOR006C.
 DR InterPro; IPR007177; DUF367.
 DR InterPro; IPR007209; RLI.
 DR Pfam; PF04034; DUF367; 1.
 DR Pfam; PF04068; RLI; 1.
 KW Hypothetical protein.
 KR SEQUENCE 313 AA; 35686 MW; 6DF4703EA7252910 CRC64;
 SQ SEQUENCE 313 AA; 35686 MW; 6DF4703EA7252910 CRC64;
 Query Match 57.4%; Score 35; DB 1; Length 313;
 Best Local Similarity 66.7%; Pred. No. 93;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RAEKVLQKLGK 12
 DB 204 RAEEMWLQKLEK 215
 RESULT 43
 AR22 HUMAN
 ID AR22 HUMAN STANDARD; PRT; 409 AA.
 AC P32121; Q8N7Y2; Q9UEO6;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Beta-arrestin 2 (Arrestin, beta 2).
 GN ARRE2 OR ARRE2 OR ARB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thyroid;
 RX MEDLINE=92267237; PubMed=1587386;
 RA Rapoport B., Kaufman K.D., Chamenbalk G.D.;
 RT "Cloning of a member of the arrestin family from a human thyroid cDNA
 library.";
 RL Mol. Cell. Endocrinol. 84:R39-R43(1992).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RA Yu Q.M., Zhou T.H., Wu Y.L., Cheng Z.J., Ma L., Pei G.;
 RT "G-protein coupled receptor interaction with beta-arrestin 2 through
 specific agonist stimulation.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Testis;
 RA Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,

RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isegai T.,
RT "NEDO human cDNA sequencing project.",
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Grimwood J., Schmutz J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [1]
CC -!- FUNCTION: Regulates beta-adrenergic receptor function. Beta-
arrestins seem to bind phosphorylated beta-adrenergic receptors,
thereby causing a significant impairment of their capacity to
activate G(s) proteins.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=1;
Name=2;
IsoId=P32121-1; Sequence=Displayed;
IsoId=P32121-2; Sequence=VSP_008194, VSP_008195;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the arrestin family.

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DR EMBL; Z11501; CAA77577.1; -;
DR EMBL; AF106941; AAC99468.1; -;
DR EMBL; AK097542; BAC05094.1; -;
DR EMBL; BC007427; AAH07427.1; -;
DR F1R; S15984; S15984.
DR HSSP; P08168; 1CPI.
DR Genew; HGNC:712; ARRB2.
DR MIM; 107941; -;
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0005886; Cytoplasmic membrane; TAS.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin; C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR ProDom; PD002059; Arrestin; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
KW Sensory transduction; Nuclear protein; Alternative splicing.
FT DOMAIN 39 399 NUCLEAR EXPORT SIGNAL (By SIMILARITY).
FT VARSPLIC 39 53 Missing (in isoform 2).
FT FTID=VSP_008194.
FT VARSPLIC 360 360 S -> SAPTPPTPLPVP (in isoform 2).

FT FTID=VSP_008195.
FT R -> P (IN REF. 1).
SQ SEQUENCE 409 AA; 46105 MW; DSEC507DA7B84FF CRC64;
Query Match 57.4%; Score 35; DB 1; Length 409;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 RAQKVLQKLGK 12
Db 100 RLQDRLLRLKLG 111
RESULT 44
ARR2 MOUSE
ID ARR2 MOUSE STANDARD; PRT; 410 AA.
AC Q31Y74;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-arrestin 2 (Arrestin, beta 2).
GN ARRB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Grimwood J., Schmutz J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RP NUCLEOCYTOPLASMIC SHUTTLING.
RX MEDLINE=22241956; PubMed=12167659;
RA Scott M.G., Le Rouzic E., Perianin A., Pierotti V., Enslin H.,
RA Benichou S., Marullo S., Benmerah A.,
RT "Differential nucleocytoplasmic shuttling of beta-arrestins.
Characterization of a leucine-rich nuclear export signal in
beta-arrestin2.",
RL J. Biol. Chem. 277:37693-37701(2002).
CC -!- FUNCTION: Regulates beta-adrenergic receptor function. Beta-
arrestins seem to bind phosphorylated beta-adrenergic receptors,
thereby causing a significant impairment of their capacity to
activate G(s) proteins.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- TISSUE SPECIFICITY: Predominantly localized in neuronal tissues
and in the spleen.
CC -!- SIMILARITY: Belongs to the arrestin family.

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CC CC
DR EMBL; BC016642; AAH16642.1; -.
DR MGD; MGI:99474; Artd2.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PRODOM; PD002099; ARRESTIN; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
DR Sensory transduction; Nuclear protein.
KW DOMAIN 390 400 NUCLEAR EXPORT SIGNAL.
FT DOMAIN 390 400 NUCLEAR EXPORT SIGNAL (BY SIMILARITY).
SQ SEQUENCE 410 AA; 4634 MW; ODFA7A1C532AE03 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 410;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
DB 100 RLQDRLLKLGK 111

RESULT 45
ARR2 RAT STANDARD; PRT; 410 AA.
AC P29067;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-arrestin 2 (Arrestin, beta 2).
GN ARRB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=92388146; PubMed=1517224;
RA Attramadal H., Arriza J.L., Acki C., Dawson T.M., Codina J.,
RA Kwatra M.M., Snyder S.H., Caron M.G., Lefkowitz R.J.;
RT "Beta-arrestin2, a novel member of the arrestin/beta-arrestin gene
RT family.";
RL J. Biol. Chem. 267:17882-17890(1992).
RN [2]
RP SEQUENCE OF 295-410 FROM N.A.
RC TISSUE=Pineal gland;
RX MEDLINE=94140898; PubMed=8308033;
RA Craft C.M., Whitmore D.H., Wlechmann A.F.;
RT "Cone arrestin identified by targeting expression of a functional
RT family.";
RL J. Biol. Chem. 269:4613-4619(1994).
RN [3]
RP SEQUENCE OF 305-386 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Retina;
RX MEDLINE=99145674; PubMed=9767391;
RA Komori N., Cain S.D., Roch J.-M., Miller K.E., Matsumoto H.;
RT "Differential expression of alternative splice variants of
RT beta-arrestin-1 and -2 in rat central nervous system and peripheral
RT tissues.";
RL Eur. J. Neurosci. 10:2607-2616(1998).
CC -!- FUNCTION: Regulates beta-adrenergic receptor function. Beta-
CC arrestins seem to bind phosphorylated beta-adrenergic receptors,
CC thereby causing a significant impairment of their capacity to
CC activate G(s) proteins.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Predominantly localized in neuronal tissues
CC and in the spleen.
CC -!- SIMILARITY: Belongs to the arrestin family.
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CC CC
DR EMBL; BC016642; AAH16642.1; -.
DR MGD; MGI:99474; Artd2.
DR InterPro; IPR000698; Arrestin.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00339; arrestin; 1.
DR Pfam; PF02752; arrestin C; 1.
DR PRINTS; PR00309; ARRESTIN.
DR PRODOM; PD002099; ARRESTIN; 1.
DR PROSITE; PS00295; ARRESTINS; 1.
DR Sensory transduction; Nuclear protein.
KW DOMAIN 390 400 NUCLEAR EXPORT SIGNAL.
FT DOMAIN 390 400 NUCLEAR EXPORT SIGNAL (BY SIMILARITY).
SQ SEQUENCE 410 AA; 4634 MW; ODFA7A1C532AE03 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 410;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGK 12
DB 100 RLQDRLLKLGK 111

RESULT 46
ARLY OCEIH STANDARD; PRT; 459 AA.
AC OCELT9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Argininosuccinate lyase (EC 4.3.2.1) (Argininosuccinase) (ASAL).
GN ARGH OR OB3128.
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -!- CATALYTIC ACTIVITY: N-(L-arginino)succinate = fumarate + L-
CC arginine.
CC -!- PATHWAY: Arginine biosynthesis; eighth (last) step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the lyase 1 family. Argininosuccinate lyase
CC subfamily.
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CC CC
DR EMBL; AP004603; BAC15084.1; -.
DR HAMAP; MF 00006; -.
DR InterPro; IPR005049; argH.
DR InterPro; IPR000362; Fumarate_lyase.
DR InterPro; IPR008948; L-Aspartase-like.

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DR Pfam: PF00206; lyase 1; 1.
DR PRINTS: PR00149; FUMARATELYASE.
DR TIGRFAMs: TIGR00838; argH; 1.
DR PROSITE: PS00163; FUMARATE LYASES; 1.
DR Arginine biosynthesis; Lyase; Complete proteome.
KW SEQUENCE 459 AA; 51230 MW; C100878/5B890964 CRC64;
SQ SEQUENCE 459 AA; 51230 MW; C100878/5B890964 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 459;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AOEKVLQKLGKA 13
|:|:|:|:|
DB 440 AKESVLOQIAKA 451

RESULT 47
GATB_STRCO STANDARD; PRT; 504 AA.
AC Q92578;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Asparyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
DE (EC 6.3.5.-) (Asp/Glu-ADT subunit B).
GN GATB OR SC05501 OR SC899.13.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieseer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieseer T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajadream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RA ?Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn)
CC or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
CC tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
CC of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction
CC takes place in the presence of glutamine and ATP through an
CC activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (by
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
CC + phosphate + L-glutamyl-tRNA(Gln) + L-glutamate.
CC -!- CATALYTIC ACTIVITY: ATP + L-asparaginyl-tRNA(Asn) + L-glutamine = ADP
CC + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate.
CC -!- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
CC -!- SIMILARITY: Belongs to the gatB/gatE family. GatB subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL939124; CAB37577.1; -.
CC PIR; T35817; T35817.
CC HAMAP; MF_00121; -.
CC InterPro; IPR004413; GatB.
CC InterPro; IPR006107; GatB_cent.

DR Pfam: PF00206; lyase 1; 1.
DR PRINTS: PR00149; FUMARATELYASE.
DR TIGRFAMs: TIGR00838; argH; 1.
DR PROSITE: PS00163; FUMARATE LYASES; 1.
DR Arginine biosynthesis; Lyase; Complete proteome.
KW SEQUENCE 459 AA; 51230 MW; C100878/5B890964 CRC64;
SQ SEQUENCE 459 AA; 51230 MW; C100878/5B890964 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 459;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AOEKVLQKLGKA 13
|:|:|:|:|
DB 440 AKESVLOQIAKA 451

RESULT 47
GATB_STRCO STANDARD; PRT; 504 AA.
AC Q92578;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Asparyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
DE (EC 6.3.5.-) (Asp/Glu-ADT subunit B).
GN GATB OR SC05501 OR SC899.13.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieseer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieseer T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajadream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RA ?Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn)
CC or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
CC tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
CC of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction
CC takes place in the presence of glutamine and ATP through an
CC activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (by
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
CC + phosphate + L-glutamyl-tRNA(Gln) + L-glutamate.
CC -!- CATALYTIC ACTIVITY: ATP + L-asparaginyl-tRNA(Asn) + L-glutamine = ADP
CC + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate.
CC -!- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
CC -!- SIMILARITY: Belongs to the gatB/gatE family. GatB subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL939124; CAB37577.1; -.
CC PIR; T35817; T35817.
CC HAMAP; MF_00121; -.
CC InterPro; IPR004413; GatB.
CC InterPro; IPR006107; GatB_cent.

DR Pfam: PF00206; lyase 1; 1.
DR PRINTS: PR00149; FUMARATELYASE.
DR TIGRFAMs: TIGR00838; argH; 1.
DR PROSITE: PS00163; FUMARATE LYASES; 1.
DR Arginine biosynthesis; Lyase; Complete proteome.
KW SEQUENCE 459 AA; 51230 MW; C100878/5B890964 CRC64;
SQ SEQUENCE 459 AA; 51230 MW; C100878/5B890964 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 504;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RAOEKVLQKLGKA 13
|:|:|:|:|
DB 490 RVKELILEKLGVA 502

RESULT 48
REC_N_HELPJ STANDARD; PRT; 522 AA.
AC Q92780;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA repair protein recN (Recombination protein N).
DE REC_N_HELPJ OR JHP1434.
GN Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.B., Noonan B., Guild B.C., deJonghe B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -!- FUNCTION: MAY BE INVOLVED IN RECOMBINATIONAL REPAIR OF DAMAGED
CC -!- DNA (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the recN family.
CC
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CC
CC EMBL; AE001566; AB007019.1; -.
CC PIR; B71807; B71807.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR003439; ABC_transporter.
CC SMART; SM00382; AAA; 1.
CC NP_BIND 36 43 ATP (POTENTIAL).
CC SEQUENCE 522 AA; 59349 MW; 000D7EE3C0632EA5 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 522;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EKVLEKLG 11
|:|:|:|:|
DB 282 EKVLEKLG 289
```


RESULT 49
NAFI HUMAN
ID NAF1 HUMAN STANDARD; PRT; 636 AA.
AC Q15025; Q76008; Q96EL9; Q99833; Q9H1J3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nef-associated factor 1 (Naf1) (Hiv-1 Nef interacting protein)
DE (Viron-associated nuclear shuttling protein) (VAN) (hVAN) (TNFAIP3
DE interacting protein 1)
GN TNFIP1 OR NAF1 OR KIAA0113.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP TISSUE=Peripheral blood;
RC MEDLINE=99120485; PubMed=9923610;
RA Fukushima M., Dixon J., Kimura T., Teurutani N., Dixon M.J.,
RA Yamamoto N.;
RT "Identification and cloning of a novel cellular protein Naf1, Nef-
RT associated factor 1, that increases cell surface CD4 expression.";
RN FEBS Lett. 442:83-88(1999).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Leukocyte;
RC MEDLINE=20541981; PubMed=11090181;
RX Gupta K., Ott D., Hope T.J., Siliciano R.P., Boeke J.D.;
RA "A human nuclear shuttling protein that interacts with human
RT immunodeficiency virus type 1 matrix is packaged into virions.";
RJ J. Virol. 74:11811-11824(2000).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Lung;
RC MEDLINE=22386257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN SEQUENCE OF 136-636 FROM N.A. (ISOFORM 2).
RP TISSUE=Craniofacial;
RC MEDLINE=96276047; PubMed=8681136;
RX Loftus S.K., Dixon J., Koprivnikar K., Dixon M.J., Wasmuth J.J.;
RA "Transcriptional map of the Treacher Collins candidate gene region.";
RL Genome Res. 6:26-34(1996).
[5]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP Ohara O., Nagase T., Kikuno R., Nomura N.;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE OF 341-636 FROM N.A. (ISOFORM 1).
RP TISSUE=Bone marrow;
RC MEDLINE=95308325; PubMed=7788527;
RX Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
RA Tabata S., Ishikawa K.-I., Kawarabayashi Y., Kotani H., Nomura N.;

"Prediction of the coding sequences of unidentified human genes. III.
The coding sequences of 40 new genes (K1AA0081-K1AA0120) deduced by
analysis of cDNA clones from human cell line KG-1.";
DNA Res. 2:37-43(1995).
[7]
RN SEQUENCE OF 94-412 FROM N.A.
RP Fukushima M., Kimura T., Yamamoto N.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RC FUNCTION: Interacts with zinc finger protein A20/TNFAIP3 and
inhibits TNF-induced NF-kappa-B-dependent gene expression by
interfering with an RIP- or TRAF2-mediated transactivation signal
(By similarity). Increases cell surface CD4(T4) antigen
expression. Interacts with HIV-1 matrix protein and is packaged
into virions and overexpression can inhibit viral replication. May
regulate matrix nuclear localization, both nuclear import of p1C
(preintegration complex) and export of GAG polypeptide and viral
genomic RNA during virion production.
CC -1 SUBUNIT: Interacts with TNFAIP3 (By similarity). Interacts with
CC HIV-1 matrix protein.
CC -1 SUBCELLULAR LOCATION: Cytoplasmic. Shuttles between the nucleus
CC and cytoplasm in a CRM1-dependent manner.
CC -1 ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Alpha;
CC IsoId=Q15025-1; Sequence=Displayed;
CC Name=2; Synonyms=Beta;
CC IsoId=Q15025-2; Sequence=VSP_003913;
CC Note=No experimental confirmation available;
CC -1 TISSUE SPECIFICITY: Ubiquitous. Strongly expressed in peripheral
CC blood lymphocytes, spleen and skeletal muscle, and is weakly
CC expressed in the brain.
CC -1 CAUTION: Ref.7 sequence differs from that shown due to frameshifts
CC in positions 152 and 154.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; AJ011895; CAA09855.1; -
CC EMBL; AJ011896; CAA09856.1; -
CC EMBL; AY012155; AAG42154.1; -
CC EMBL; BC012133; AAH12133.1; -
CC EMBL; BC014008; AAH14008.1; -
CC EMBL; U39403; AAC99999.1; -
CC EMBL; D30755; BAA06416.2; -
CC EMBL; U83844; AAB41438.1; ALT_FRAME.
CC Genew; HGNC:16903; TNFIP1.
CC MIM; 607714; -
CC GO; GO:0005622; C:intracellular; TAS.
CC GO; GO:0005515; P:protein binding; TAS.
CC GO; GO:0009101; P:glycoprotein biosynthesis; IDA.
CC GO; GO:0045071; P:negative regulation of viral genome replica. .; TAS.
CC Coiled coil; Nuclear protein; Alternative splicing.
CC FT DOMAIN 20 73
CC FT COILED COIL (POTENTIAL).
CC FT DOMAIN 196 258
CC FT COILED COIL (POTENTIAL).
CC FT DOMAIN 294 535
CC FT COILED COIL (POTENTIAL).
CC FT DOMAIN 94 412
CC FT INTERACTS WITH NEF.
CC FT DOMAIN 524 530
CC FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT DOMAIN 539 636
CC FT PRO-RICH.
CC FT VARSPLIC 627 636
CC FT SPKNDREGPQ -> PADLRLPRN (in isoform 2).
CC FT FTID=VSP_003913.
CC FT CONFLICT 148 148
CC FT G -> D (IN REF. 3; AAH12133).
CC FT CONFLICT 299 299
CC FT A -> P (IN REF. 2).
CC FT SEQUENCE 636 AA; 71864 MW; D81B96BEAD50D871 CRC64;
Query Match 57.4%; Score 35; DB 1; Length 636;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:38:36 ; Search time 30.6129 Seconds
(without alignments)
133.987 Million cell updates/sec

Title: US-10-069-540A-2_COPY_23_35

Perfect score: 61

Sequence: 1 RAQEKVLQKLGA 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

SPTREMBL 25:**

1: sp archaea:**

2: sp bacteria:**

3: sp fungi:**

4: sp human:**

5: sp invertebrate:**

6: sp mammal:**

7: sp mbc:**

8: sp organelle:**

9: sp phage:**

10: sp plant:**

11: sp rodent:**

12: sp virus:**

13: sp vertebrate:**

14: sp unclassified:**

15: sp rvirus:**

16: sp bacteriophage:**

17: sp archaea:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	250	11	Q8BXH2
2	61	100.0	385	4	Q8NFI3
3	61	100.0	439	4	Q8BTH3
4	61	100.0	478	13	Q7ZNP5
5	61	100.0	490	4	Q8WHH9
6	61	100.0	564	4	Q9UKN4
7	61	100.0	565	4	Q9UBW5
8	61	100.0	565	4	Q86VV0
9	61	100.0	685	11	Q7TGF7
10	61	100.0	695	4	Q8N4G0
11	57	93.4	524	13	Q803I3
12	49	80.3	414	5	Q8WQ54
13	47	77.0	602	5	Q9YQ94
14	41	67.2	461	10	Q9FP28
15	41	67.2	570	16	P94544
16	41	67.2	651	16	Q8E5M0

17	41	67.2	651	16	Q8DX0	Q8DX0 streptococ
18	41	67.2	874	10	Q84PYS	Q84PYS oryza sativ
19	41	67.2	876	10	Q943V8	Q943V8 oryza sativ
20	41	67.2	876	10	Q7XXG7	Q7XXG7 oryza sativ
21	41	67.2	1235	5	Q8SX64	Q8SX64 drosophila
22	41	67.2	1381	5	Q9VZT7	Q9VZT7 drosophila
23	40	65.6	176	16	Q9EHL3	Q9EHL3 deinococcus
24	39	63.9	502	16	Q8J132	Q8J132 tropheryma
25	39	63.9	505	16	Q97PES	Q97PES streptococ
26	39	63.9	510	16	Q8DNU7	Q8DNU7 streptococ
27	39	63.9	513	16	Q8RBN7	Q8RBN7 thermococ
28	39	63.9	516	10	Q42701	Q42701 catharanthu
29	39	63.9	522	16	Q83G32	Q83G32 tropheryma
30	39	63.9	524	10	Q42700	Q42700 catharanthu
31	39	63.9	700	16	Q8ET76	Q8ET76 corynebacte
32	38	62.3	88	4	Q9BS66	Q9BS66 homo sapien
33	38	62.3	193	4	Q8IU96	Q8IU96 homo sapien
34	38	62.3	250	4	Q9UEN2	Q9UEN2 homo sapien
35	38	62.3	257	4	Q8IX25	Q8IX25 homo sapien
36	38	62.3	300	17	Q8T25	Q8T25 methanosarc
37	38	62.3	331	4	Q9S278	Q9S278 homo sapien
38	38	62.3	408	13	Q7T2D2	Q7T2D2 brachydanio
39	38	62.3	445	16	Q89AC2	Q89AC2 buchnera ap
40	38	62.3	452	16	Q8FJR9	Q8FJR9 xanthomonas
41	38	62.3	461	5	Q21004	Q21004 caenorhabdi
42	38	62.3	474	16	Q9KTE0	Q9KTE0 vibrio chol
43	38	62.3	474	16	Q8RCI2	Q8RCI2 salmonella
44	38	62.3	474	16	Q8DFE8	Q8DFE8 vibrio vuln
45	38	62.3	474	16	Q8CX45	Q8CX45 shewanella
46	38	62.3	474	16	Q87RP4	Q87RP4 vibrio para
47	38	62.3	474	16	Q83LY3	Q83LY3 shigella fl
48	38	62.3	475	16	Q87AP4	Q87AP4 xylella fas
49	38	62.3	475	16	Q7VE74	Q7VE74 haemophilus
50	38	62.3	485	16	Q8F8B5	Q8F8B5 xanthomonas
51	38	62.3	488	16	Q8Z8G5	Q8Z8G5 salmonella
52	38	62.3	496	16	Q9AD76	Q9AD76 streptomyce
53	38	62.3	497	16	Q9PEX2	Q9PEX2 xylella fas
54	38	62.3	509	5	Q9VTZ7	Q9VTZ7 drosophila
55	38	62.3	535	17	Q8Z2Q9	Q8Z2Q9 pyrobaculum
56	38	62.3	552	4	Q9N089	Q9N089 homo sapien
57	38	62.3	552	11	Q91YNO	Q91YNO mus musculu
58	38	62.3	574	16	Q9ZLM0	Q9ZLM0 rhizobium m
59	38	62.3	817	16	Q83DJ0	Q83DJ0 coxiella bu
60	38	62.3	908	17	Q8Q0E6	Q8Q0E6 methanosarc
61	37	60.7	81	17	Q34794	Q34794 methanobact
62	37	60.7	81	2	Q03115	Q03115 streptococ
63	37	60.7	168	2	Q9AGA2	Q9AGA2 streptococ
64	37	60.7	186	16	Q7VLQ5	Q7VLQ5 haemophilus
65	37	60.7	316	11	Q8BHS4	Q8BHS4 mus musculu
66	37	60.7	386	17	Q97C57	Q97C57 thermoplas
67	37	60.7	386	17	Q97A29	Q97A29 thermoplas
68	37	60.7	393	17	Q979E8	Q979E8 thermoplas
69	37	60.7	395	10	Q7XQW1	Q7XQW1 oryza sativ
70	37	60.7	403	17	Q26176	Q26176 methanobact
71	37	60.7	441	5	Q8MP09	Q8MP09 caenorhabdi
72	37	60.7	444	11	Q8JZT3	Q8JZT3 mus musculu
73	37	60.7	461	4	Q8N2L3	Q8N2L3 homo sapien
74	37	60.7	461	4	Q8H173	Q8H173 homo sapien
75	37	60.7	465	11	Q9EPK6	Q9EPK6 mus musculu
76	37	60.7	465	11	Q91V34	Q91V34 mus musculu
77	37	60.7	468	10	Q94J76	Q94J76 oryza sativ
78	37	60.7	472	10	Q98RQ7	Q98RQ7 guillardia
79	37	60.7	526	17	Q98616	Q98616 pyrococcus
80	37	60.7	545	16	Q8EEX1	Q8EEX1 shewanella
81	37	60.7	585	11	Q8BHY7	Q8BHY7 mus musculu
82	37	60.7	591	10	Q9LU46	Q9LU46 arabidopsis
83	37	60.7	636	10	Q7XWT1	Q7XWT1 oryza sativ
84	37	60.7	669	10	Q7XRD9	Q7XRD9 oryza sativ
85	37	60.7	684	10	Q7X8V4	Q7X8V4 oryza sativ
86	37	60.7	728	10	Q7XWRO	Q7XWRO oryza sativ
87	37	60.7	784	16	Q88QC2	Q88QC2 pseudomonas
88	37	60.7	820	10	Q7XLC2	Q7XLC2 oryza sativ
89	37	60.7	823	10	Q7XPA8	Q7XPA8 oryza sativ

```

90 37 60.7 839 10 Q7XP88
91 37 60.7 858 10 Q7XMB9
92 37 60.7 876 10 Q7XV39
93 37 60.7 876 10 Q7XNA9
94 37 60.7 897 10 Q8S6T5
95 37 60.7 905 11 Q8CHD8
96 37 60.7 1110 3 Q8NIU9
97 37 60.7 1148 10 Q8H897
98 37 60.7 1209 4 Q7Z570
99 37 60.7 1274 10 Q9ZQR2
100 36 59.0 82 16 Q93MT9
101 36 59.0 99 9 Q8SDT2
102 36 59.0 124 6 Q7YS73
103 36 59.0 131 5 Q7YX99
104 36 59.0 217 15 Q8NTA9
105 36 59.0 227 15 Q90QX6
106 36 59.0 275 16 Q830T9
107 36 59.0 296 16 Q8F2V6
108 36 59.0 296 16 Q9ABP4
109 36 59.0 334 10 Q9FFP2
110 36 59.0 384 6 Q8F299
111 36 59.0 410 11 Q8BNT5
112 36 59.0 418 5 Q8YB1
113 36 59.0 418 11 Q8BNG8
114 36 59.0 439 16 Q8AIL2
115 36 59.0 442 16 Q9JXV8
116 36 59.0 442 16 Q9JW12
117 36 59.0 443 16 Q8ZS17
118 36 59.0 447 16 Q7V286
119 36 59.0 451 16 Q8DAD1
120 36 59.0 457 16 Q8Y206
121 36 59.0 462 16 Q9F0Z2
122 36 59.0 462 16 Q8NTY4
123 36 59.0 463 16 Q8ZCA7
124 36 59.0 475 16 Q7WMN3
125 36 59.0 475 16 Q7WB66
126 36 59.0 500 5 Q9XUB5
127 36 59.0 512 10 Q9LUD3
128 36 59.0 856 16 Q8Y320
129 36 59.0 933 5 Q23360
130 36 59.0 1070 3 P78734
131 36 59.0 1113 5 Q9LSV7
132 36 59.0 1123 5 Q8I3M5
133 36 59.0 1275 16 Q99YA0
134 36 59.0 1275 16 Q8ZK6
135 36 59.0 1275 16 Q8K600
136 36 59.0 1277 16 Q879K2
137 35 57.4 49 5 Q7YVY9
138 35 57.4 60 5 Q7YVW9
139 35 57.4 72 15 Q72102
140 35 57.4 91 15 Q76445
141 35 57.4 99 15 Q9IH00
142 35 57.4 102 16 Q8FFV7
143 35 57.4 139 15 Q8AKJ7
144 35 57.4 148 2 Q9L8S0
145 35 57.4 148 2 Q845X5
146 35 57.4 158 2 Q8CHP4
147 35 57.4 179 16 Q8G403
148 35 57.4 183 16 Q87633
149 35 57.4 201 8 Q9T227
150 35 57.4 220 2 Q87952

```

ALIGNMENTS

```

RESULT 1
Q8BXH2 PRELIMINARY; PRT; 250 AA.
AC Q8BXH2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

```

```

DE Similar to MVC box dependent interacting protein 1.
GN AMPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "The Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK047144; BAC32971.1; -.
DR MGI; MGI:103574; Amph.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00721; BAR; 1.
SQ SEQUENCE 250 AA; 29125 MW; 568A3D55CC6C37CE CRC64;

Query Match 100.0%; Score 61; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 19 RAQEKVLQKLGKA 31
|||||
|

RESULT 2
Q8NPL3 PRELIMINARY; PRT; 385 AA.
AC Q8NPL3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Amphiphysin I variant NT2 (Fragment).
GN AMPH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22017878; PubMed=12023042;
RX Terada Y., Teutsui K., Sano K., Hosoya O., Ohtsuki H., Tokunaga A.,
RA Tsutsui K.;
RT "Novel splice variants of amphiphysin I are expressed in retina.";
RL FEBS Lett. 519:185-190 (2002).
DR EMBL; AF498097; AA044811.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR003017; Amphiphysin_1.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR_dom.
DR Pfam; PF03114; BAR; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR ProDom; PD003208; Amphiphysin_1; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00721; BAR; 1.
FT NON TER 385
SQ SEQUENCE 385 AA; 43753 MW; 4B9AB0A3136711AA CRC64;

Query Match 100.0%; Score 61; DB 4; Length 385;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 RAQEKVLQKLGKA 13
DB 19 RAQEKVLQKLGKA 31

RESULT 3
Q9BTH3 ID Q9BTH3 PRELIMINARY; PRT; 439 AA.
AC Q9BTH3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Similar to bridging integrator 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; BC004101; AA04101.1; -.
DR EMBL; BT006865; AAP35511.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR dom.
DR InterPro; IPR000875; Cectropin.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PROSITE; PS00268; CECROPIN; 1.
DR PROSITE; PS00002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 439 AA; 48286 MW; 350E428C8E198136 CRC64;

Query Match 100.0%; Score 61; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RAQEKVLQKLGKA 13
DB 24 RAQEKVLQKLGKA 36

RESULT 4
Q7ZWP5 ID Q7ZWP5 PRELIMINARY; PRT; 478 AA.
AC Q7ZWP5;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to bridging integrator 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Query Match 100.0%; Score 61; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8395;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046852; AA046852.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PROSITE; PS00452; SH3DOMAIN.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
SQ SEQUENCE 478 AA; 53445 MW; 042A1A94D59095A8 CRC64;

Query Match 100.0%; Score 61; DB 13; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RAQEKVLQKLGKA 13
DB 23 RAQEKVLQKLGKA 35

RESULT 5
Q8WH9 ID Q8WH9 PRELIMINARY; PRT; 490 AA.
AC Q8WH9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Amphiphysin IIB-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kim K.-C., Kim T.-S., Kang K.-H., Choi K.-H.;
RT "Amphiphysin IIB-1, a novel splicing variant of amphiphysin II,
RT regulates p73b function through protein-protein interactions."
RL Oncogene 0:0-0(2002).
DR EMBL; AF411606; AAL38509.1; -.
DR GO; GO:0006897; P: endocytosis; IEA.
DR GO; GO:0007268; P: synaptic transmission; IEA.
DR InterPro; IPR003005; Amphiphysin.
DR InterPro; IPR006632; BAR.
DR InterPro; IPR004148; BAR dom.
DR InterPro; IPR001452; SH3.
DR Pfam; PF03114; BAR; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR01251; AMPHIPHYSIN.
DR PROSITE; PS00002; SH3; 1.
DR SMART; SM00721; BAR; 1.
DR SMART; SM00326; SH3; 1.
SQ SEQUENCE 490 AA; 53167 MW; 8F50F36F7B6E9690 CRC64;

Query Match 100.0%; Score 61; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RAQEKVLQKLGKA 13
DB 24 RAQEKVLQKLGKA 36

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LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-454-4

Query Match 100.0%; Score 61; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 21 RAQEKVLQKLGKA 33

RESULT 3

US-08-652-972A-4

Sequence 4, Application US/08652972A

Patent No. 5723581

GENERAL INFORMATION: ISSUED 3/2/1998

APPLICANT: Prendergast, George C.

APPLICANT: Sakamuro, Daitoku

TITLE OF INVENTION: Murine and Human Box-Dependent

TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P O Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,972A

FILING DATE: 24-MAY-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,454

FILING DATE: 05-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: RST608USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-652-972A-4

Query Match 100.0%; Score 61; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 21 RAQEKVLQKLGKA 33

RESULT 4

US-08-919-145-6

Sequence 6, Application US/08919145

Patent No. 5958753

GENERAL INFORMATION:

APPLICANT: Prendergast, George C.

TITLE OF INVENTION: Bau, A Binl Interacting Protein, and

TITLE OF INVENTION: Uses Therefor

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,145

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/025,482

FILING DATE: 23-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kodroff, Cathy A.

REGISTRATION NUMBER: 33,980

REFERENCE/DOCKET NUMBER: WST73AUSA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 451 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-919-145-6

Query Match 100.0%; Score 61; DB 2; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.016; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RAQEKVLQKLGKA 13
DB 21 RAQEKVLQKLGKA 33

RESULT 5

US-08-870-126-4

Sequence 4, Application US/08870126

Patent No. 6048702

GENERAL INFORMATION:

APPLICANT: Prendergast, George C.

APPLICANT: Sakamuro, Daitoku

TITLE OF INVENTION: Murine and Human Box-Dependent

TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P O Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/870,126

FILING DATE:

CLASSIFICATION: 530

101 35.5 37.4 724 4 US-09-562-737-23
 102 35.5 37.4 916 4 US-09-562-991A-23637
 103 35.5 37.4 1441 4 US-09-562-991A-28143
 104 35.5 37.4 12 3 US-09-060-039-22
 105 35.5 36.8 54 2 US-08-592-646A-15
 106 35.5 36.8 54 4 US-09-165-422-15
 107 35.5 36.8 83 4 US-09-134-000C-4372
 108 35.5 36.8 96 4 US-09-621-976-4959
 109 35.5 36.8 139 4 US-08-107-532A-4424
 110 35.5 36.8 153 3 US-09-154-083-12
 111 35.5 36.8 153 3 US-09-154-083-20
 112 35.5 36.8 181 4 US-09-134-000C-6757
 113 35.5 36.8 218 4 US-09-562-991A-26105
 114 35.5 36.8 222 4 US-09-543-681A-6244
 115 35.5 36.8 267 4 US-09-134-001C-5042
 116 35.5 36.8 283 4 US-08-107-532A-6360
 117 35.5 36.8 318 4 US-09-107-532A-6731
 118 35.5 36.8 325 4 US-09-540-236-2444
 119 35.5 36.8 329 4 US-09-107-532A-7038
 120 35.5 36.8 329 4 US-09-543-681A-4790
 121 35.5 36.8 361 1 US-08-537-434-1
 122 35.5 36.8 398 4 US-10-083-889-4
 123 35.5 36.8 398 4 US-10-083-889-4
 124 35.5 36.8 408 4 US-10-083-889-22
 125 35.5 36.8 415 4 US-09-134-000C-3595
 126 35.5 36.8 419 4 US-09-562-991A-30457
 127 35.5 36.8 429 4 US-09-134-001C-4960
 128 35.5 36.8 458 4 US-09-252-991A-22614
 129 35.5 36.8 463 4 US-09-252-991A-24757
 130 35.5 36.8 464 4 US-08-297-468-2
 131 35.5 36.8 495 4 US-09-479-645A-2
 132 35.5 36.8 495 4 US-09-479-645A-4
 133 35.5 36.8 608 4 US-09-489-039A-12785
 134 35.5 36.8 611 4 US-09-107-532A-4988
 135 35.5 36.8 640 4 US-09-177-165A-30
 136 35.5 36.8 675 1 US-08-386-495-10
 137 35.5 36.8 675 5 PCT-US96-02331-10
 138 35.5 36.8 699 4 US-09-808-701A-34
 139 35.5 36.8 715 4 US-09-808-701A-33
 140 35.5 36.8 742 4 US-09-500-123-12
 141 35.5 36.8 771 4 US-09-462-284-2
 142 35.5 36.8 771 4 US-09-079-592-2
 143 35.5 36.8 811 4 US-09-500-123-9
 144 35.5 36.8 811 4 US-09-540-236-2412
 145 35.5 36.8 817 4 US-09-562-991A-20757
 146 35.5 36.8 871 4 US-09-500-123-7
 147 35.5 36.8 895 4 US-09-489-039A-13127
 148 35.5 36.8 915 4 US-09-562-991A-24992
 149 35.5 36.8 944 4 US-09-134-000C-5578
 150 35.5 36.8 962 4 US-09-594-777A-24

ALIGNMENTS

RESULT 1
 US-08-630-915A-24
 ; Sequence/24, Application US/08630915A
 ; Patent No. 6309820
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: HOFFMAN, No. 6309820h
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: FOWLES, Dana M.
 ; APPLICANT: MCCONNELL, Stephen J.
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
 ; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
 ; TITLE OF INVENTION: USING SAME
 ; NUMBER OF SEQUENCES: 227
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York

STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/630,915A
 APPLICATION NUMBER: US/08/630,915A
 FILING DATE: 03-APR-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-174
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 404 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-630-915A-24

Query Match 100.0%; Score 95; DB 4; Length 404;
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0;

Qy 1 RIAGKRLVDYDSARH 18
 Db 104 RIAGKRLVDYDSARH 121

RESULT 2
 US-08-630-915A-22
 ; Sequence/22, Application US/08630915A
 ; Patent No. 6309820
 ; GENERAL INFORMATION:
 ; APPLICANT: SPARKS, Andrew B.
 ; APPLICANT: HOFFMAN, No. 6309820h
 ; APPLICANT: KAY, Brian K.
 ; APPLICANT: FOWLES, Dana M.
 ; APPLICANT: MCCONNELL, Stephen J.
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
 ; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
 ; TITLE OF INVENTION: USING SAME
 ; NUMBER OF SEQUENCES: 227
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/630,915A
 FILING DATE: 03-APR-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 1101-174
 TELECOMMUNICATION INFORMATION:

B

102 (e)

B

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-22

Query Match 100.0%; Score 95; DB 4; Length 434;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRGKLVYDSARHH 18
Db 139 RIAGRGKLVYDSARHH 156

RESULT 3
US-08-435-454-4
Sequence 4, Application US/08435454
Patent No. 5605830
GENERAL INFORMATION:
APPLICANT: Prendergast, George C.
APPLICANT: Sakamuro, Daitoku

TITLE OF INVENTION: Murine and Human C-Myc Interacting
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,454
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-9818

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-435-454-4

Query Match 100.0%; Score 95; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRGKLVYDSARHH 18
Db 136 RIAGRGKLVYDSARHH 153

RESULT 4
US-08-652-972A-4

Sequence 4, Application US/08652972A
Patent No. 5723581
GENERAL INFORMATION:
APPLICANT: Prendergast, George C.
APPLICANT: Sakamuro, Daitoku
TITLE OF INVENTION: Murine and Human Box-Dependent
TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,972A
FILING DATE: 24-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-972A-4

Query Match 100.0%; Score 95; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIAGRGKLVYDSARHH 18
Db 136 RIAGRGKLVYDSARHH 153

RESULT 5
US-08-919-145-6
Sequence 6, Application US/08919145
Patent No. 5958753
GENERAL INFORMATION:
APPLICANT: Prendergast, George C.
APPLICANT: Bau, A Binl Interacting Protein, and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: